



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 178609**

**TO: Jeffrey Parkin**  
**Location: rem/3D39/3C18**  
**Art Unit: 1648**  
**Friday, February 17, 2006**  
**Case Serial Number: 09/669187**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**REM-1A59**  
**Phone: 571-272-2523**  
  
**[toby.port@uspto.gov](mailto:toby.port@uspto.gov)**

### **Search Notes**

**Examiner Parkin,**

**See attached results.**

**If you have any questions about this search feel free to contact me at any time.**

**Thank you for using STIC search services!**

**Toby Port**  
**X22523**

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STIC-Biotech/ChemLib

178609

mg

From: Parkin, Jeffrey  
Sent: Friday, February 03, 2006 6:25 PM  
To: STIC-Biotech/ChemLib  
Subject: U.S. Serial No. 09/669,187

Aloha!

Please search **SEQ ID NOS.: 73, 80, 81, 148, and 906** from U.S. Serial No. **09/669,187** v. all relevant databases, including interference. Please limit search results to oligonucleotides less than 50 nt in length, if possible. Place results on both paper and electronic format (i.e., disk, e-mail, etc.). Thanks!

Jeffrey S. Parkin, Ph.D.  
Primary Examiner  
Art Unit 1648  
REM 3D39  
2-0908

3C18

RECEIVED  
FEB - 6 2006  
STIC

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Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:51:58 ; Search time 479.835 Seconds  
(without alignments)  
2369.293 Million cell updates/sec

Title: US-09-669-187A-73

Perfect score: 20

Sequence: 1 ttttggggttttggggtttt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_ov.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vi.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 20    | 100.0       | 20     | 6     | AX103881 Sequence  |
| 2          | 20    | 100.0       | 20     | 6     | AX546934 Sequence  |
| 3          | 20    | 100.0       | 28     | 6     | CS077910 Sequence  |
| 4          | 20    | 100.0       | 28     | 6     | CS077991 Sequence  |
| 5          | 20    | 100.0       | 36     | 2     | OFREP2             |
| 6          | 20    | 100.0       | 39     | 6     | AR074313 Sequence  |
| 7          | 20    | 100.0       | 39     | 6     | AX032675 Sequence  |
| 8          | 20    | 100.0       | 44     | 6     | AR104530 Sequence  |
| 9          | 20    | 100.0       | 44     | 6     | AR175791 Sequence  |
| 10         | 20    | 100.0       | 44     | 6     | E37018 Human telom |
| 11         | 20    | 100.0       | 44     | 6     | AR390695 Sequence  |
| 12         | 20    | 100.0       | 44     | 6     | AR393309 Sequence  |
| 13         | 20    | 100.0       | 44     | 6     | AR592667 Sequence  |
| 14         | 20    | 100.0       | 44     | 6     | AX810603 Sequence  |
| 15         | 20    | 100.0       | 44     | 6     | BD011269 Human tel |
| 16         | 20    | 100.0       | 46     | 6     | AR104529 Sequence  |
| 17         | 20    | 100.0       | 46     | 6     | AR175790 Sequence  |
| 18         | 20    | 100.0       | 46     | 6     | E37017 Human telom |

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|----|------|-------|----|---|--------------------|
| 19 | 20   | 100.0 | 46 | 6 | AR390694           |
| 20 | 20   | 100.0 | 46 | 6 | AR393308 Sequence  |
| 21 | 20   | 100.0 | 46 | 6 | AR592666 Sequence  |
| 22 | 20   | 100.0 | 46 | 6 | AX810602 Sequence  |
| 23 | 20   | 100.0 | 46 | 6 | BD011268 Human tel |
| 24 | 20   | 100.0 | 48 | 6 | AR104525 Sequence  |
| 25 | 20   | 100.0 | 48 | 6 | AR104528 Sequence  |
| 26 | 20   | 100.0 | 48 | 6 | AR175786 Sequence  |
| 27 | 20   | 100.0 | 48 | 6 | AR175789 Sequence  |
| 28 | 20   | 100.0 | 48 | 6 | E37014 Human telom |
| 29 | 20   | 100.0 | 48 | 6 | AR390691 Sequence  |
| 30 | 20   | 100.0 | 48 | 6 | AR393305 Sequence  |
| 31 | 20   | 100.0 | 48 | 6 | AR592662 Sequence  |
| 32 | 20   | 100.0 | 48 | 6 | AR592665 Sequence  |
| 33 | 20   | 100.0 | 48 | 6 | AX810599 Sequence  |
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| 35 | 20   | 100.0 | 50 | 6 | AR104527 Sequence  |
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| 37 | 20   | 100.0 | 50 | 6 | E37016 Human telom |
| 38 | 20   | 100.0 | 50 | 6 | AR390693 Sequence  |
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| 41 | 20   | 100.0 | 50 | 6 | AX810601 Sequence  |
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| 50 | 18   | 90.0  | 50 | 6 | BD011267 Human tel |
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| 54 | 16.8 | 84.0  | 44 | 6 | E37018 Human telom |
| 55 | 16.8 | 84.0  | 44 | 6 | AR390695 Sequence  |
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| 59 | 16.8 | 84.0  | 44 | 6 | BD011269 Human tel |
| 60 | 16.8 | 84.0  | 46 | 6 | AR104529 Sequence  |
| 61 | 16.8 | 84.0  | 46 | 6 | AR175790 Sequence  |
| 62 | 16.8 | 84.0  | 46 | 6 | E37017 Human telom |
| 63 | 16.8 | 84.0  | 46 | 6 | AR390694 Sequence  |
| 64 | 16.8 | 84.0  | 46 | 6 | AR393308 Sequence  |
| 65 | 16.8 | 84.0  | 46 | 6 | AR592666 Sequence  |
| 66 | 16.8 | 84.0  | 46 | 6 | AX810602 Sequence  |
| 67 | 16.8 | 84.0  | 46 | 6 | BD011268 Human tel |
| 68 | 16.8 | 84.0  | 48 | 6 | AR104525 Sequence  |
| 69 | 16.8 | 84.0  | 48 | 6 | AR104528 Sequence  |
| 70 | 16.8 | 84.0  | 48 | 6 | AR175786 Sequence  |
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| 73 | 16.8 | 84.0  | 48 | 6 | AR390691 Sequence  |
| 74 | 16.8 | 84.0  | 48 | 6 | AR393305 Sequence  |
| 75 | 16.8 | 84.0  | 48 | 6 | AR592662 Sequence  |
| 76 | 16.8 | 84.0  | 48 | 6 | AR592665 Sequence  |
| 77 | 16.8 | 84.0  | 48 | 6 | AX810599 Sequence  |
| 78 | 16.8 | 84.0  | 48 | 6 | BD011265 Human tel |
| 79 | 16   | 80.0  | 16 | 6 | AR104544 Sequence  |
| 80 | 16   | 80.0  | 16 | 6 | AR175805 Sequence  |
| 81 | 16   | 80.0  | 16 | 6 | E36807 Human telom |
| 82 | 16   | 80.0  | 16 | 6 | AR390484 Sequence  |
| 83 | 16   | 80.0  | 16 | 6 | AR393098 Sequence  |
| 84 | 16   | 80.0  | 16 | 6 | AR592679 Sequence  |
| 85 | 16   | 80.0  | 16 | 6 | AX810149 Sequence  |
| 86 | 16   | 80.0  | 16 | 6 | BD011058 Human tel |
| 87 | 15   | 80.0  | 20 | 2 | OFREP1             |
| 88 | 15.2 | 76.0  | 20 | 6 | CS013559 Sequence  |
| 89 | 15.2 | 76.0  | 22 | 6 | CS113618 Sequence  |
| 90 | 14.8 | 74.0  | 24 | 6 | AR207616 Sequence  |
| 91 | 14.8 | 74.0  | 24 | 6 | AX104500 Sequence  |

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| 92    | 14.8 | 74.0 | 24 | 6 | AX104502 | AX104502 Sequence  | 165   | 13.2 | 66.0 | 29 | 6  | CS125435 | CS125435 Sequence  |
| 93    | 14.8 | 74.0 | 24 | 6 | AX104691 | AX104691 Sequence  | 166   | 13.2 | 66.0 | 29 | 6  | AX928232 | AX928232 Sequence  |
| 94    | 14.8 | 74.0 | 24 | 6 | AX137294 | AX137294 Sequence  | 167   | 13.2 | 66.0 | 30 | 6  | AR000058 | AR000058 Sequence  |
| 95    | 14.8 | 74.0 | 24 | 6 | AX355707 | AX355707 Sequence  | 168   | 13.2 | 66.0 | 30 | 6  | AR064881 | AR064881 Sequence  |
| 96    | 14.8 | 74.0 | 24 | 6 | AX547553 | AX547553 Sequence  | c 169 | 13.2 | 66.0 | 30 | 6  | CQ869331 | CQ869331 Sequence  |
| 97    | 14.8 | 74.0 | 24 | 6 | AX547555 | AX547555 Sequence  | 170   | 13.2 | 66.0 | 41 | 6  | CQ817934 | CQ817934 Sequence  |
| 98    | 14.8 | 74.0 | 24 | 6 | AX547744 | AX547744 Sequence  | 171   | 13.2 | 66.0 | 43 | 6  | AX058564 | AX058564 Sequence  |
| 99    | 14.8 | 74.0 | 24 | 6 | AX593918 | AX593918 Sequence  | 172   | 13.2 | 66.0 | 49 | 6  | AX058563 | AX058563 Sequence  |
| 100   | 14.8 | 74.0 | 24 | 6 | AX961611 | AX961611 Sequence  | c 173 | 13.2 | 66.0 | 50 | 6  | I42216   | I42216 Sequence    |
| 101   | 14.8 | 74.0 | 24 | 6 | BD014843 | BD014843 Universal | c 174 | 13.2 | 66.0 | 50 | 6  | BD014161 | BD014161 Probe for |
| 102   | 14.8 | 74.0 | 40 | 6 | CS131752 | CS131752 Sequence  | 175   | 12.8 | 64.0 | 18 | 6  | AR297501 | AR297501 Sequence  |
| c 103 | 14.8 | 74.0 | 46 | 6 | AR207615 | AR207615 Sequence  | 176   | 12.8 | 64.0 | 18 | 6  | AX599218 | AX599218 Sequence  |
| c 104 | 14.8 | 74.0 | 46 | 6 | AX137293 | AX137293 Sequence  | 177   | 12.8 | 64.0 | 18 | 6  | AX599352 | AX599352 Sequence  |
| c 105 | 14.8 | 74.0 | 46 | 6 | BD014842 | BD014842 Universal | 178   | 12.8 | 64.0 | 18 | 6  | AX599695 | AX599695 Sequence  |
| c 106 | 14.2 | 71.0 | 23 | 6 | E35795   | E35795 Process for | 179   | 12.8 | 64.0 | 18 | 6  | AX599696 | AX599696 Sequence  |
| c 107 | 14.2 | 71.0 | 26 | 6 | AR104518 | AR104518 Sequence  | 180   | 12.8 | 64.0 | 18 | 6  | AX599792 | AX599792 Sequence  |
| c 108 | 14.2 | 71.0 | 26 | 6 | AR104543 | AR104543 Sequence  | 181   | 12.8 | 64.0 | 18 | 6  | AX767670 | AX767670 Sequence  |
| c 109 | 14.2 | 71.0 | 26 | 6 | AR175779 | AR175779 Sequence  | 182   | 12.8 | 64.0 | 18 | 6  | AX796126 | AX796126 Sequence  |
| c 110 | 14.2 | 71.0 | 26 | 6 | AR175804 | AR175804 Sequence  | 183   | 12.8 | 64.0 | 18 | 6  | AX796226 | AX796226 Sequence  |
| c 111 | 14.2 | 71.0 | 26 | 6 | E37007   | E37007 Human telom | c 184 | 12.8 | 64.0 | 20 | 6  | AR236874 | AR236874 Sequence  |
| c 112 | 14.2 | 71.0 | 26 | 6 | AR390684 | AR390684 Sequence  | c 185 | 12.8 | 64.0 | 21 | 6  | CQ799734 | CQ799734 Sequence  |
| c 113 | 14.2 | 71.0 | 26 | 6 | AR393298 | AR393298 Sequence  | 186   | 12.8 | 64.0 | 21 | 6  | AR296682 | AR296682 Sequence  |
| c 114 | 14.2 | 71.0 | 26 | 6 | AR592655 | AR592655 Sequence  | 187   | 12.8 | 64.0 | 24 | 6  | CQ903961 | CQ903961 Sequence  |
| c 115 | 14.2 | 71.0 | 26 | 6 | AR592678 | AR592678 Sequence  | 188   | 12.8 | 64.0 | 24 | 6  | AX104112 | AX104112 Sequence  |
| c 116 | 14.2 | 71.0 | 26 | 6 | AX810592 | AX810592 Sequence  | 189   | 12.8 | 64.0 | 24 | 6  | AX104166 | AX104166 Sequence  |
| c 117 | 14.2 | 71.0 | 26 | 6 | BD011258 | BD011258 Human tel | 190   | 12.8 | 64.0 | 24 | 6  | AX104243 | AX104243 Sequence  |
| c 118 | 14.2 | 71.0 | 29 | 6 | BD225589 | BD225589 Assay for | 191   | 12.8 | 64.0 | 24 | 6  | AX105106 | AX105106 Sequence  |
| c 119 | 14.2 | 71.0 | 32 | 6 | AX394124 | AX394124 Sequence  | 192   | 12.8 | 64.0 | 24 | 6  | AX355699 | AX355699 Sequence  |
| c 120 | 14.2 | 71.0 | 35 | 6 | E06305   | E06305 Primer. 9/1 | 193   | 12.8 | 64.0 | 24 | 6  | AX355819 | AX355819 Sequence  |
| c 121 | 14.2 | 71.0 | 35 | 6 | E06501   | E06501 Primer. 9/1 | 194   | 12.8 | 64.0 | 24 | 6  | AX355820 | AX355820 Sequence  |
| c 122 | 14   | 70.0 | 15 | 6 | AR095959 | AR095959 Sequence  | 195   | 12.8 | 64.0 | 24 | 6  | AX547165 | AX547165 Sequence  |
| c 123 | 14   | 70.0 | 15 | 6 | AR104531 | AR104531 Sequence  | 196   | 12.8 | 64.0 | 24 | 6  | AX547219 | AX547219 Sequence  |
| c 124 | 14   | 70.0 | 15 | 6 | AR104533 | AR104533 Sequence  | 197   | 12.8 | 64.0 | 24 | 6  | AX547296 | AX547296 Sequence  |
| c 125 | 14   | 70.0 | 15 | 6 | AR175792 | AR175792 Sequence  | 198   | 12.8 | 64.0 | 24 | 6  | AX593909 | AX593909 Sequence  |
| c 126 | 14   | 70.0 | 15 | 6 | AR175794 | AR175794 Sequence  | 199   | 12.8 | 64.0 | 24 | 6  | AX593920 | AX593920 Sequence  |
| c 127 | 14   | 70.0 | 15 | 6 | E36806   | E36806 Human telom | c 200 | 12.8 | 64.0 | 24 | 6  | AX593921 | AX593921 Sequence  |
| c 128 | 14   | 70.0 | 15 | 6 | AR359628 | AR359628 Sequence  | c 201 | 12.8 | 64.0 | 28 | 6  | CQ894850 | CQ894850 Sequence  |
| c 129 | 14   | 70.0 | 15 | 6 | AR390483 | AR390483 Sequence  | c 202 | 12.8 | 64.0 | 31 | 6  | BD247607 | BD247607 Streptoco |
| c 130 | 14   | 70.0 | 15 | 6 | AR393097 | AR393097 Sequence  | c 203 | 12.8 | 64.0 | 31 | 6  | AR198761 | AR198761 Sequence  |
| c 131 | 14   | 70.0 | 15 | 6 | AR526688 | AR526688 Sequence  | c 204 | 12.6 | 63.0 | 19 | 6  | AX599175 | AX599175 Sequence  |
| c 132 | 14   | 70.0 | 15 | 6 | AR592669 | AR592669 Sequence  | c 205 | 12.6 | 63.0 | 21 | 6  | CS059446 | CS059446 Sequence  |
| c 133 | 14   | 70.0 | 15 | 6 | AX033371 | AX033371 Sequence  | c 206 | 12.6 | 63.0 | 21 | 6  | AR296307 | AR296307 Sequence  |
| c 134 | 14   | 70.0 | 15 | 6 | AX033372 | AX033372 Sequence  | 207   | 12.6 | 63.0 | 22 | 6  | CQ807573 | CQ807573 Sequence  |
| c 135 | 14   | 70.0 | 15 | 6 | AX810148 | AX810148 Sequence  | 208   | 12.6 | 63.0 | 22 | 6  | AX116710 | AX116710 Sequence  |
| c 136 | 14   | 70.0 | 15 | 6 | BD011057 | BD011057 Human tel | 209   | 12.6 | 63.0 | 22 | 6  | AX511797 | AX511797 Sequence  |
| c 137 | 14   | 70.0 | 20 | 6 | AX339139 | AX339139 Sequence  | 210   | 12.6 | 63.0 | 23 | 6  | CS048929 | CS048929 Sequence  |
| c 138 | 13.8 | 69.0 | 19 | 6 | AR444879 | AR444879 Sequence  | 211   | 12.6 | 63.0 | 23 | 6  | CS048932 | CS048932 Sequence  |
| c 139 | 13.8 | 69.0 | 49 | 6 | AX772455 | AX772455 Sequence  | c 212 | 12.6 | 63.0 | 24 | 6  | CS013792 | CS013792 Sequence  |
| 140   | 13.8 | 69.0 | 50 | 6 | AR356126 | AR356126 Sequence  | c 213 | 12.6 | 63.0 | 24 | 6  | AX114887 | AX114887 Sequence  |
| 141   | 13.8 | 69.0 | 50 | 6 | AR537682 | AR537682 Sequence  | c 214 | 12.6 | 63.0 | 29 | 6  | AR142922 | AR142922 Sequence  |
| 142   | 13.6 | 68.0 | 21 | 6 | AR074334 | AR074334 Sequence  | 215   | 12.6 | 63.0 | 30 | 6  | CQ857114 | CQ857114 Sequence  |
| 143   | 13.6 | 68.0 | 21 | 6 | I21708   | I21708 Sequence 4  | 216   | 12.6 | 63.0 | 30 | 6  | AX793377 | AX793377 Sequence  |
| 144   | 13.6 | 68.0 | 21 | 6 | AX032696 | AX032696 Sequence  | 217   | 12.6 | 63.0 | 40 | 6  | AR083586 | AR083586 Sequence  |
| 145   | 13.6 | 68.0 | 26 | 6 | I26260   | I26260 Sequence 7  | 218   | 12.6 | 63.0 | 40 | 6  | AR160411 | AR160411 Sequence  |
| 146   | 13.6 | 68.0 | 29 | 6 | AX104113 | AX104113 Sequence  | 219   | 12.6 | 63.0 | 40 | 6  | AR216833 | AR216833 Sequence  |
| 147   | 13.6 | 68.0 | 29 | 6 | AX355103 | AX355103 Sequence  | 220   | 12.6 | 63.0 | 40 | 6  | AR369636 | AR369636 Sequence  |
| 148   | 13.6 | 68.0 | 29 | 6 | AX547166 | AX547166 Sequence  | 221   | 12.6 | 63.0 | 40 | 6  | BD008982 | BD008982 SpSA poly |
| 149   | 13.6 | 68.0 | 32 | 6 | AX104237 | AX104237 Sequence  | 222   | 12.6 | 63.0 | 40 | 6  | BD009195 | BD009195 Novel Sps |
| 150   | 13.6 | 68.0 | 32 | 6 | AX355706 | AX355706 Sequence  | 223   | 12.6 | 63.0 | 40 | 15 | AJ838493 | AJ838493 Arabidops |
| 151   | 13.6 | 68.0 | 32 | 6 | AX547290 | AX547290 Sequence  | c 224 | 12.6 | 63.0 | 40 | 15 | AJ838543 | AJ838543 Arabidops |
| c 152 | 13.6 | 68.0 | 40 | 6 | AX394946 | AX394946 Sequence  | c 225 | 12.6 | 63.0 | 50 | 6  | CQ003524 | CQ003524 Sequence  |
| 153   | 13.6 | 68.0 | 43 | 6 | AX058571 | AX058571 Sequence  | c 226 | 12.4 | 62.0 | 18 | 6  | AR060409 | AR060409 Sequence  |
| 154   | 13.6 | 68.0 | 47 | 6 | AR289107 | AR289107 Sequence  | c 227 | 12.4 | 62.0 | 18 | 6  | AR094563 | AR094563 Sequence  |
| 155   | 13.6 | 68.0 | 47 | 6 | AR290741 | AR290741 Sequence  | 228   | 12.4 | 62.0 | 18 | 6  | AR094564 | AR094564 Sequence  |
| c 156 | 13.6 | 68.0 | 50 | 6 | CQ003525 | CQ003525 Sequence  | c 229 | 12.4 | 62.0 | 18 | 6  | AR128967 | AR128967 Sequence  |
| c 157 | 13.4 | 67.0 | 20 | 6 | AR032105 | AR032105 Sequence  | c 230 | 12.4 | 62.0 | 19 | 6  | AX817169 | AX817169 Sequence  |
| c 158 | 13.4 | 67.0 | 21 | 6 | CQ873830 | CQ873830 Sequence  | 231   | 12.4 | 62.0 | 19 | 6  | AX817184 | AX817184 Sequence  |
| c 159 | 13.4 | 67.0 | 30 | 6 | AX394125 | AX394125 Sequence  | 232   | 12.4 | 62.0 | 19 | 6  | AX824393 | AX824393 Sequence  |
| c 160 | 13.4 | 67.0 | 32 | 6 | AR287340 | AR287340 Sequence  | 233   | 12.4 | 62.0 | 20 | 6  | BD090050 | BD090050 A method  |
| c 161 | 13.2 | 66.0 | 25 | 6 | CQ857416 | CQ857416 Sequence  | 234   | 12.4 | 62.0 | 21 | 6  | E33097   | E33097 Tetrahydroc |
| 162   | 13.2 | 66.0 | 25 | 6 | CQ894348 | CQ894348 Sequence  | c 235 | 12.4 | 62.0 | 21 | 6  | AR299170 | AR299170 Sequence  |
| 163   | 13.2 | 66.0 | 25 | 6 | AX786820 | AX786820 Sequence  | 236   | 12.4 | 62.0 | 22 | 6  | CQ807361 | CQ807361 Sequence  |
| 164   | 13.2 | 66.0 | 26 | 6 | AB2168   | AB2168 Sequence 3  | 237   | 12.4 | 62.0 | 22 | 6  | AX795983 | AX795983 Sequence  |

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| 238   | 12.4 | 62.0 | 22 | 6  | AX822515 | Sequence    | AX822515.1 | GI:13920078 | linear | PAT 01-MAR-2003 |
| 239   | 12.4 | 62.0 | 22 | 6  | AX826155 | Sequence    |            |             |        |                 |
| C 240 | 12.4 | 62.0 | 29 | 6  | BD076698 | Lentiviru   |            |             |        |                 |
| C 241 | 12.4 | 62.0 | 29 | 6  | BD076703 | Lentiviru   |            |             |        |                 |
| C 242 | 12.4 | 62.0 | 29 | 6  | AX600339 | Sequence    |            |             |        |                 |
| 243   | 12.4 | 62.0 | 35 | 10 | C75714   | Homo sapien |            |             |        |                 |
| 244   | 12.2 | 61.0 | 17 | 6  | CQ808548 | Sequence    |            |             |        |                 |
| 245   | 12.2 | 61.0 | 17 | 6  | CS114151 | Sequence    |            |             |        |                 |
| 246   | 12.2 | 61.0 | 17 | 6  | CS125229 | Sequence    |            |             |        |                 |
| 247   | 12.2 | 61.0 | 17 | 6  | AR188758 | Sequence    |            |             |        |                 |
| 248   | 12.2 | 61.0 | 17 | 6  | AR324611 | Sequence    |            |             |        |                 |
| 249   | 12.2 | 61.0 | 17 | 6  | AR598071 | Sequence    |            |             |        |                 |
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| 256   | 12.2 | 61.0 | 20 | 6  | AX599081 | Sequence    |            |             |        |                 |
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| 259   | 12.2 | 61.0 | 20 | 6  | AX795989 | Sequence    |            |             |        |                 |
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| C 264 | 12.2 | 61.0 | 21 | 6  | AX599104 | Sequence    |            |             |        |                 |
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| C 266 | 12.2 | 61.0 | 21 | 6  | AX796018 | Sequence    |            |             |        |                 |
| C 267 | 12.2 | 61.0 | 21 | 6  | AX811415 | Sequence    |            |             |        |                 |
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| C 277 | 12.2 | 61.0 | 24 | 6  | CS029142 | Sequence    |            |             |        |                 |
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| C 279 | 12.2 | 61.0 | 24 | 6  | CS029173 | Sequence    |            |             |        |                 |
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| C 287 | 12.2 | 61.0 | 25 | 6  | CS075292 | Sequence    |            |             |        |                 |
| C 288 | 12.2 | 61.0 | 25 | 6  | AX609190 | Sequence    |            |             |        |                 |
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| C 293 | 12.2 | 61.0 | 27 | 6  | CS029186 | Sequence    |            |             |        |                 |
| C 294 | 12.2 | 61.0 | 27 | 6  | CS029188 | Sequence    |            |             |        |                 |
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| C 297 | 12.2 | 61.0 | 28 | 6  | CS029116 | Sequence    |            |             |        |                 |
| C 298 | 12.2 | 61.0 | 28 | 6  | CS029118 | Sequence    |            |             |        |                 |
| C 299 | 12.2 | 61.0 | 28 | 6  | CS029138 | Sequence    |            |             |        |                 |
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| LOCUS      | AX103881   | Sequence   | 73 from Patent WO0122972. |     |        |                 |
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| ACCESSION  | AX103881   |  |                           |     |        |                 |
| VERSION    | AX103881.1 | GI:13920078  |                           |     |        |                 |
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| SOURCE     |            | synthetic construct  |                           |     |        |                 |
| ORGANISM   |            | other sequences; artificial sequences.   |                           |     |        |                 |
| REFERENCE  | 1          | Bates, P.J., Miller, D.M., Trent, J.O. and Xu, X. A method for the treatment of malignant diseases by inhibiting nucleolin |                           |     |        |                 |

JOURNAL Patent: WO 2005035579-A 28 21-APR-2005;  
University of Louisville Research Foundation (US)

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LOCUS CS097991 28 bp DNA linear PAT 03-JUN-2005  
DEFINITION Sequence 29 from Patent WO2005037323.  
ACCESSION CS097991  
VERSION CS097991.1 GI:66954236  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Bates,P.J., Girvan,A.C. and Barve,S.S.  
TITLE Method for inhibiting nf-kappa b signaling and use to treat or prevent human diseases  
JOURNAL Patent: WO 2005037323-A 29 28-APR-2005;  
University of Louisville Research Foundation, Inc. (US)  
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RESULT 5  
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LOCUS Oxytricha fallax right end of linear DNA fragments in macronucleus.  
DEFINITION V01083  
ACCESSION V01083.1 GI:9755  
VERSION repetitive sequence.  
KEYWORDS Oxytricha fallax  
SOURCE Oxytricha fallax  
ORGANISM Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia; Stichotrichida; Oxytrichidae; Oxytricha.  
REFERENCE 1 (bases 1 to 36)  
AUTHORS Dawson,D. and Herrick,G.  
TITLE Micronuclear DNA sequences of Oxytricha fallax homologous to the macronuclear inverted terminal repeat  
JOURNAL Nucleic Acids Res. 10 (9), 2911-2924 (1982)  
PUBMED 7099969  
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Db 5 TTTTGGGGTTTGGGGTTTT 24

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LOCUS AR074313 39 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 121 from patent US 5952490.  
ACCESSION AR074313  
VERSION AR074313.1 GI:10001068  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y., Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and Imbach,J.Louis.  
TITLE Oligonucleotides having a conserved G4 core sequence  
JOURNAL Patent: US 5952490-A 121 14-SEP-1999;  
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RESULT 7  
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LOCUS Sequence 121 from Patent EP1016715.  
DEFINITION AX032675  
ACCESSION AX032675  
VERSION AX032675.1 GI:10279613  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1  
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J., Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and Wyatt,J.R.  
TITLE Oligonucleotides having a conserved g4 core sequence  
JOURNAL Patent: EP 1016715-A 121 05-JUL-2000;  
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LOCUS AR104530 linear PAT 14-FEB-2001
DEFINITION Sequence 42 from patent US 6093809.
ACCESSION AR104530
VERSION AR104530.1 GI:12817238
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 42 25-JUL-2000;
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Db 25 TTTTGGGGTTTGGGGTTTT 44

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LOCUS AR175791 linear PAT 17-DEC-2001
DEFINITION Sequence 42 from patent US 6309867.
ACCESSION AR175791
VERSION AR175791.1 GI:17917090
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 42 30-OCT-2001;
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Db 25 TTTTGGGGTTTGGGGTTTT 44

RESULT 10
LOCUS E37018 linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E37018
VERSION E37018.1 GI:13022981
KEYWORDS JP 1999253177-A/226.
SOURCE unidentified
ORGANISM unclassified.

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REFERENCE 1 (bases 1 to 44)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 226 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
PN JP 1999253177-A/226
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503 PI THOMAS
R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN.
PI CALVIN B HAREI, WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K48/00,
PC C12Q1/02,
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C07K16/40,
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FH Key Location/Qualifiers
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LOCUS AR390695 44 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 568 from patent US 6610839.
ACCESSION AR390695
VERSION AR390695.1 GI:40112629
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Morin,G.B. and Andrews,W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 568 26-AUG-2003;
Geron Corporation, Menlo Park, CA
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Db 25 TTTTGGGGTTTGGGGTTTT 44

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ACCESSION AR393309  
VERSION AR393309.1 GI:40118689  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 44)  
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,  
Harley,C.B. and Andrews,W.H.  
TITLE Cells immortalized with telomerase reverse transcriptase for use in  
drug screening  
JOURNAL Patent: US 6617110-A 568 09-SEP-2003;  
Geron Corporation and University Technology Corporation; Menlo  
Park, CA  
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Db 25 TTTTGGGGTTTGGGGTTTT 44

RESULT 13  
AR592667  
LOCUS AR592667 44 bp DNA linear PAT 15-DEC-2004  
DEFINITION Sequence 42 from patent US 6808880.  
ACCESSION AR592667  
VERSION AR592667.1 GI:56641387  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 44)  
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,  
Harley,C. and Andrews,W.H.  
TITLE Method for detecting polynucleotides encoding telomerase  
JOURNAL Patent: US 6808880-A 42 26-OCT-2004;  
Geron Corporation and Regents of the University of Colorado; Menlo  
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Db 25 TTTTGGGGTTTGGGGTTTT 44

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DEFINITION Sequence 568 from Patent EP1333094.  
ACCESSION AX810603

VERSION AX810603.1 GI:38524092  
KEYWORDS  
SOURCE Unidentified  
ORGANISM unclassified  
REFERENCE 1  
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,  
Harley,C.B. and Andrews,W.H.  
TITLE Human telomerase catalytic subunit  
JOURNAL Patent: EP 1333094-A 568 06-AUG-2003;  
Geron Corporation (US); University Technology Corporation (US)  
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LOCUS BD011269 44 bp DNA linear PAT 31-JAN-2002  
DEFINITION Human telomerase catalytic subunit.  
ACCESSION BD011269  
VERSION BD011269.1 GI:18639642  
KEYWORDS  
SOURCE Unidentified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 44)  
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,  
Harley,C.B. and Andrews,W.H.  
TITLE Human telomerase catalytic subunit  
JOURNAL Patent: JP 2001081042-A 226 27-MAR-2001;  
GERON CORP,UNIVERSITY TECHNOLOGY CORP  
COMMENT OS Unidentified  
PN JP 2001081042-A/226  
PD 27-MAR-2001  
PF 27-JUL-2000 JP 2000227474  
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR  
25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR  
09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR  
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS  
R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B  
MORIN,  
PI CALVIN B HARLEY,WILLIAM H ANDREWS  
PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,  
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LOCUS AR104529 46 bp DNA PAT 14-FEB-2001  
DEFINITION Sequence 41 from patent US 6093809.  
ACCESSION AR104529  
VERSION AR104529.1 GI:12817237  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Cech,T.R. and Lingner,J.  
TITLE Telomerase  
JOURNAL Patent: US 6093809-A 41 25-JUL-2000;  
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ACCESSION AR175790  
VERSION AR175790.1 GI:17917089  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Cech,T.R. and Nakamura,T.  
TITLE Telomerase  
JOURNAL Patent: US 6309867-A 41 30-OCT-2001;  
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DEFINITION Human telomerase catalytic subunit promoter.  
ACCESSION E37017  
VERSION E37017.1 GI:13022980

KEYWORDS JP 1999253177-A/225.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M., Calvin,B.H. and William,H.A.  
TITLE Human telomerase catalytic subunit promoter  
JOURNAL Patent: JP 1999253177-A 225 21-SEP-1999;  
JERON CORP. UNIVERSITY TECHNOLOGY CORP  
OS Unidentified  
PN JP 1999253177-A/225  
PD 21-SEP-1999  
PF 15-OCT-1998 JP 1998320169  
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR 25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR 09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR 14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503, PI THOMAS R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B MORIN,  
PI CALVIN B HAREI,WILLIAM H ANDREWS  
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,  
PC C12Q1/02,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC C07K16/40,  
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PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84), PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC  
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RESULT 19  
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DEFINITION Sequence 567 from patent US 6610839.  
ACCESSION AR390694  
VERSION AR390694.1 GI:40112628  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Morin,G.B. and Andrews,W.H.  
TITLE Promoter for telomerase reverse transcriptase  
JOURNAL Patent: US 6610839-A 567 26-AUG-2003;  
Geron Corporation, Menlo Park, CA  
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DEFINITION Sequence 567 from patent US 6617110.
ACCESSION AR393308
VERSION AR393308.1 GI:40118687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
         Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
        drug screening
JOURNAL Patent: US 6617110-A 567 09-SEP-2003;
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DEFINITION Sequence 41 from patent US 6808880.
ACCESSION AR592666
VERSION AR592666.1 GI:56641386
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
         Harley,C. and Andrews,W.H.
TITLE Method for detecting polynucleotides encoding telomerase
JOURNAL Patent: US 6808880-A 41 26-OCT-2004;
        Geron Corporation and Regents of the University of Colorado; Menlo
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Db 27 TTTTGGGTTTGGGGTTTT 46

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DEFINITION Sequence 567 from Patent EPI333094.
ACCESSION AX810602
VERSION AX810602.1 GI:38524091
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
         Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: EP 1333094-A 567 06-AUG-2003;
        Geron Corporation (US) ; University Technology Corporation (US)
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DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011268
VERSION BD011268.1 GI:18639641
KEYWORDS JP 2001081042-A/225.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
         Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 225 27-MAR-2001;
        GERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
        PN JP 2001081042-A/225
        PD 27-MAR-2001
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        25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
        09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
        14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
        R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI
        MORIN,
        PI CALVIN B HARLEY,WILLIAM H ANDREWS
        PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
        PC C07K5/10,
        PC C07K5/107, C07K5/117, C07K7/06, C07K7/08, C07K16/40, C12N9/12, PC
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        PC C12Q1/02, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 27 TTTTGGGGTTTGGGGTTTT 46

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DEFINITION Sequence 37 from patent US 6093809.  
ACCESSION AR104525  
VERSION AR104525.1 GI:12817233  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Cech,T.R. and Lingner,J.  
TITLE Telomerase  
JOURNAL Patent: US 6093809-A 37 25-JUL-2000;  
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
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RESULT 25  
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DEFINITION Sequence 40 from patent US 6093809.  
ACCESSION AR104528  
VERSION AR104528.1 GI:12817236  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Cech,T.R. and Lingner,J.  
TITLE Telomerase  
JOURNAL Patent: US 6093809-A 40 25-JUL-2000;  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 26  
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DEFINITION Sequence 37 from patent US 6309867.  
ACCESSION AR175786  
VERSION AR175786.1 GI:17917085  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Cech,T.R. and Nakamura,T.  
TITLE Telomerase  
JOURNAL Patent: US 6309867-A 37 30-OCT-2001;  
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Db 29 TTTTGGGGTTTGGGGTTTT 48

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DEFINITION Sequence 40 from patent US 6309867.  
ACCESSION AR175789  
VERSION AR175789.1 GI:17917088  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Cech,T.R. and Nakamura,T.  
TITLE Telomerase  
JOURNAL Patent: US 6309867-A 40 30-OCT-2001;  
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
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Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 28  
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DEFINITION Human telomerase catalytic subunit promoter.  
ACCESSION E37014  
VERSION E37014.1 GI:13022977  
KEYWORDS JP 199253177-A/222.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,  
Calvin,B.H. and William,H.A.  
TITLE Human telomerase catalytic subunit promoter  
JOURNAL Patent: JP 199253177-A 222 21-SEP-1999;  
COMMENT JERON CORP,UNIVERSITY TECHNOLOGY CORP  
OS Unidentified

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PN JP 19992531177-A/222
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724.643,18-APR-1997 US 08/844.419, PR
25-APR-1997 US 08/846.017,06-MAY-1997 US 08/851.843, PR
09-MAY-1997 US 08/854.050,14-AUG-1997 US 08/911.312, PR
14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/915.503 PI THOMAS
R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HARELI,WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
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C07K16/40,
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DEFINITION
Sequence 564 from patent US 6610839.
ACCESSION
AR390691
VERSION
AR390691.1 GI:40112625
KEYWORDS
Unknown.
ORGANISM
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REFERENCE
1 (bases 1 to 48)
AUTHORS
Morin,G.B. and Andrews,W.H.
TITLE
Promoter for telomerase reverse transcriptase
JOURNAL
Patent: US 6610839-A 564 26-AUG-2003;
Geron Corporation; Menlo Park, CA
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Db 29 TTTTGGGGTTTGGGGTTTT 48

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Sequence 564 from patent US 6617110.
ACCESSION
AR393305
VERSION
AR393305.1 GI:40118681
KEYWORDS
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ORGANISM
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REFERENCE
1 (bases 1 to 48)
AUTHORS
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE
Method for detecting polynucleotides encoding telomerase
JOURNAL
Patent: US 680880-A 37 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
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Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 32
AR592665
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DEFINITION
Sequence 40 from patent US 680880.
ACCESSION
AR592665
VERSION
AR592665.1 GI:56641385
KEYWORDS
Unknown.
ORGANISM
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REFERENCE
1 (bases 1 to 48)
AUTHORS
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE
Method for detecting polynucleotides encoding telomerase
JOURNAL
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Geron Corporation and Regents of the University of Colorado; Menlo
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RESULT 33
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DEFINITION
Sequence 40 from patent US 680880.
ACCESSION
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VERSION
AR592665.1 GI:56641385
KEYWORDS
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ORGANISM
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REFERENCE
1 (bases 1 to 48)
AUTHORS
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE
Method for detecting polynucleotides encoding telomerase
JOURNAL
Patent: US 680880-A 37 26-OCT-2004;
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Db 29 TTTTGGGGTTTGGGGTTTT 48

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ACCESSION AR393305
VERSION AR393305.1 GI:40118681
KEYWORDS
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ORGANISM
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REFERENCE
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AUTHORS
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Harley,C.B. and Andrews,W.H.
TITLE
Cells immortalized with telomerase reverse transcriptase for use in
drug screening
JOURNAL
Patent: US 6617110-A 564 09-SEP-2003;
Geron Corporation and University Technology Corporation; Menlo
Park, CA
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Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 31
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DEFINITION
Sequence 37 from patent US 680880.
ACCESSION
AR592662
VERSION
AR592662.1 GI:56641382
KEYWORDS
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ORGANISM
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REFERENCE
1 (bases 1 to 48)
AUTHORS
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C. and Andrews,W.H.
TITLE
Method for detecting polynucleotides encoding telomerase
JOURNAL
Patent: US 680880-A 37 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
Park, CA
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Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 32
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DEFINITION
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ACCESSION
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VERSION
AR592665.1 GI:56641385
KEYWORDS
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ORGANISM
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REFERENCE
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AUTHORS
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE
Method for detecting polynucleotides encoding telomerase
JOURNAL
Patent: US 680880-A 37 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
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RESULT 33
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LOCUS
DEFINITION
Sequence 40 from patent US 680880.
ACCESSION
AR592665
VERSION
AR592665.1 GI:56641385
KEYWORDS
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ORGANISM
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REFERENCE
1 (bases 1 to 48)
AUTHORS
Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE
Method for detecting polynucleotides encoding telomerase
JOURNAL
Patent: US 680880-A 37 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
Park, CA
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TITLE Harley, C. and Andrews, W.H.  
JOURNAL Method for detecting polynucleotides encoding telomerase  
Patent: US 6808880-A 40 26-OCT-2004;  
Geron Corporation and Regents of the University of Colorado; Menlo  
Park, CA

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RESULT 33  
AX810599 48 bp DNA linear PAT 25-NOV-2003  
LOCUS  
DEFINITION Sequence 564 from Patent EP1333094.  
ACCESSION AX810599  
VERSION AX810599.1 GI:38524088

KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.

REFERENCE 1  
AUTHORS Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B.,  
Harley, C.B. and Andrews, W.H.  
TITLE Human telomerase catalytic subunit  
JOURNAL Patent: EP 1333094-A 564 06-AUG-2003;  
Geron Corporation (US); University Technology Corporation (US)

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/db\_xref="taxon:32644"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
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Db 29 TTTTGGGTTTGGGGTTTT 48  
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RESULT 34  
BD011265 48 bp DNA linear PAT 31-JAN-2002  
LOCUS  
DEFINITION Human telomerase catalytic subunit.  
ACCESSION BD011265  
VERSION BD011265.1 GI:18639638

KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 48)  
AUTHORS Sechi, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Mori, G.B.,  
Harley, C.B. and Andrews, W.H.  
TITLE Human telomerase catalytic subunit  
JOURNAL Patent: JP 2001081042-A 222 27-MAR-2001;  
GERON CORP, UNIVERSITY TECHNOLOGY CORP

COMMENT  
OS Unidentified  
PN JP 2001081042-A/222  
PD 27-MAR-2001  
PF 27-JUL-2000 JP 2000227474  
PR 01-OCT-1996 US 08/724643, 18-APR-1997 US 08/844419 PR

25-APR-1997 US 08/846017, 06-MAY-1997 US 08/851843 PR  
09-MAY-1997 US 08/854050, 14-AUG-1997 US 08/911312 PR  
14-AUG-1997 US 08/912951, 14-AUG-1997 US 08/915503 PI THOMAS  
R SECHI, JOACHIM LINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B  
MORIN,

PI CALVIN B HARLEY, WILLIAM H ANDREWS  
PC A61K38/00, A61K31/7088, A61K39/00, A61K48/00, A61P35/00, A61P43/00,  
PC C07K5/10,  
PC C07K5/107, C07K5/117, C07K7/06, C07K7/08, C07K16/40, C12N9/12, PC  
C12N15/09,

PC C12Q1/02, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC  
G01N33/53,  
PC G01N33/566, G01N33/573//C12P21/08, A61K37/02, C12N15/00 CC  
Strandedness: Single;  
CC Topology: Linear;

FT Key Location/Qualifiers  
FT source 1. .48  
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source Location/Qualifiers  
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/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGTTTGGGGTTTT 48  
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RESULT 35  
AR104527 50 bp DNA linear PAT 14-FEB-2001  
LOCUS  
DEFINITION Sequence 39 from patent US 6093809.  
ACCESSION AR104527  
VERSION AR104527.1 GI:12817235

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Cech, T.R. and Lingner, J.  
TITLE Telomerase  
JOURNAL Patent: US 6093809-A 39 25-JUL-2000;  
FEATURES  
source Location/Qualifiers  
1. .50  
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/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 31 TTTTGGGTTTGGGGTTTT 50  
|||||

RESULT 36  
AR175788 50 bp DNA linear PAT 17-DEC-2001  
LOCUS  
DEFINITION Sequence 39 from patent US 6309867.  
ACCESSION AR175788  
VERSION AR175788.1 GI:17917087

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

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REFERENCE 1 (bases 1 to 50)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 39 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
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Db 31 TTTTGGGGTTTGGGGTTTT 50

RESULT 37
E37016
LOCUS Human telomerase catalytic subunit promoter. PAT 18-JUN-2001
DEFINITION E37016
ACCESSION E37016
VERSION E37016.1 GI:13022979
KEYWORDS JP 199253177-A/224.
SOURCE unclassified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 50)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 199253177-A 224 21-SEP-1999;
COMMENT JERON CORP./UNIVERSITY TECHNOLOGY CORP
OS Unidentified
PN JP 199253177-A/224
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503 PI THOMAS
R SECHI, JOCHIMU RINGER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HAREI, WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
PC C12Q1/02,
PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
C12R1:84),
PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..50
FT /organism='Unidentified'.
FEATURES source
1..50
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 31 TTTTGGGGTTTGGGGTTTT 50

REFERENCE 1 (bases 1 to 50)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 39 30-OCT-2001;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
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Db 31 TTTTGGGGTTTGGGGTTTT 50

RESULT 38
AR390693
LOCUS Sequence 566 from patent US 6610839. PAT 18-DEC-2003
DEFINITION AR390693
ACCESSION AR390693
VERSION AR390693.1 GI:40112627
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Morin,G.B. and Andrews,W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 566 26-AUG-2003;
COMMENT Geron Corporation; Menlo Park, CA
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 31 TTTTGGGGTTTGGGGTTTT 50

RESULT 39
AR393307
LOCUS Sequence 566 from patent US 6617110. PAT 18-DEC-2003
DEFINITION AR393307
ACCESSION AR393307
VERSION AR393307.1 GI:40118685
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
drug screening
JOURNAL Patent: US 6617110-A 566 09-SEP-2003;
COMMENT Geron Corporation and University Technology Corporation; Menlo
Park, CA
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
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Db 31 TTTTGGGGTTTGGGGTTTT 50

RESULT 40
AR592664
LOCUS Sequence 39 from patent US 680880. PAT 15-DEC-2004
DEFINITION AR592664
ACCESSION AR592664
VERSION AR592664.1 GI:56641384
KEYWORDS
SOURCE Unknown.
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C., and Andrews,W.H.
TITLE Method for detecting polynucleotides encoding telomerase
JOURNAL Patent: US 6809880-A 39 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
Park, CA
FEATURES
source Location/Qualifiers
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/mol_type="unknown"
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTGGGGTTTGGGGTTT 20
|||||
Db 31 TTTTGGGGTTTGGGGTTT 50
|||||

RESULT 41
AX810601
LOCUS AX810601 50 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 566 from Patent EP1333094.
ACCESSION AX810601
VERSION AX810601.1 GI:38524090
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified sequences.
REFERENCE 1
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: EP 1333094-A 566 06-AUG-2003;
Geron Corporation (US) ; University Technology Corporation (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32644"
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Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTGGGGTTTGGGGTTT 20
|||||
Db 31 TTTTGGGGTTTGGGGTTT 50
|||||

RESULT 42
BD011267
LOCUS BD011267 50 bp DNA linear PAT 31-JAN-2002
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011267
VERSION BD011267.1 GI:18639640
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 224 27-MAR-2001;
GERON CORP., UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified

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PN JP 2001081042-A/224
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
PR 01-JUL-1996 US 08/724643,18-APR-1997 US 08/844419 PR
25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
03-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN,PI GREG B
MORIN,
PI CALVIN B HARLEY,WILLIAM H ANDREWS
PC A61K39/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
PC C07K5/10,
PC C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12,PC
C12N15/09,
PC C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,PC
G01N33/53,
PC G01N33/566,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..50
FT /organism='Unidentified'.
FT Location/Qualifiers
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/mol_type="unidentified"
/db_xref="taxon:32644"
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Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTGGGGTTTGGGGTTT 20
|||||
Db 31 TTTTGGGGTTTGGGGTTT 50
|||||

RESULT 43
AR104527/c
LOCUS AR104527 50 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 39 from patent US 6093809.
ACCESSION AR104527
VERSION AR104527.1 GI:12817235
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 39 25-JUL-2000;
FEATURES
source Location/Qualifiers
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Query Match 90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTGGGGTTTGGGGTTT 18
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Db 18 TTTTGGGGTTTGGGGTTT 1
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RESULT 44
AR175788/c
LOCUS AR175788 50 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 39 from patent US 6309867.
ACCESSION AR175788
VERSION AR175788.1 GI:17917087

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Cech,T.R. and Nakamura,T.
TITLE       Telomerase
JOURNAL     Patent: US 6309867-A 39 30-OCT-2001;
FEATURES    Location/Qualifiers
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ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTT 18
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Db 18 TTTTGGGGTTTGGGGTT 1

RESULT 45
E37016/c
LOCUS       E37016      50 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION   E37016
VERSION     E37016.1 GI:13022979
KEYWORDS    JP 1999253177-A/224.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 50)
AUTHORS     Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
            Calvin,B.H. and William,H.A.
TITLE       Human telomerase catalytic subunit promoter
JOURNAL     Patent: JP 1999253177-A 224 21-SEP-1999;
            JERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT     OS Unidentified
            PN JP 1999253177-A/224
            PD 21-SEP-1999
            PF 15-OCT-1998 JP 1998320169
            PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
            25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
            09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
            14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503 PI THOMAS
            R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
            MORIN,
            PI CALVIN B HARRI,WILLIAM H ANDREWS
            PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K48/00,
            PC C12Q1/02,
            PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
            C07K16/40,
            PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
            C12R1:84),
            PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
            PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
            Strandedness: Single;
            CC Topology: Linear;
            FH Key
            FT source
            FT source
            Location/Qualifiers
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            /db_xref="taxon:32644"

ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTT 18
    |||||
Db 18 TTTTGGGGTTTGGGGTT 1

RESULT 46
AR390693/c
LOCUS       AR390693    50 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 566 from patent US 6610839.
ACCESSION   AR390693
VERSION     AR390693.1 GI:40112627
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Morin,G.B. and Andrews,W.H.
TITLE       Promoter for telomerase reverse transcriptase
JOURNAL     Patent: US 6610839-A 566 26-AUG-2003;
            Geron Corporation; Menlo Park, CA
FEATURES    Location/Qualifiers
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ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTT 18
    |||||
Db 18 TTTTGGGGTTTGGGGTT 1

RESULT 47
AR393307/c
LOCUS       AR393307    50 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 566 from patent US 6617110.
ACCESSION   AR393307
VERSION     AR393307.1 GI:40118685
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
            Harley,C.B. and Andrews,W.H.
TITLE       Cells immortalized with telomerase reverse transcriptase for use in
            drug screening
JOURNAL     Patent: US 6617110-A 566 09-SEP-2003;
            Geron Corporation and University Technology Corporation; Menlo
            Park, CA
FEATURES    Location/Qualifiers
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ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTT 18
    |||||
Db 18 TTTTGGGGTTTGGGGTT 1

RESULT 48
AR592664/c
LOCUS       AR592664    50 bp      DNA      linear      PAT 15-DEC-2004
DEFINITION Sequence 39 from patent US 6808880.
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
            Harley,C.B. and Andrews,W.H.
TITLE       Cells immortalized with telomerase reverse transcriptase for use in
            drug screening
JOURNAL     Patent: US 6617110-A 566 09-SEP-2003;
            Geron Corporation and University Technology Corporation; Menlo
            Park, CA
FEATURES    Location/Qualifiers
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            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TTTTGGGGTTTGGGGTT 18
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Db 18 TTTTGGGGTTTGGGGTT 1

RESULT 46
AR390693/c
LOCUS       AR390693    50 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 566 from patent US 6610839.
ACCESSION   AR390693
VERSION     AR390693.1 GI:40112627
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Morin,G.B. and Andrews,W.H.
TITLE       Promoter for telomerase reverse transcriptase
JOURNAL     Patent: US 6610839-A 566 26-AUG-2003;
            Geron Corporation; Menlo Park, CA
FEATURES    Location/Qualifiers
            source
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            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTT 18
    |||||
Db 18 TTTTGGGGTTTGGGGTT 1

RESULT 47
AR393307/c
LOCUS       AR393307    50 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 566 from patent US 6617110.
ACCESSION   AR393307
VERSION     AR393307.1 GI:40118685
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
            Harley,C.B. and Andrews,W.H.
TITLE       Cells immortalized with telomerase reverse transcriptase for use in
            drug screening
JOURNAL     Patent: US 6617110-A 566 09-SEP-2003;
            Geron Corporation and University Technology Corporation; Menlo
            Park, CA
FEATURES    Location/Qualifiers
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            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTT 18
    |||||
Db 18 TTTTGGGGTTTGGGGTT 1

RESULT 48
AR592664/c
LOCUS       AR592664    50 bp      DNA      linear      PAT 15-DEC-2004
DEFINITION Sequence 39 from patent US 6808880.
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
            Harley,C.B. and Andrews,W.H.
TITLE       Cells immortalized with telomerase reverse transcriptase for use in
            drug screening
JOURNAL     Patent: US 6617110-A 566 09-SEP-2003;
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AUTHORS Cecchi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C. and Andrews,W.H.
TITLE Method for detecting polynucleotides encoding telomerase
JOURNAL Patent: US 680880-A 39 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
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AUTHORS Cecchi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: EP 1333094-A 566 06-AUG-2003;
Geron Corporation (US) ; University Technology Corporation (US)
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AUTHORS Cecchi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
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        MORIN,
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| 260 | 12.8 | 64.0 | 31 | 2  | AAQ44765 | Aaq44765 Steroid h |
| 261 | 12.8 | 64.0 | 31 | 3  | AAA49331 | Aaa49331 Primer us |
| 262 | 12.8 | 64.0 | 35 | 11 | ADO77990 | Ado77990 Chimeric  |
| 263 | 12.8 | 64.0 | 35 | 11 | ADO77989 | Ado77989 Chimeric  |
| 264 | 12.8 | 64.0 | 37 | 6  | ACN19904 | Acn19904 WNV Zinz  |
| 265 | 12.8 | 64.0 | 41 | 12 | ADK17690 | Adk17690 Cytochrom |
| 266 | 12.8 | 64.0 | 41 | 14 | AE991290 | Aeb91290 Reverse p |
| 267 | 12.8 | 64.0 | 45 | 2  | AAE67449 | Aat67449 H. pylori |
| 268 | 12.8 | 64.0 | 46 | 2  | AAE6508  | Aat6508 WO 990919  |
| 269 | 12.8 | 64.0 | 50 | 6  | ABH05136 | Abh05136 Human leu |
| 270 | 12.6 | 63.0 | 13 | 5  | ABH09453 | Abh09453 Oligonuc  |
| 271 | 12.6 | 63.0 | 13 | 5  | ABH09452 | Abh09452 Oligonuc  |
| 272 | 12.6 | 63.0 | 19 | 8  | ABZ10375 | Abz10375 Haematopo |
| 273 | 12.6 | 63.0 | 20 | 12 | ADJ25248 | Adj25248 Human end |
| 274 | 12.6 | 63.0 | 20 | 12 | ADJ25340 | Adj25340 Human end |
| 275 | 12.6 | 63.0 | 20 | 12 | ADK74370 | Adk74370 Chimeric  |
| 276 | 12.6 | 63.0 | 20 | 12 | ADK76005 | Adk76005 Chimeric  |
| 277 | 12.6 | 63.0 | 20 | 12 | ADK73634 | Adk73634 Chimeric  |
| 278 | 12.6 | 63.0 | 20 | 12 | ADK76773 | Adk76773 Chimeric  |
| 279 | 12.6 | 63.0 | 20 | 12 | ADK79971 | Adk79971 Chimeric  |
| 280 | 12.6 | 63.0 | 20 | 12 | ADK81477 | Adk81477 Chimeric  |
| 281 | 12.6 | 63.0 | 21 | 3  | AAZ73686 | Aaz73686 Human bia |
| 282 | 12.6 | 63.0 | 21 | 14 | ADY94237 | Ady94237 Sequencin |
| 283 | 12.6 | 63.0 | 22 | 4  | AAH39037 | Aah39037 SNP speci |
| 284 | 12.6 | 63.0 | 22 | 6  | ABS59605 | Abs59605 Real-time |
| 285 | 12.6 | 63.0 | 22 | 12 | ADL56894 | Adl56894 Human NOV |
| 286 | 12.6 | 63.0 | 22 | 12 | ADQ39278 | Ado39278 Human NOV |
| 287 | 12.6 | 63.0 | 22 | 13 | ADS90007 | Ads90007 Human PCR |
| 288 | 12.6 | 63.0 | 23 | 9  | ADA13696 | Ada13696 Short int |
| 289 | 12.6 | 63.0 | 23 | 10 | ADG29769 | Adg29769 EGFR-targ |
| 290 | 12.6 | 63.0 | 23 | 11 | ADL80060 | Adl80060 Human HBR |
| 291 | 12.6 | 63.0 | 23 | 11 | ADM65565 | Adm65565 Human Y C |
| 292 | 12.6 | 63.0 | 23 | 11 | ADM65562 | Adm65562 Human Y C |
| 293 | 12.6 | 63.0 | 23 | 12 | ADQ78147 | Adq78147 PCR prime |
| 294 | 12.6 | 63.0 | 23 | 12 | ADQ78164 | Adq78164 PCR prime |
| 295 | 12.6 | 63.0 | 23 | 13 | ADS78188 | Ads78188 RASSF1A g |
| 296 | 12.6 | 63.0 | 23 | 13 | ADS78213 | Ads78213 RASSF1A g |
| 297 | 12.6 | 63.0 | 23 | 13 | ADX59095 | Adx59095 Human liv |
| 298 | 12.6 | 63.0 | 23 | 14 | ADV46309 | Adv46309 Human Cpg |
| 299 | 12.6 | 63.0 | 24 | 2  | AAV09446 | Aav09446 Cpg-conta |
| 300 | 12.6 | 63.0 | 24 | 2  | AAV09582 | Aav09582 MSP ampli |

ALIGNMENTS

RESULT 1  
ID AAF98948 standard; DNA; 20 BP.  
XX  
AC AAF98948;  
XX

DT 12-JUN-2001 (first entry)  
XX Immunostimulatory nucleic acid #64.  
DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
XX immunostimulatory; tumour; viral infection; bacterial infection;  
KW fungal infection; parasitic infection; cancer; asthma;  
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
XX Synthetic.  
XX WO200122972-A2.  
PN 05-APR-2001.  
XX 25-SEP-2000; 2000WO-US026383.  
PD 25-SEP-1999; 99US-0156113P.  
XX 27-SEP-1999; 99US-0156135P.  
XX 23-AUG-2000; 2000US-0227436P.  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLB-) COLEY PHARM GMBH.  
PA Krieg AM, Schetter C, Vollmer J;  
XX WPI; 2001-273485/28.  
XX Vaccinating against tumors, infectious diseases, allergies and asthma  
PT using immunostimulatory Py-rich and TG nucleic acids.  
PT Disclosure; Page 39; 338pp; English.  
CC The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
CC acid to a non-rodent subject in sufficient quantity to stimulate an  
CC immune response. The present sequence is one such immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone  
XX Sequence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 20; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTTTGGGTTTGGGGTTT 20  
Db 1 TTTTGGGTTTGGGGTTT 20  
RESULT 2  
ABS77589  
ID ABS77589 standard; DNA; 20 BP.  
XX  
AC ABS77589;  
XX  
XX 13-DEC-2002 (first entry)  
XX Angiogenesis inhibitory oligonucleotide #73.  
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX Synthetic.  
XX  
XX WO200253141-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 14-DEC-2001; 2001WO-US048458.  
XX PF  
XX 14-DEC-2000; 2000US-0255534P.  
XX PR  
XX (COLE-) COLLEY PHARM GROUP INC.  
XX PA  
XX Bratzler RL;  
XX PI  
XX WPI; 2002-566690/60.  
XX DR  
XX Inhibiting angiogenesis in a subject, involves administering at least one  
XX PT antiangiogenic nucleic acid molecule to the subject.  
XX PT  
XX Claim 2; Page 20; 276pp; English.  
XX PS  
XX The invention relates to inhibiting angiogenesis in a subject, comprising  
XX CC administering at least one antiangiogenic nucleic acid molecule. Also  
XX CC included is a kit comprising a first container housing the antiangiogenic  
XX CC nucleic acids, and instructions for administering them to a subject  
XX CC having a condition characterised by unwanted angiogenesis. The method is  
XX CC useful for inhibiting angiogenesis associated with solid tumour growth,  
XX CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
XX CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
XX CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
XX CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
XX CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
XX CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
XX CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
XX CC acid of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGTTTGGGGTTTT 20  
|||  
DB 1 TTTTGGGTTTGGGGTTTT 20  
|||  
  
RESULT 3  
ACD99381  
ID ACD99381 standard; DNA; 20 BP.  
XX  
XX  
XX ACD99381;  
XX  
XX 25-SEP-2003 (first entry)  
XX  
XX Immunostimulatory nucleic acid #67.  
XX  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
XX KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
XX KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
XX KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX  
XX Synthetic.  
XX OS  
XX US2003050268-A1.  
XX PN  
XX 13-MAR-2003.  
XX PD  
XX

PF 29-MAR-2002; 2002US-00112653.  
XX  
XX 29-MAR-2001; 2001US-0279642P.  
XX  
XX (KRIE/) KRIEG A M.  
XX PA (BERG/) BERG D J.  
XX  
XX Krieg AM, Berg DJ;  
XX PI  
XX WPI; 2003-521815/49.  
XX DR  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
XX PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
XX PT disease by administering an immunostimulatory nucleic acid.  
XX  
XX Disclosure; Page 10; 229pp; English.  
XX  
XX The invention describes a method of treating non-allergic inflammatory  
XX CC disease comprising administering to a subject having or at risk of  
XX CC developing a non-allergic inflammatory disease an immunostimulatory  
XX CC nucleic acid for prevention or treatment of the disease. The method is  
XX CC useful for treating non-allergic inflammatory diseases, such as  
XX CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
XX CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
XX CC This sequence represents an immunostimulatory nucleic acid  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGTTTGGGGTTTT 20  
|||  
DB 1 TTTTGGGTTTGGGGTTTT 20  
|||  
  
RESULT 4  
ADB36450  
ID ADB36450 standard; DNA; 20 BP.  
XX  
XX ADB36450;  
XX  
XX 04-DEC-2003 (first entry)  
XX  
XX Immunostimulatory nucleic acid #64.  
XX  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
XX KW hypo-responsive subject; immunostimulatory.  
XX  
XX Synthetic.  
XX OS  
XX US2003087848-A1.  
XX PN  
XX 08-MAY-2003.  
XX PD  
XX 02-FEB-2001; 2001US-00776479.  
XX PF  
XX 03-FEB-2000; 2000US-0179991P.  
XX PR  
XX (BRAT/) BRATZLER R L.  
XX PA (PETE/) PETERSEN D M.  
XX PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX PI  
XX WPI; 2003-657977/62.  
XX DR  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
XX PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX  
XX Disclosure; Page 6; 221pp; English.  
XX



RESULT 7  
 AAD64883  
 ID AAD64883 standard; DNA; 28 BP.  
 XX  
 AC AAD64883;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Non-antisense oligonucleotide, GRO J1.  
 XX  
 KW Neoplastic; malignancy; lung carcinoma; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003194754-A1.  
 XX  
 PD 16-OCT-2003.  
 XX  
 PF 08-APR-2002; 2002US-00118854.  
 XX  
 PR 08-APR-2002; 2002US-00118854.  
 XX  
 PA (MILL/) MILLER D M.  
 PA (BATE/) BATES P J.  
 PA (TREN/) TRENT J O.  
 PA (AUXK/) XU X.  
 XX  
 PI Miller DM, Bates PJ, Trent JO, Xu X;  
 XX  
 XX WPI; 2003-875400/81.  
 XX  
 PT Determining neoplastic state of cell, involves detecting presence of  
 PT plasma membrane nucleotide in cell or quantifying amount of plasma  
 PT membrane nucleolin in cell.  
 XX  
 PS Claim 11; SEQ ID NO 28; Opp; English.  
 XX  
 CC The present invention relates to method for determining neoplastic state  
 CC of a cell, involves detecting the presence of plasma membrane nucleotide  
 CC in the cell or quantifying the amount of plasma membrane nucleolin in the  
 CC cell. The invention is useful for diagnosing pre-malignant cells,  
 CC malignant cells and lung small cell carcinoma. The present sequence is a  
 CC non-antisense oligonucleotide  
 XX  
 XX Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 10; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTTTT 20  
 DB 5 TTTTGGGGTTTGGGGTTTT 24  
 RESULT 8  
 ADJ94159  
 ID ADJ94159 standard; DNA; 28 BP.  
 XX  
 AC ADJ94159;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Oligonucleotide of the invention #26.  
 XX  
 KW ds; linear polynucleotide; cation; telomere repeat.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2003169676-A.  
 XX  
 PD 17-JUN-2003.  
 XX

XX  
 PF 05-DEC-2001; 2001JP-00371975.  
 XX  
 PR 05-DEC-2001; 2001JP-00371975.  
 XX  
 PA (TAKE/) TAKENAKA S.  
 PA (TUMK-) TUM KENYUSHO KK.  
 XX  
 XX WPI; 2003-639772/61.  
 DR  
 XX  
 PT Quantitative method of cation for clinical laboratory test, involves  
 PT adding linear polynucleotide containing telomere repeat sequence with  
 PT donor and acceptor at edge portions, to solution containing cation.  
 XX  
 PS Disclosure; Page 29; 8pp; Japanese.  
 XX  
 CC The invention relates to a novel quantitative method for adding linear  
 CC polynucleotide to solution containing a cation. The linear polynucleotide  
 CC contains telomere repeat sequence with donor at one edge portion and  
 CC acceptor at another edge portion. The optical detection is performed  
 CC using this linear polynucleotide. The method of the invention is useful  
 CC in medical fields such as clinical laboratory test and fields with cation  
 CC fixed assay. The present sequence is used in the exemplification of the  
 CC invention.  
 XX  
 SQ Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTTTT 20  
 DB 5 TTTTGGGGTTTGGGGTTTT 24  
 RESULT 9  
 ADI28732  
 ID ADI28732 standard; DNA; 28 BP.  
 XX  
 AC ADI28732;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Guanosine-rich oligonucleotide GRO J, used in apoptosis detection.  
 XX  
 KW Apoptosis; nucleolin; AIDS; cancer; neurodegenerative disease;  
 KW autoimmune disease; infection; diagnosis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004003554-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 26-JUN-2003; 2003WO-US020167.  
 XX  
 PR 26-JUN-2002; 2002US-0392143P.  
 XX  
 PA (UYLO-) UNIV LOUISVILLE RES FOUND INC.  
 PA (BATE/) BATES P J.  
 PA (MIYY/) MI Y.  
 XX  
 PI Bates PJ, Mi Y;  
 XX  
 XX WPI; 2004-083166/08.  
 DR  
 PT Detecting apoptosis comprises preparing a sample from which cells have  
 PT been removed and detecting at least one of nucleolin and PARP-I in the  
 PT sample.  
 XX  
 XX Claim 9; SEQ ID NO 28; 66pp; English.  
 XX



CC The present sequence is that of guanosine-rich oligonucleotide GRO J,  
CC which can be used in the method of the invention. The method is for the  
CC detection of apoptosis. It involves preparing a sample from which cells  
CC have been removed, and detecting nucleolin and/or poly(ADP-ribose)  
CC polymerase (PARP-1) in the sample, where the sample is blood, serum,  
CC plasma, tissue, tissue culture medium or sputum. Detection of nucleolin  
CC involves detection of a complex between nucleolin and a nucleolin binding  
CC molecule, preferably an anti-nucleolin antibody or a GRO, such as GRO J,  
CC which is characterised as a good plasma membrane nucleolin-binding GRO.  
CC The method allows detection of excessive apoptosis in a subject suspected  
CC of having AIDS, a neurodegenerative disease, an ischaemic injury, an  
CC autoimmune disease, a tumour, a cancer (especially endocervical  
CC adenocarcinoma, prostatic carcinoma, breast cancer, leukaemia and non-  
CC small cell lung carcinoma), a viral infection, an acute inflammatory  
CC condition or sepsis (all claimed).

XX Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 28;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTTTGGGGTTTT 20  
Db 5 TTTTGGGTTTTTGGGGTTTT 24

## RESULT 10

ADY53924  
ID ADY53924 standard; DNA; 28 BP.

XX AC ADY53924;

XX 19-MAY-2005 (first entry)

XX Non-antisense GRO nucleolin-binding oligonucleotide GRO29A.

XX Diagnosis; therapy; tumor; cancer; neoplasm; cytostatic; nucleolin; ss;  
KW guanine-rich oligonucleotide; gene silencing; RNA interference; melanoma;  
KW lymphoma; sarcoma; glioma; leukemia; hepatocellular carcinoma.

XX Synthetic.

XX US2005053607-A1.

XX 10-MAR-2005.

XX 09-OCT-2003; 2003US-00683480.

XX 08-APR-2002; 2002US-00118854.

PA (BATE/) BATES P J.

PA (MILL/) MILLER D M.

PA (TREN/) TRENT J O.

PA (XUXX/) XU X.

XX Bates PJ, Miller DM, Trent JO, Xu X;

XX WPI; 2005-213006/22.

PT Treating cancer in a subject comprises administering to the subject a  
PT therapeutically effective amount of an anti-nucleolin agent and a  
PT carrier.

XX Disclosure; SEQ ID NO 28; 32pp; English.

XX The invention relates to treating cancer in a subject comprises  
CC administering to the subject a therapeutically effective amount of an  
CC anti-nucleolin agent and a carrier. Also included is a pharmaceutical  
CC composition comprising a nucleolin antibody or an inhibitory RNA against  
CC nucleolin, and a carrier. The method and antibodies, RNA and composition  
CC are useful for treating cancer, such as melanoma, lymphoma, plasmocytoma,  
CC sarcoma, glioma, thymoma, leukemia, hepatoma, or breast, prostate, colon,

CC liver, esophageal, brain, lung, ovary, or cervical cancer. The present  
CC sequence is a GRO (guanine-rich oligonucleotide) which binds to nucleolin  
CC (thereby inhibiting cancer cell growth).

XX Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 28;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTTTGGGGTTTT 20  
Db 5 TTTTGGGTTTTTGGGGTTTT 24

## RESULT 11

ADZ58647  
ID ADZ58647 standard; DNA; 28 BP.

XX AC ADZ58647;

XX 14-JUL-2005 (first entry)

XX Inflammation treatment-related GRO J oligonucleotide SeqID29.

XX Inflammation; antiinflammatory; analgesic; gynecological; hepatotropic;  
KW neuroprotective; nootropic; antiarthritic; antirheumatic;  
KW gastrointestinal-Gen.; antiulcer; gene therapy; dysmenorrhea;  
KW alcoholic hepatitis; pancreatitis; Alzheimers disease;  
KW rheumatoid arthritis; asthma; gastrointestinal disease; psoriasis;  
KW atherosclerosis; Crohns disease; ulcerative colitis; GRO J; ss.

XX Unidentified.

XX WO2005037323-A2.

XX 28-APR-2005.

XX 08-OCT-2004; 2004WO-US033185.

XX 10-OCT-2003; 2003US-0510466P.

XX (UYLO-) UNIV LOUISVILLE RES FOUND INC.

XX Bates PJ, Girvan AC, Barve SS;

XX WPI; 2005-315628/32.

XX Treating inflammation, e.g. acute or chronic inflammation such as  
PT rheumatoid arthritis, asthma, psoriasis, and atherosclerosis, in a  
PT patient comprises administering to the patient a composition comprising a  
GRO.

XX Claim 2; SEQ ID NO 29; 60pp; English.

XX This invention relates to a novel method for treating inflammation in a  
CC patient which comprises administering to the patient a composition  
CC comprising a GRO (guanosine-rich oligonucleotide). The invention may be  
CC useful for the development of compounds with an antiinflammatory,  
CC analgesic, gynecological, hepatotropic, neuroprotective, nootropic,  
CC antiarthritic, antirheumatic, gastrointestinal-Gen. or antiulcer activity  
CC whilst the disclosed sequence may prove useful for gene therapy. The  
CC methods are useful for treating inflammation associated with an acute  
CC inflammatory condition. The acute inflammatory condition is selected from  
CC primary dysmenorrhea, acute alcoholic liver disease and acute  
CC pancreatitis. The inflammation may also be of Alzheimer's disease or  
CC associated with a chronic inflammatory disease. The chronic inflammatory  
CC disease is selected from rheumatoid arthritis, asthma, gastrointestinal  
CC tract disease, psoriasis, atherosclerosis, Crohns disease, ulcerative  
CC colitis alcohol, chronic alcoholic liver disease, non-alcoholic  
CC steatohepatitis and chronic pancreatitis. The present sequence is that of  
CC the oligonucleotide GRO J which was used during the development of the  
CC novel method of the invention.

XX SQ Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 28;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 5 TTTTGGGGTTTGGGGTTTT 24

RESULT 12

AD225617  
ID AD225617 standard; DNA; 28 BP.  
XX AC AD225617;  
XX DT 14-JUL-2005 (first entry)  
DE G-quadruplex-forming carbazole-binding DNA Oxy28, SEQ ID NO:11.  
XX KW Telomere; stabilizer; telomerase inhibitor; cancer; neoplasm; cytostatic;  
XX OS ss.  
XX Unidentified.  
XX US2005090671-A1.  
XX PN US2005090671-A1.  
XX PD 28-APR-2005.  
XX PF 22-OCT-2003; 2003US-00690984.  
XX PS 22-OCT-2003; 2003US-00690984.  
XX (CHAN/) CHANG T.  
XX PA (CHAN/) CHANG C.  
XX PU (WUJU/) WU J.  
XX Chang T, Chang C, Wu J;  
XX WPI; 2005-331984/34.  
XX New carbazole compound stabilizing G-quadruplex of telomere, useful to  
treat telomerase-related disease e.g. cancer.  
XX Example 9; SEQ ID NO 11; 12pp; English.

The invention relates to novel carbazole compounds which thermally  
stabilize the intramolecular G-quadruplex structure of human telomeres.  
The folding of telomeric DNA into G-quadruplexes inhibits telomerase, the  
enzyme present in over 85% of tumor cells which adds nucleotides to  
telomeres, preventing them from reducing in length during cell division.  
The carbazole compounds of the invention may be used to treat telomere-  
related disease, e.g., cancer. Sequences AD225610-AD225619 represent DNA  
sequences capable of duplex or quadruplex formation which were  
demonstrated to be bound by a carbazole compound of the invention. The  
present sequence represents a G-quadruplex-forming DNA capable of being  
bound by a carbazole compound. Note: The specification states that this  
sequence forms a G-quadruplex structure; however, further details on how  
the structure is formed has not been provided.

XX SQ Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 28;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 5 TTTTGGGGTTTGGGGTTTT 24

RESULT 13

AA257146  
ID AA257146 standard; DNA; 32 BP.  
XX AC AA257146;  
XX DT 24-MAR-2000 (first entry)  
XX Exemplary quadruplex nucleic acid SEQ ID NO:9.  
DE Quadruplex DNA; antibody; binding; detection; isolation; purification;  
XX KW ss.  
XX OS Synthetic.  
XX PN US6001657-A.  
XX PD 14-DEC-1999.  
XX PF 11-OCT-1996; 96US-00729598.  
XX PR 12-OCT-1995; 95US-0005242P.  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX PA (JACK-) JACKSON LAB.  
XX Roberts JF, Pelsue SC, Hardin CC, Brown BA;  
XX WPI; 2000-096139/08.  
XX Quadruplex nucleic acid and antibody binding assay useful for detecting  
and purifying antibodies and nucleic acids from a biological sample.  
XX Disclosure; Col 3; 11pp; English.

A method has been developed for binding quadruplex nucleic acids. The  
method comprises contacting a quadruplex nucleic acid with a monoclonal  
antibody that selectively binds to quadruplex nucleic acid to form an  
antibody-quadruplex nucleic acid complex. The method can be used for  
detecting antibodies that bind to quadruplex nucleic acids and to collect  
antibodies that bind to quadruplex nucleic acids. The method is also  
suitable for detecting, isolating and purifying quadruplex nucleic acids.  
The detecting step can be carried out on a biological sample such as  
cerebrospinal fluid, tissues samples, blood samples or other sample  
suspected of containing quadruplex nucleic acids. The method can be used  
for the purification of quadruplex nucleic acids from solutions and to  
purify aptamers from combinatorial libraries or heterogeneous solutions,  
in particular to purify or detect DNA aptamers that specifically bind the  
thrombin molecule critical in the thrombin-catalysed, fibrin-clot  
formation cascade of blood platelets. The antibodies can then be used to  
detect levels of a known therapeutic aptamer in a patient and monitor  
clearance and dosage levels in a treatment protocol involving the  
aptamer. The present sequence represents an oligonucleotide used in the  
exemplification of the present invention

XX SQ Sequence 32 BP; 0 A; 0 C; 16 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 1 TTTTGGGGTTTGGGGTTTT 20

RESULT 14

AAQ61979  
ID AAQ61979 standard; DNA; 39 BP.  
XX AC AAQ61979;  
XX DT 25-MAR-2003 (revised)

DT 04-NOV-1994 (first entry)  
 XX Oxytricha telomeric sequence.  
 XX  
 XX Inhibition; replication; herpes simplex virus; HSV; HIV; aging; length;  
 KW human cytomegalovirus; influenza virus; inflammation; telomere  
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;  
 KW malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.  
 XX  
 XX Oxytricha sp.  
 XX  
 XX W09408053-A1.  
 XX  
 XX 14-APR-1994.  
 XX  
 XX 29-SEP-1993; 93WO-US009297.  
 XX  
 XX 29-SEP-1992; 92US-00954185.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;  
 PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;  
 XX  
 XX WPI; 1994-135613/16.  
 XX  
 XX New modified oligo-nucleotide contg guanine quartet - inhibits activity  
 PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length  
 PT of chromosomes.  
 XX  
 XX Example 7; Page 36; 144pp; English.  
 XX  
 XX This sequence represents a guanine rich sequence derived from the  
 CC Oxytricha telomeric region. This sequence forms an unusual structure  
 CC termed a G quartet. The formation of this structure is monovalent cation  
 CC dependant and is disrupted by high temperature. Sequences which share the  
 CC guanine rich nature of this telomeric sequence may be used to inhibit  
 CC human type II phospholipase A2 activity. Oligonucleotides such as these  
 CC may also be used for inhibiting activity of HSV, HIV, human  
 CC cytomegalovirus or influenza virus, or for treating inflammatory and  
 CC neurological disorders caused by phospholipase A2 activity in cases of  
 CC hyperproliferation, malignancy, cardiovascular disease and snake bite.  
 CC They may also be used for inhibiting division of malignant cells by  
 CC modulating telomere length, which may also retard aging. (Updated on 25-  
 CC MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 39 BP; 0 A; 0 C; 20 G; 16 T; 0 U; 3 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 2; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTTT 20  
 |||||  
 Db 8 TTTTGGGGTTTGGGGTTT 27  
 |||||  
 RESULT 15  
 AAV17009  
 ID AAV17009 standard; DNA; 44 BP.  
 XX  
 AC AAV17009;  
 XX  
 DT 13-AUG-1998 (first entry)  
 XX  
 DE Telomerase substrate utilisation primer 28-30.  
 XX  
 KW Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;  
 KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX

PN GB2317891-A.  
 XX  
 PD 08-APR-1998.  
 XX  
 PF 01-OCT-1997; 97GB-00020890.  
 XX  
 PR 01-OCT-1996; 96US-00724643.  
 PR 18-APR-1997; 97US-00844419.  
 PR 25-APR-1997; 97US-00846017.  
 PR 06-MAY-1997; 97US-00851843.  
 PR 09-MAY-1997; 97US-00854050.  
 PR 14-AUG-1997; 97US-00911312.  
 PR 14-AUG-1997; 97US-00912951.  
 PR 14-AUG-1997; 97US-00915503.  
 XX  
 XX (GERO-) GERON CORP.  
 PA (UYTB-) UNIV TECHNOLOGY CORP.  
 XX  
 XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;  
 PI Andrews WH;  
 PI  
 XX WPI; 1998-171633/16.  
 DR  
 XX Pure and recombinant human Telomerase Reverse Transcriptase and its  
 PT variants - are useful in the diagnosis, prognosis and treatment of cell  
 PT proliferation conditions especially cancer and ageing.  
 XX  
 PS Example 1; Page 200; 387pp; English.  
 XX  
 CC The present sequence represents a primer from the present invention which  
 CC describes human telomerase reverse transcriptase (hTERT). The present  
 CC invention also describes the following methods: (A) determining whether a  
 CC test compound is a modulator of hTERT, by detecting the change in hTERT  
 CC recombinant protein or polynucleotide, on administration of the compound;  
 CC (B) preparation of recombinant telomerase by contacting a protein  
 CC preparation of hTERT with a telomerase RNA component; (C) detection of the  
 CC hTERT RNA or protein in a sample by binding a relevant probe to the sample  
 CC and detecting the product and correlating the presence of complex or  
 CC amplifying the product with presence of hTERT in the sample; and (D)  
 CC amplification product with presence of hTERT in the sample; and (E)  
 CC increasing the proliferation of a vertebrate cell by increasing hTERT  
 CC expression; and (E) the use of an agent that causes an increase in cell  
 CC vertebrate cell proliferation to create a medication that inhibits  
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding  
 CC hTERT can be used in the manufacture of medicaments for inhibiting the  
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be used  
 CC to treat conditions that are associated with high telomerase activity. A  
 CC protein preparation of hTERT can also be used in the new methods  
 XX  
 SQ Sequence 44 BP; 10 A; 10 C; 12 G; 12 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTTT 20  
 |||||  
 Db 25 TTTTGGGGTTTGGGGTTT 44  
 |||||  
 RESULT 16  
 AAV17008  
 ID AAV17008 standard; DNA; 46 BP.  
 XX  
 AC AAV17008;  
 XX  
 DT 13-AUG-1998 (first entry)  
 XX  
 DE Telomerase substrate utilisation primer 25-27.  
 XX  
 KW Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;  
 KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.  
 OS  
 XX

```

OS Synthetic.
OS Homo sapiens.
PN GB2317891-A.
PD 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
XX Example 1; Page 200; 387pp; English.
XX
XX The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX
XX Sequence 46 BP; 10 A; 12 C; 12 G; 12 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20
Db |||||
27 TTTTGGGTTTGGGGTTT 46

RESULT 17
AAV17007
ID AAV17007 standard; DNA; 48 BP.
XX
XX AAV17007;
XX
XX 13-AUG-1998 (first entry)
XX
XX Telomerase substrate utilisation primer 22-24.
XX

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KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX GB2317891-A.
XX
XX 08-APR-1998.
PD
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
XX Example 1; Page 200; 387pp; English.
XX
XX The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX
XX Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20
Db |||||
29 TTTTGGGTTTGGGGTTT 48

RESULT 18
AAV17004
ID AAV17004 standard; DNA; 48 BP.
XX
XX AAV17004;
XX
XX 13-AUG-1998 (first entry)
XX

```

```
XX Telomerase substrate utilisation primer 13-15.
DE Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
XX Synthetic.
OS Homo sapiens.
XX GB2317891-A.
XX 08-APR-1998.
XX 01-OCT-1997; 97GB-00020890.
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX Example 1; Page 200; 387pp; English.
XX The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 20; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGGGTTTGGGGTTTT 20
DB 29 TTTTGGGTTTGGGGTTTT 48
RESULT 19
AAV17006
ID AAV17006 standard; DNA; 50 BP.
XX
```

```
AC AAV17006;
XX 13-AUG-1998 (first entry)
DE Telomerase substrate utilisation primer 19-21.
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
XX Synthetic.
OS Homo sapiens.
XX GB2317891-A.
XX 08-APR-1998.
XX 01-OCT-1997; 97GB-00020890.
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX Example 1; Page 200; 387pp; English.
XX The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX Sequence 50 BP; 12 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 20; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGGGTTTGGGGTTTT 20
DB 31 TTTTGGGTTTGGGGTTTT 50
RESULT 20
AAV17006
ID AAV17006 standard; DNA; 50 BP.
XX
```

ADP69702  
ID ADF69702 standard; DNA; 29 BP.  
XX  
AC ADF69702;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
XX Human HLTf methylation detection PCR primer.  
DE  
XX human; SLC5A8; cell surface protein; cytostatic; gene therapy;  
KW SLC5A8-associated cancer; colon cancer; breast cancer; thyroid cancer;  
KW stomach cancer; cancer; HLTf; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO2003104427-A2.  
XX  
XX 18-DEC-2003.  
PD  
XX 05-JUN-2003; 2003WO-US019239.  
PF  
XX 05-JUN-2002; 2002US-0386653P.  
PR  
XX (UYCA-) UNIV CASE WESTERN RESERVE.  
PA  
XX Markowitz SD;  
PI  
XX WPI; 2004-062348/06.  
DR  
XX New SLC5A8 polypeptide, useful for detecting and treating SLC5A8-  
PT associated cancer, e.g. colon, breast, thyroid or stomach cancer.  
XX  
XX Claim 77; Page 99; 207pp; English.  
PS  
XX The present invention describes the human SLC5A8 protein (I), which is a  
CC cell surface protein. (I) has cytostatic activity, and can be used in  
CC gene therapy. (I) can be used in detecting and treating SLC5A8-associated  
CC cancer, e.g. colon cancer, breast cancer, thyroid cancer or stomach  
CC cancer. (I) is also useful in screening assays, predictive medicine and  
CC in diagnostic and prognostic assays. The human SLC5A8 gene is located on  
CC chromosome 12. The present sequence is used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;  
Query Match 92.0%; Score 18.4; DB 12; Length 29;  
Best Local Similarity 95.0%; Pred. No. 2.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTT 20  
Db 3 TTTTGGGGTTTGGGGTTT 22  
RESULT 21  
ADV09385  
ID ADV09385 standard; DNA; 29 BP.  
XX  
AC ADV09385;  
XX  
DT 24-FEB-2005 (first entry)  
XX  
DE Human HLTf 5' unmethylated DNA amplifying PCR primer, P-HLTf1347UF.  
XX  
KW DNA methylation; HLTf; helicase-like transcription factor; HPI16a; Zbul;  
KW RUSHia; Smarca; proliferative disease; colon neoplasia; cytostatic; PCR;  
KW primer; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2004242510-A1.  
XX

PD 02-DEC-2004.  
XX  
PF 07-OCT-2002; 2002US-00266103.  
XX  
PR 05-OCT-2001; 2001US-0327537P.  
XX  
PA (MARK/) MARKOWITZ S D.  
XX  
PI Markowitz SD;  
XX  
DR WPI; 2005-011663/01.  
XX  
PT Detecting differential methylation patterns in an HLTf nucleotide  
PT sequence, useful for diagnosing or treating colon neoplasia, comprises  
PT assay samples for the presence of methylation within a specific  
PT nucleotide sequence.  
XX  
PS Example; SEQ ID NO 50; 117pp; English.  
XX  
CC The present invention relates to a method for detecting differential  
CC methylation patterns in an helicase-like transcription factor (HLTf, also  
CC called HPI16a, Zbul, RUSHia and Smarca) nucleotide sequence. The method  
CC involves obtaining samples from a patient and a healthy subject, assaying  
CC the samples for the presence of methylation within a nucleotide sequence  
CC and comparing the methylation patterns in the sample from the subject to  
CC those in the normal sample. HLTf modulator is useful for treating an HLTf  
CC -associated proliferative disease in a subject, where the disease is  
CC associated with methylation of an HLTf nucleic acid sequence, i.e. colon  
CC neoplasia and the compound induces HLTf expression. The method of the  
CC invention is useful in gene therapy. The present sequence is the human  
CC HLTf 5' unmethylated DNA fragment amplifying PCR primer.  
XX  
SQ Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;  
Query Match 92.0%; Score 18.4; DB 14; Length 29;  
Best Local Similarity 95.0%; Pred. No. 2.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTT 20  
Db 3 TTTTGGGGTTTGGGGTTT 22  
RESULT 22  
ADV09348  
ID ADV09348 standard; DNA; 29 BP.  
XX  
AC ADV09348;  
XX  
DT 24-FEB-2005 (first entry)  
XX  
DE Human HLTf unmethylated DNA amplifying forward PCR primer, 1347UF.  
XX  
KW DNA methylation; HLTf; helicase-like transcription factor; HPI16a; Zbul;  
KW RUSHia; Smarca; proliferative disease; colon neoplasia; cytostatic; PCR;  
KW primer; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2004242510-A1.  
XX  
PD 02-DEC-2004.  
XX  
PF 07-OCT-2002; 2002US-00266103.  
XX  
PR 05-OCT-2001; 2001US-0327537P.  
XX  
PA (MARK/) MARKOWITZ S D.  
XX  
PI Markowitz SD;  
XX  
DR WPI; 2005-011663/01.  
XX

PT Detecting differential methylation patterns in an HMTF nucleotide  
PT sequence, useful for diagnosing or treating colon neoplasia, comprises  
PT assay samples for the presence of methylation within a specific  
PT nucleotide sequence.

PS Claim 10; SEQ ID NO 13; 117pp; English.

XX The present invention relates to a method for detecting differential  
CC methylation patterns in an helicase-like transcription factor (HMTF, also  
CC called HPI16a, Zbul, RUSH1a and Smarca) nucleotide sequence. The method  
CC involves obtaining samples from a patient and a healthy subject, assaying  
CC the samples for the presence of methylation within a nucleotide sequence  
CC and comparing the methylation patterns in the sample from the subject to  
CC those in the normal sample. HMTF modulator is useful for treating an HMTF  
CC -associated proliferative disease in a subject, where the disease is  
CC associated with methylation of an HMTF nucleic acid sequence, i.e. colon  
CC neoplasia and the compound induces HMTF expression. The method of the  
CC invention is useful in gene therapy. The present sequence is the human  
CC HMTF unmethylated DNA amplifying PCR primer.

XX  
SQ Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 14; Length 29;  
Best Local Similarity 95.0%; Pred. No. 2.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTT 20  
|||||  
Db 3 TTTTGGGGTTTGGGGTTT 22  
|||||

RESULT 23  
AAT28342  
ID AAT28342 standard; DNA; 18 BP.

XX  
AC AAT28342;  
XX  
XX 20-NOV-1996 (first entry)  
XX  
DE Multi-G oligonucleotide T3-G4-T4-G4-T3.

XX Multi-G oligonucleotide; antisense sequence; c-myb; nuclease resistant;  
KW phosphorothioate linkage; phosphorodithioate linkage; inhibitor; therapy;  
KW cell proliferation; smooth muscle cell; proliferation protein;  
KW vascular restenosis; arterial restenosis; ss.

XX Synthetic.  
OS  
XX WO9611266-A2.  
XX  
XX 18-APR-1996.  
XX  
XX 03-OCT-1995; 95WO-US012770.  
XX  
XX 05-OCT-1994; 94US-00318458.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Burgess TL, Farrell CL, Fisher EF;  
XX  
XX WPI; 1996-209848/21.  
XX  
XX New modified oligo:nucleotide(s) contg. consecutive guanine residues -  
PT inhibit proliferation of smooth muscle cells, esp. to prevent arterial  
PT restenosis.

XX Example 6; Page 32; 67pp; English.

PS  
PS AAT28317-T28347 represent multi-G oligonucleotides. AAT28336-T28347 are  
CC multi-G oligonucleotides with multiple G strings, or G strings of 4 bases  
CC and over. These sequences are oligonucleotides of the invention. These  
CC sequences can be modified to become more nuclease resistant, using  
CC phosphorothioate, phosphorodithioate, or 3'-carbon modified links. To

CC screen for modified multi-G sequences that inhibit cell proliferation,  
CC cultured smooth muscle cells that are arrested in the G0 phase, are  
CC induced to proliferate in the presence of the multi-G sequence. The  
CC cultured smooth muscle cells used in this method are attached to a solid  
CC support, and growth arrest is achieved on a starvation medium, followed  
CC by transfer to a normal growth medium to induce proliferation. The  
CC compounds that provide over 50% inhibition at a set dosage are selected  
CC as being useful for inhibiting vascular restenosis. The multi-G  
CC oligonucleotides are used to inhibit proliferation of smooth muscle  
CC cells, such as to prevent arterial restenosis. These sequences are not  
CC antisense sequences, but are thought to work in a similar way. The  
CC sequences are thought to act by binding to proteins involved in the  
CC proliferation process. Compounds containing these multi-G  
CC oligonucleotides are not toxic, and their effect on cell proliferation is  
CC fully reversible

XX  
SQ Sequence 18 BP; 0 A; 0 C; 8 G; 10 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTTGGGGTTTGGGGTTT 19  
|||||  
Db 1 TTTGGGGTTTGGGGTTT 18  
|||||

RESULT 24  
AAV17006/C  
ID AAV17006 standard; DNA; 50 BP.

XX  
AC AAV17006;  
XX  
XX 13-AUG-1998 (first entry)  
XX  
DE Telomerase substrate utilisation primer 19-21.

XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;  
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.

XX Synthetic.  
OS  
XX Homo sapiens.  
XX  
XX GB2317891-A.  
XX  
XX 08-APR-1998.  
XX  
XX 01-OCT-1997; 97GB-00020890.  
XX  
XX 01-OCT-1996; 96US-00724643.  
XX 18-APR-1997; 97US-00844419.  
XX 25-APR-1997; 97US-00846017.  
XX 06-MAY-1997; 97US-00851843.  
XX 09-MAY-1997; 97US-00854050.  
XX 14-AUG-1997; 97US-00911312.  
XX 14-AUG-1997; 97US-00912951.  
XX 14-AUG-1997; 97US-00915503.  
XX  
XX (GERO-) GERON CORP.  
XX (UTTE-) UNIV TECHNOLOGY CORP.

XX  
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;  
XX Andrews WH;  
XX WPI; 1998-171633/16.  
XX  
XX Pure and recombinant human Telomerase Reverse Transcriptase and its  
PT variants - are useful in the diagnosis, prognosis and treatment of cell  
PT proliferation conditions especially cancer and ageing.

XX Example 1; Page 200; 387pp; English.

XX The present sequence represents a primer from the present invention which

CC describes human telomerase reverse transcriptase (hTERT). The present  
CC invention also describes the following methods: (A) determining whether a  
CC test compound is a modulator of hTERT, by detecting the change in hTERT  
CC recombinant protein or polynucleotide, on administration of the compound;  
CC (B) preparation of recombinant telomerase by contacting a protein  
CC preparation of hTERT with a telomerase RNA component; (C) detection of the  
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample  
CC and detecting the complex formed or in the case of RNA detection,  
CC amplifying the product and correlating the presence of complex or  
CC amplification product with presence of hTERT in the sample; and (D)  
CC increasing the proliferation of a vertebrate cell by increasing hTERT  
CC expression; and (E) the use of an agent that causes an increase in cell  
CC vertebrate cell proliferation to create a medicament that inhibits  
CC ageing. A protein preparation of hTERT and the polynucleotide encoding the  
CC hTERT can be used in the manufacture of medicaments for inhibiting the  
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used  
CC to treat conditions that are associated with high telomerase activity. A  
CC protein preparation of hTERT can also be used in the new methods  
XX  
SQ Sequence 50 BP; 12 A; 14 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 18  
Db 18 TTTTGGGGTTTGGGGTTT 1

RESULT 25  
AAQ44008  
ID AAQ44008 standard; DNA; 26 BP.  
XX  
AC AAQ44008;  
XX  
DT 25-MAR-2003 (revised)  
DT 28-OCT-1993 (first entry)  
XX  
DE Target sequence #4.  
XX  
KW Purine; pyrimidine; tracts; therapeutic; diagnostic; control;  
KW gene expression; mRNA synthesis suppression; ds.  
XX  
OS Synthetic.  
XX  
PN WO9312230-A1.  
XX  
PD 24-JUN-1993.  
XX  
PF 11-DEC-1992; 92WO-US010792.  
XX  
PR 13-DEC-1991; 91US-00808452.  
PR 21-JAN-1992; 92US-00826934.  
XX  
PA (STRI ) SRI INT.  
XX  
PI Jayasena SD, Johnston BH;  
XX  
XX WPI; 1993-214172/26.  
DR  
PT New oligo:nucleotide(s) forming triple helix with target nucleic acid -  
PT contain purine and pyrimidine tracts in specific orientations, useful  
PT therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.  
XX  
PS Example; Fig 14a; 101pp; English.

CC The sequence is that of the target sequence #4 which was used in an  
CC experiment to determine the in vitro cleavage of target duplexes to  
CC evaluate the lengths of purine and pyrimidine tracts which are useful in  
CC obtaining oligonucleotides capable of triple helix formation with target  
CC nucleic acids. The complementary strand overhangs the 3' end by the  
CC sequence CTAG and the sense strand overhangs the complementary strand by

CC the sequence AATT. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 26 BP; 2 A; 1 C; 13 G; 10 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 2; Length 26;  
Best Local Similarity 94.7%; Pred. No. 6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTTGGGGTTTGGGGTTT 20  
Db 3 TTTGGGGTTTGGGGTTT 21

RESULT 26  
AAQ04992  
ID AAQ04992 standard; DNA; 28 BP.  
XX  
AC AAQ04992;  
XX  
DT 25-MAR-2003 (revised)  
DT 31-OCT-1990 (first entry)  
XX  
DE Sequence binding to and inhibiting the gene controlling Alzheimer's  
DE disease plaque formation.  
XX  
KW C-myc; cancer; HIV-1; AIDS; collagenase; Alzheimers disease; EGF;  
KW epidermal growth factor; GSTpi; HMGCoA; thalassaemia;  
KW Herpes simplex virus; nerve growth factor receptor; globin; ss.  
XX  
OS Synthetic.  
XX  
PN EP375408-A.  
XX  
PD 27-JUN-1990.  
XX  
PF 20-DEC-1989; 89EP-00313391.  
XX  
PR 20-DEC-1988; 88US-00287359.  
XX  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (HOGA/) HOGAN M E.  
XX  
PI Hogan ME, Kessler DJ;  
XX  
XX WPI; 1990-195509/26.  
XX  
PT Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-  
PT linear triplex to control transcription process in gene-specific fashion.

Claim 35; Page 30; 40pp; English.  
XX  
CC Sequence forms triplex with the double stranded target sequence with G  
CC binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel  
CC orientation and when targeted to a specific sequence will deactivate it.  
CC This allows for growth inhibition in cancerous cells; manipulation of  
CC cellular structural protein content; inhibition of IL-2 chain receptor;  
CC disubursing plaque formation in Alzheimer's disease; inhibiting EGF gene;  
CC modulating cholesterol synthesis through the HMGCoA gene; suppressing NGF  
CC gene expression; arresting HSV-1 replication and suppressing Beta- globin  
CC expression in thalassaemia and sickle cell anaemia patients. (Updated on  
CC 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA  
CC field.)  
XX  
SQ Sequence 28 BP; 0 A; 0 C; 9 G; 19 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 2; Length 28;  
Best Local Similarity 90.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20  
Db 6 TTTTGGGGTTTGGGGTTT 25



```

RESULT 27
AAQ36268
ID AAQ36268 standard; DNA; 28 BP.
XX
AC AAQ36268;
XX
DT 25-MAR-2003 (revised)
DT 07-JUN-1993 (first entry)
XX
DE APP4par, targetted to a region of APP770 gene.
XX
KW Alzheimer's disease; amyloid precursor protein; plaque; triplex; target;
KW duplex; ss.
XX
OS Synthetic.
XX
PN US5176996-A.
XX
PD 05-JAN-1993.
XX
PF 22-DEC-1989; 89US-00453532.
XX
PR 20-DEC-1988; 88US-00287359.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI Hogan ME, Kessler DJ;
XX
WPI; 1993-035718/04.
XX
PT Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT which bind to target sequence in duplex DNA forming colinear triplex by
PT binding to major groove.
XX
PS Example 6; Col 22; 29pp; English.
XX
CC The APP770 gene is the precursor protein responsible for production of
CC plaque in Alzheimer's disease. Expression of this gene may be prevented
CC by the formation of a triplex between the duplex target DNA sequence and
CC an anti parallel or parallel synthetic oligonucleotide. A suitable target
CC sequence is that from base -434 to -407 of the APP770 gene and a suitable
CC antiparallel synthetic oligonucleotide sequence is shown. See also
CC AAQ36219-362. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 28 BP; 0 A; 0 C; 9 G; 19 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 2; Length 28;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
   ||||| ||||| |||||
Db 6 TTTTGGGGTTTGGGGTTT 25

RESULT 28
AAQ36269
ID AAQ36269 standard; DNA; 28 BP.
XX
AC AAQ36269;
XX
DT 25-MAR-2003 (revised)
DT 07-JUN-1993 (first entry)
XX
DE APP4anti, targetted to a region of APP770 gene.
XX
KW Alzheimer's disease; amyloid precursor protein; plaque; triplex; target;
KW 3'-5'; duplex; ss.
XX
OS Synthetic.
XX
PN US5176996-A.
XX

Query Match 84.0%; Score 16.8; DB 2; Length 28;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
   ||||| ||||| |||||
Db 6 TTTTGGGGTTTGGGGTTT 25

RESULT 29
AAV17009/c
ID AAV17009 standard; DNA; 44 BP.
XX
AC AAV17009;
XX
DT 13-AUG-1998 (first entry)
XX
DE Telomerase substrate utilisation primer 28-30.
XX
KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;

```

PI Andrews WH;  
 XX WPI; 1998-171633/16.  
 XX Pure and recombinant human Telomerase Reverse Transcriptase and its  
 PT variants - are useful in the diagnosis, prognosis and treatment of cell  
 PT proliferation conditions especially cancer and ageing.  
 XX Example 1; Page 200; 387pp; English.  
 XX The present sequence represents a primer from the present invention which  
 CC describes human telomerase reverse transcriptase (hTERT). The present  
 CC invention also describes the following methods: (A) determining whether a  
 CC test compound is a modulator of hTERT, by detecting the change in hTERT  
 CC recombinant protein or polynucleotide, on administration of the compound;  
 CC (B) preparation of recombinant telomerase by contacting a protein  
 CC preparation of hTERT with a telomerase RNA component; (C) detection of the  
 CC hTERT RNA or protein in a sample by binding a relevant probe to the sample  
 CC and detecting the complex formed or in the case of RNA detection,  
 CC amplifying the product and correlating the presence of complex or  
 CC increasing the proliferation of a vertebrate cell by increasing hTERT  
 CC expression; and (E) the use of an agent that causes an increase in cell  
 CC vertebrate cell proliferation to create a medicament that inhibits  
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding  
 CC hTERT can be used in the manufacture of medicaments for inhibiting the  
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be used  
 CC to treat conditions that are associated with high telomerase activity. A  
 CC protein preparation of hTERT can also be used in the new methods  
 XX Sequence 44 BP; 10 A; 10 C; 12 G; 12 T; 0 U; 0 Other;  
 SQ Query Match 84.0%; Score 16.8; DB 2; Length 44;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTTTT 20  
 Db 20 TGTGGGGTTTGGGGTTTT 1  
 RESULT 30  
 AAV17008/c  
 ID AAV17008 standard; DNA; 46 BP.  
 XX AC AAV17008;  
 XX DT 13-AUG-1998 (first entry)  
 XX DE Telomerase substrate utilisation primer 25-27.  
 XX KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;  
 KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX PN GB2317891-A.  
 XX PD 08-APR-1998.  
 XX PF 01-OCT-1997; 97GB-00020890.  
 XX PR 01-OCT-1996; 96US-00724643.  
 PR 18-APR-1997; 97US-00844419.  
 PR 25-APR-1997; 97US-00846017.  
 PR 06-MAY-1997; 97US-00851843.  
 PR 14-AUG-1997; 97US-00911312.  
 PR 14-AUG-1997; 97US-00912951.  
 PR 14-AUG-1997; 97US-00915503.  
 XX (GERO-) GERON CORP.

PA (UYTE-) UNIV TECHNOLOGY CORP.  
 XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;  
 PI Andrews WH;  
 XX WPI; 1998-171633/16.  
 DR Pure and recombinant human Telomerase Reverse Transcriptase and its  
 XX variants - are useful in the diagnosis, prognosis and treatment of cell  
 PT proliferation conditions especially cancer and ageing.  
 XX Example 1; Page 200; 387pp; English.  
 XX The present sequence represents a primer from the present invention which  
 CC describes human telomerase reverse transcriptase (hTERT). The present  
 CC invention also describes the following methods: (A) determining whether a  
 CC test compound is a modulator of hTERT, by detecting the change in hTERT  
 CC recombinant protein or polynucleotide, on administration of the compound;  
 CC (B) preparation of recombinant telomerase by contacting a protein  
 CC preparation of hTERT with a telomerase RNA component; (C) detection of the  
 CC hTERT RNA or protein in a sample by binding a relevant probe to the sample  
 CC and detecting the complex formed or in the case of RNA detection,  
 CC amplifying the product and correlating the presence of complex or  
 CC increasing the proliferation of a vertebrate cell by increasing hTERT  
 CC expression; and (E) the use of an agent that causes an increase in cell  
 CC vertebrate cell proliferation to create a medicament that inhibits  
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding  
 CC hTERT can be used in the manufacture of medicaments for inhibiting the  
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be used  
 CC to treat conditions that are associated with high telomerase activity. A  
 CC protein preparation of hTERT can also be used in the new methods  
 XX Sequence 46 BP; 10 A; 12 C; 12 G; 12 T; 0 U; 0 Other;  
 SQ Query Match 84.0%; Score 16.8; DB 2; Length 46;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTTTT 20  
 Db 22 TGTGGGGTTTGGGGTTTT 3  
 RESULT 31  
 AAV17007/c  
 ID AAV17007 standard; DNA; 48 BP.  
 XX AC AAV17007;  
 XX DT 13-AUG-1998 (first entry)  
 XX DE Telomerase substrate utilisation primer 22-24.  
 XX KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;  
 KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX PN GB2317891-A.  
 XX PD 08-APR-1998.  
 XX PF 01-OCT-1997; 97GB-00020890.  
 XX PR 01-OCT-1996; 96US-00724643.  
 PR 18-APR-1997; 97US-00844419.  
 PR 25-APR-1997; 97US-00846017.  
 PR 06-MAY-1997; 97US-00851843.  
 PR 09-MAY-1997; 97US-00854050.  
 PR 14-AUG-1997; 97US-00911312.  
 PR 14-AUG-1997; 97US-00912951.  
 PR 14-AUG-1997; 97US-00912951.

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PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
XX Example 1; Page 200; 387pp; English.
XX
XX The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX
XX Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
SQ
Query Match 84.0%; Score 16.8; DB 2; Length 48;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
Db | | | | | | | | | | | | | | | | | |
24 TGTGGGGTTTGGGGTTT 5

RESULT 32
AAV17004/c
ID AAV17004 standard; DNA; 48 BP.
XX
XX AAV17004;
XX
XX 13-AUG-1998 (first entry)
XX
XX Telomerase substrate utilisation primer 13-15.
XX
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
XX
XX Synthetic.
OS
OS Homo sapiens.
XX
XX GB2317891-A.
PN
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR

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PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
XX Example 1; Page 200; 387pp; English.
XX
XX The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX
XX Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
SQ
Query Match 84.0%; Score 16.8; DB 2; Length 48;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
Db | | | | | | | | | | | | | | | | | |
24 TGTGGGGTTTGGGGTTT 5

RESULT 33
ABZ05743
ID ABZ05743 standard; DNA; 50 BP.
XX
XX ABZ05743;
XX
XX 09-JAN-2003 (first entry)
XX
XX Human leukocyte gene expression profiling probe SEQ ID NO 5734.
DE
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
XX Homo sapiens.
OS
XX WO200257414-A2.
PN
XX
XX 25-JUL-2002.
PD
XX 22-OCT-2001; 2001WO-US047856.
PF
XX

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PR 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quettermous T, Johnson F;
XX
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 513; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
XX Sequence 50 BP; 6 A; 6 C; 20 G; 18 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 6; Length 50;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 14 TGTGGGGTTTGGGGTTTT 33

RESULT 34
AAA39694/c
ID AAA39694 standard; DNA; 20 BP.
XX
XX AAA39694;
AC
XX 18-SEP-2000 (first entry)
XX
XX S. lemnae alpha-tubulin telomerase primer DNA.
XX
XX Regulatory sequence; eukaryotic protist; telomere; alpha-tubulin; primer;
KW ss.
XX
XX Stylonychia lemnae.
XX
XX WO200023604-A1.
XX
XX 27-APR-2000.
XX
XX 20-OCT-1999; 99WO-BP007958.
XX
XX 21-OCT-1998; 98DE-01048485.
XX
XX 21-OCT-1998; 98DE-01048486.
XX
XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
XX Gallert K, Huels C, Muellner S, Steinbrueck G, Jacob NK;
XX
XX WPI; 2000-339703/29.
XX
XX Expression vector functional in eukaryotic protist, useful for expression
PT of heterologous proteins, contains a coding sequence and regulatory
PT flanking regions from a protist.

us-09-669-187a-73.szlm50.rng
Claim 4; Page 45; 51pp; German.
XX
XX This invention describes a novel expression vector (A) for eukaryotic
CC protists comprises a sequence (I) encoding a protein and having, at its
CC 3' and 5'-ends, native flanking regulatory sequences (RS) selected from
CC Stylonychia lemnae and with terminal telomeric sequences. (A) are used
CC for production of proteins in protists, particularly functional
CC heterologous proteins. (A) provide overexpression of foreign proteins in
CC protists, e.g. at 7-15% of total proteins. Eukaryotic protists can be
CC grown simply and on a large scale to high cell density with short
CC generation times and have metabolic and other properties similar to those
CC of multicellular organisms (contrast prokaryotes). In the macronucleus
CC genome of protists, most genes are amplified, resulting in high
CC expression rates even under normal conditions. This sequence represents a
CC primer used in the construction of the expression vector described in the
CC invention
XX
XX Sequence 20 BP; 8 A; 12 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGG 16
Db 16 TTTTGGGGTTTGGGG 1

RESULT 35
AAA39699/c
ID AAA39699 standard; DNA; 30 BP.
XX
XX AAA39699;
AC
XX 18-SEP-2000 (first entry)
XX
XX S. lemnae expression vector construct primer XbaApatel.
XX
XX Regulatory sequence; eukaryotic protist; telomere; primer; ss.
XX
XX Stylonychia lemnae.
XX
XX WO200023604-A1.
XX
XX 27-APR-2000.
XX
XX 20-OCT-1999; 99WO-BP007958.
XX
XX 21-OCT-1998; 98DE-01048485.
XX
XX 21-OCT-1998; 98DE-01048486.
XX
XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
XX Gallert K, Huels C, Muellner S, Steinbrueck G, Jacob NK;
XX
XX WPI; 2000-339703/29.
XX
XX Expression vector functional in eukaryotic protist, useful for expression
PT of heterologous proteins, contains a coding sequence and regulatory
PT flanking regions from a protist.

Example 1; Page 27; 51pp; German.
XX
XX This invention describes a novel expression vector (A) for eukaryotic
CC protists comprises a sequence (I) encoding a protein and having, at its
CC 3' and 5'-ends, native flanking regulatory sequences (RS) selected from
CC Stylonychia lemnae and with terminal telomeric sequences. (A) are used
CC for production of proteins in protists, particularly functional
CC heterologous proteins. (A) provide overexpression of foreign proteins in
CC protists, e.g. at 7-15% of total proteins. Eukaryotic protists can be
CC grown simply and on a large scale to high cell density with short
CC generation times and have metabolic and other properties similar to those
```

CC of multicellular organisms (contrast prokaryotes). In the macronucleus  
CC genome of protists, most genes are amplified, resulting in high  
CC expression rates even under normal conditions. This sequence represents a  
CC primer used in the construction of the expression vector described in the  
CC invention  
XX

SQ Sequence 30 BP; 10 A; 13 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 80.0%; Score 16; DB 3; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGG 16  
|||||  
Db 28 TTTTGGGGTTTGGG 13

RESULT 36  
ADV45884/c  
ID ADV45884 standard; DNA; 19 BP.  
XX  
AC ADV45884;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE Human CpG site probe SEQ ID NO 1411.  
XX  
DE DNA methylation; ss; probe; cancer; neoplasm; squamous cell carcinoma.  
XX  
OS Homo sapiens.  
XX  
PN WC2004110246-A2.  
XX  
PD 23-DEC-2004.  
XX  
PF 14-MAY-2004; 2004WO-US015382.  
XX  
PR 15-MAY-2003; 2003US-0471488P.  
XX  
PA (ILLU-) ILLUMINA INC.  
XX  
PI Fan J, Bibikova M;  
XX  
DR WPI; 2005-057693/06.  
XX

PS Identifying differentially methylated genomic CpG dinucleotide sequences  
PT associated with cancer, comprises measuring level of methylated genomic  
PT CpG dinucleotide sequences for genomic targets in sample and comparing to  
PT reference level.  
XX  
PS Claim 28; SEQ ID NO 1411; 89pp; English.  
XX

CC The invention relates to a method of identifying differentially  
CC methylated genomic CpG dinucleotide sequences associated with cancer,  
CC comprising measuring the level of methylated genomic CpG dinucleotide  
CC sequences for two or more of the genomic targets in sample, and comparing  
CC the level of methylation at genomic CpG dinucleotide sequences in the  
CC sample to a reference level of methylated genomic CpG dinucleotide  
CC sequences. The method is useful for identifying differentially methylated  
CC genomic CpG dinucleotide sequences associated with cancer in an  
CC individual. The level of methylation of the differentially methylated  
CC genomic CpG dinucleotide sequences is used to diagnose cancer in the  
CC individual, predict the course of cancer, predict the susceptibility of  
CC cancer, stage the progression of cancer, predict the likelihood of  
CC overall survival, and predict the likelihood of recurrence of cancer for  
CC individual. The level of methylation of the differentially methylated  
CC genomic CpG dinucleotide sequences in the sample is also used to  
CC determine the effectiveness of a treatment course undergone by the  
CC individual. The cancer is preferably adenocarcinoma or squamous cell  
CC carcinoma. The probes are useful for detecting methylation of genomic CpG  
CC dinucleotide sequences of two or more genomic targets. The present  
XX sequence represents a CpG site probe.

SQ Sequence 19 BP; 11 A; 8 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 77.0%; Score 15.4; DB 14; Length 19;  
Best Local Similarity 94.1%; Pred. No. 3.9e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTGGGGTTT 20  
|||||  
Db 19 TGGGGTTTGGGGTTT 3

RESULT 37  
ACF58129  
ID ACF58129 standard; DNA; 43 BP.  
XX  
AC ACF58129;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE HMTF non-methylation-specific PCR forward primer.  
XX  
KW Disease diagnostic; CpG; nucleic acid amplification; cancer detection;  
KW p14; HMTF; MINT31; MINT2; methylation; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WC2003087390-A2.  
XX  
PD 23-OCT-2003.  
XX  
PF 11-APR-2003; 2003WO-US011023.  
XX  
PR 11-APR-2002; 2002US-00123071.  
XX  
PA (EXAC-) EXACT SCI CORP.  
XX  
PI Shuber AP;  
XX  
DR WPI; 2003-845337/78.  
XX

PT Detecting an indicium of a disease in a heterogeneous biological sample  
PT comprises contacting the nucleic acid sample with an agent that modifies  
PT unmethylated cytosine, and detecting hypermethylated or hypomethylated  
PT nucleic acid.  
XX

PS Example 4; Page 17; Opp; English.  
XX

CC The invention relates to detecting an indicium of a disease in a  
CC heterogeneous biological sample. The method involves (a) isolating a  
CC heterogeneous nucleic-acid sample comprising a CpG-containing target  
CC template from a heterogeneous biological sample; (b) contacting the  
CC nucleic acid sample with an agent that modifies unmethylated cytosine;  
CC (c) performing an amplification reaction on the target template using at  
CC least one chimeric primer that comprises a first portion that is not  
CC specific for the target template and a second portion 3' to the first  
CC portion, where the second portion is specific for the CpG-containing  
CC target template if the template comprises an unmethylated cytosine at a  
CC predetermined position; and (d) detecting the presence of an  
CC amplification product as an indicium of a disease. The method is useful  
CC for detecting indicia of cancer in a biological sample, for detecting  
CC abnormal methylation in a homogenous sample, such as a biopsy sample. The  
CC method is especially suitable in clinical assays involving sporadic  
CC cancer detection, for infectious disease diagnostics, or inherited  
CC disease diagnostics. The new method makes it possible to detect a disease  
CC in a biological sample without using an invasive procedure. Sequences  
CC ACF58127-134 represent non-methylation-specific primer used for PCR  
CC assaying of hypermethylation markers on genes p14, HMTF, MINT31 and  
CC MINT2, used in detection of hypermethylation at multiple loci, which  
CC indicate a higher risk of colorectal cancer  
XX

SQ Sequence 43 BP; 4 A; 5 C; 16 G; 18 T; 0 U; 0 Other;  
Query Match 77.0%; Score 15.4; DB 10; Length 43;

Best Local Similarity 94.1%; Pred. No. 4e+03; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTGGGGTTT 20  
 |||||  
 Db 20 TGGGGTTTGGGGTTT 36

RESULT 38  
 ADW84828/c  
 ID ADW84828 standard; DNA; 20 BP.  
 AC ADW84828;  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE MAP3K9 marker amplification reverse primer #1146.  
 DE  
 DE mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9;  
 KW antiasthmatic; respiratory-gen.; antiinflammatory; antirheumatic;  
 KW antiarthritic; antipsoriatic; neuroprotective; gastrointestinal-gen.;  
 KW respiratory disease; chronic obstructive pulmonary disease;  
 KW chronic bronchitis; inflammation; ss; primer; PCR.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2005007144-A2.  
 XX  
 PD 27-JAN-2005.  
 XX  
 PF 14-JUL-2004; 2004WO-US022446.  
 XX  
 PR 14-JUL-2003; 2003US-0487072P.  
 PR 05-APR-2004; 2004US-0559611P.  
 XX  
 PA (DECO-) DECODE GENETICS EHF.  
 XX  
 PI Hakonarson H, Gurney ME, Halapi E;  
 XX  
 DR WPI; 2005-122681/13.  
 XX  
 PT Use of mixed lineage kinase family kinase inhibitor in the manufacture of  
 PT a medicament for treatment of asthma associated at-risk haplotype for  
 PT asthma, at-risk haplotype in MAP3K9 gene or increased MLK1 protein  
 PT expression or activity.  
 XX  
 PS Disclosure; Fig 12; 640pp; English.  
 XX  
 CC The invention relates to the novel use of a mixed lineage kinase (MLK)  
 CC family kinase inhibitor for treating asthma. Where the asthma is  
 CC associated with a risk factor selected from an at-risk haplotype for  
 CC asthma, at-risk haplotype in MAP3K9 gene, polymorphism in MAP3K9 nucleic  
 CC acid, dysregulation of MAP3K9 mRNA expression, dysregulation of a MAP3K9  
 CC mRNA isoform, and/or increased MLK1 protein expression. The invention  
 CC further comprises: a method for the diagnosis or identification of  
 CC susceptibility to asthma; a method for the use of a first nucleic acid  
 CC molecule for diagnosing asthma or susceptibility to asthma in a sample; a  
 CC sample; a method for assessing the presence of a first nucleic acid molecule in a  
 CC sample; a method for assessing the response to treatment with an MLK  
 CC family kinase nucleic acid inhibitor in a target population or in an  
 CC individual with an at-risk haplotype for asthma, at-risk haplotype in the  
 CC MAP3K9 gene, polymorphism in the MAP3K9 nucleic acid, dysregulation of  
 CC MAP3K9 mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased  
 CC MLK1 protein expression, increased MLK1 biochemical activity or increased  
 CC MLK1 protein isoform expression; a method for assessing the response to  
 CC treatment with an MLK1 inhibitor in a target population including an  
 CC individual with an at-risk haplotype for asthma, as above; a kit for  
 CC assaying a sample for the presence or absence of at least one haplotype  
 CC comprising 2 or more alleles associated with asthma comprising: at least  
 CC one nucleic acid capable of detecting the presence or absence of at least  
 CC one specific allele; a reagent kit for assaying the presence of at least  
 CC one haplotype comprising 2 or more alleles comprising: at least one  
 CC labeled nucleic acid capable of detecting at least one specific allele of

CC the haplotype, and reagents for detection of the label; and a reagent kit  
 CC for assaying a sample for the presence of at least one haplotype  
 CC comprising 2 or more alleles comprising: at least one nucleic acid  
 CC comprising at least one nucleotide sequence that is at least partially  
 CC complementary to a part of nucleotide sequence of MAP3K9, capable of  
 CC acting as a primer for a primer extension reaction and capable of  
 CC detecting 2 or more specific alleles of the haplotype. The MLK family  
 CC kinase inhibitor has the following activities: antiasthmatic, respiratory  
 CC -gen., antiinflammatory, antirheumatic, antiarthritic, antipsoriatic,  
 CC neuroprotective, and gastrointestinal-gen. The MLK family kinase  
 CC inhibitor is useful for the treatment of asthma associated with a risk  
 CC factor selected from at-risk haplotype for asthma, at-risk haplotype in  
 CC MAP3K9 gene, polymorphism in MAP3K9 nucleic acid, dysregulation of MAP3K9  
 CC mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased MLK1  
 CC protein expression, increased MLK1 biochemical activity and/or increased  
 CC MLK1 protein isoform expression; and in diagnosis or identification of  
 CC susceptibility to asthma. The inhibitor is also useful for the treatment  
 CC of other respiratory diseases associated with MAP3K9 or other members of  
 CC the JNK pathway such as chronic obstructive pulmonary disease, chronic  
 CC bronchitis and other inflammatory diseases such as rheumatoid arthritis,  
 CC psoriasis, multiple sclerosis and inflammatory bowel disease. This  
 CC polynucleotide sequence represents a reverse primer which is used in  
 CC amplifying a marker of the MAP3K9 kinase, where MAP3K9 is a part of  
 CC Mitogen-Activated Protein Kinase (MAPK) signal transduction pathways, of  
 CC the invention.  
 XX  
 SQ Sequence 20 BP; 11 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 14; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 4.7e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20  
 |||||  
 Db 20 TTTTGGGTTTGGGGATT 1

RESULT 39  
 AEA51773  
 ID AEA51773 standard; DNA; 22 BP.  
 XX  
 AC AEA51773;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Prostate cancer gene PCR primer SEQ ID NO 376.  
 XX  
 KW gene expression; cell proliferation; hyperproliferation; cytostatic;  
 KW neoplasm; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005054517-A2.  
 XX  
 PD 16-JUN-2005.  
 XX  
 PF 01-DEC-2004; 2004WO-US040289.  
 XX  
 PR 01-DEC-2003; 2003EP-00090414.  
 PR 10-FEB-2004; 2004EP-00090040.  
 PR 10-MAY-2004; 2004EP-00090187.  
 PR 21-JUL-2004; 2004EP-00090292.  
 XX  
 PA (EPIC-) EPICENOMICS AG.  
 XX  
 PI Day KJ, Cottrell S, Distler J, Morotti A, Yamamura S, Dekker S;  
 PI Ocamp Y, Devos T;  
 XX  
 DR WPI; 2005-425434/43.  
 XX  
 PT Detecting and/or differentiating prostate cell proliferative disorders in  
 PT a subject by contacting genomic with reagent(s) that distinguishes  
 PT between methylated and non-methylated CpG dinucleotides in target nucleic



```
QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 2 TTTAGGGGTTTAGGGGTTT 21

RESULT 42
ABZ01038
ID ABZ01038 standard; DNA; 50 BP.
XX
AC ABZ01038;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 1029.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quertermous T, Johnson F;
DR WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 357; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 13 A; 6 C; 14 G; 17 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 6; Length 50;
Best Local Similarity 85.0%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 9 TTTTGTATTGGGGTTTT 28

RESULT 43
AAF99500
ID AAF99500 standard; DNA; 24 BP.
XX
AC AAF99500;
XX
```

```
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #616.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026389.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 52; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 24 BP; 0 A; 0 C; 7 G; 17 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 4; Length 24;
Best Local Similarity 88.9%; Pred. No. 6.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 18
Db 7 TTTTGTGGTTTGTGGTT 24

RESULT 44
AAF99678
ID AAF99678 standard; DNA; 24 BP.
XX
AC AAF99678;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #794.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW
```



KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 OS Synthetic.  
 XX  
 XX WO200122972-A2.  
 PN  
 XX  
 XX 05-APR-2001.  
 PD  
 XX  
 XX 25-SEP-2000; 2000WO-US026383.  
 PF  
 XX  
 XX 25-SEP-1999; 99US-0156113P.  
 PR  
 XX 27-SEP-1999; 99US-0156135P.  
 PR  
 XX 23-AUG-2000; 2000US-0227436P.  
 PR  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 PA  
 XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 DR  
 XX  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 PT  
 XX  
 XX Claim 101; Page 55; 338pp; English.  
 PS  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 XX Sequence 24 BP; 0 A; 2 C; 8 G; 14 T; 0 U; 0 Other;  
 SQ Query Match 74.0%; Score 14.8; DB 4; Length 24;  
 Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTT 18  
 Db ||||| ||||| ||||| |||||  
 7 TTTTGGGGTTTGGGGTT 24  
 RESULT 45  
 AAF99498  
 ID AAF99498 standard; DNA; 24 BP.  
 XX  
 XX AAF99498;  
 AC  
 XX  
 XX 12-JUN-2001 (first entry)  
 DT  
 XX Immunostimulatory nucleic acid #614.  
 DE  
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200122972-A2.  
 PN  
 XX 05-APR-2001.  
 PD  
 XX

PF 25-SEP-2000; 2000WO-US026383.  
 XX  
 XX 25-SEP-1999; 99US-0156113P.  
 PR  
 XX 27-SEP-1999; 99US-0156135P.  
 PR  
 XX 23-AUG-2000; 2000US-0227436P.  
 PR  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 PA  
 XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 DR  
 XX  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 PT  
 XX  
 XX Claim 101; Page 52; 338pp; English.  
 PS  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 XX Sequence 24 BP; 0 A; 1 C; 7 G; 16 T; 0 U; 0 Other;  
 SQ Query Match 74.0%; Score 14.8; DB 4; Length 24;  
 Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTT 18  
 Db ||||| ||||| ||||| |||||  
 7 TTTTGGGGTTTGGGGTT 24  
 RESULT 46  
 AAF61386  
 ID AAF61386 standard; DNA; 24 BP.  
 XX  
 XX AAF61386;  
 AC  
 XX  
 XX 04-JUN-2001 (first entry)  
 DT  
 XX Strand displacement amplification reporter primer SEQ ID 4.  
 DE  
 XX Strand displacement amplification; primer; detection; probe; reporter;  
 KW fluorescent donor; quencher dye; ss.  
 KW  
 XX Unidentified.  
 OS  
 XX EP1087020-A2.  
 PN  
 XX 28-MAR-2001.  
 PD  
 XX 23-AUG-2000; 2000EP-00118032.  
 PF  
 XX 27-SEP-1999; 99US-00406074.  
 PR  
 XX (BECT ) BECTON DICKINSON & CO.  
 PA  
 XX Nadeau JG, Linn CP, Pitner JB, Dean CH, Walker GT;  
 PI WPI; 2001-259636/27.  
 XX  
 XX

PT Novel signal primer for detecting nucleic acid target sequences by  
PT fluorescence quenching mechanisms, comprising a reporter probe and an  
PT adaptor oligonucleotide hybridized to the probe.  
XX  
XX  
PS Example 2; Page 11; 16pp; English.  
XX  
CC This invention describes a novel signal primer (I) comprising a reporter  
CC probe (II) and an adapter oligonucleotide (III) hybridized to (II), such  
CC that (I) comprises intermolecularly base-paired portion and a single-  
CC stranded target binding sequence. (I) comprises (II), which in the  
CC absence of hybridization to a complementary sequence assumes a  
CC conformational structure which brings a fluorescent donor/quencher dye  
CC pair linked to it into sufficiently close spatial proximity to quench  
CC donor fluorescence, and an adapter oligonucleotide (III) hybridized to  
CC (II), such that (I) comprises an intermolecularly base-paired portion and  
CC a single-stranded target binding sequence. (I) is useful for detecting a  
CC nucleic acid target sequence: (I) by: (a) hybridizing with the target  
CC sequence such that formation of a secondary structure is substantially  
CC prevented; (b) separating (II) from (III) in a target-dependent manner;  
CC and (c) detecting the formation of secondary structure as an indication  
CC of the presence of the target sequence; or (2) by: (a) hybridizing (I) to  
CC the target sequence, where (I) comprises an adapter oligonucleotide  
CC hybridized to a second oligonucleotide complementary to (I) which forms a  
CC secondary structure when not hybridized to a complementary sequence; (b)  
CC separating the second oligonucleotide from (III) in a target-dependent  
CC manner; and (c) detecting the hybridization of second oligonucleotide to  
CC (I) as an indication of the presence of target sequence. Detection of a  
CC variety of different targets is simplified as the adapter polynucleotide  
CC to which the second oligonucleotide hybridizes comprises a sequence which  
CC does not hybridize to the target, as a result the 5' adapter sequence may  
CC be selected such that it is the same in a variety of adapter  
CC oligonucleotides with different target binding sequences. A single  
CC labeled reporter probe may be used for detection of a variety of  
CC different target sequences. The adapter oligonucleotides are easier, and  
CC less costly, to synthesize than reporter probes as they do not require  
CC labeling for use  
XX  
XX  
SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;  
Query Match 74.0%; Score 14.8; DB 5; Length 24;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 TTTGGGGTTTGGGTTT 19  
||| ||||| ||||| |||||  
Db 4 TTTGGGGTTTGGGTTT 21  
RESULT 47  
ABS78208  
ID ABS78208 standard; DNA; 24 BP.  
XX  
XX  
AC ABS78208;  
XX  
XX  
DT 13-DEC-2002 (first entry)  
DE  
DE Angiogenesis inhibitory oligonucleotide #692.  
XX  
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX  
XX Synthetic.  
OS  
XX WO200253141-A2.  
PN  
XX 11-JUL-2002.  
PD  
XX

PF 14-DEC-2001; 2001WO-US048458.  
XX  
PR 14-DEC-2000; 2000US-0255534P.  
XX  
XX (COLE-) COLEY PHARM GROUP INC.  
XX  
XX Bratzler RL;  
PI  
XX WPI; 2002-566690/60.  
DR  
XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.  
XX  
PS Claim 2; Page 31; 276pp; English.  
XX  
CC The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
XX  
SQ Sequence 24 BP; 0 A; 1 C; 7 G; 16 T; 0 U; 0 Other;  
Query Match 74.0%; Score 14.8; DB 6; Length 24;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGTTT 18  
||||| ||||| ||||| |||||  
Db 7 TTTTGGGGTTTGGGTTT 24  
RESULT 48  
ABS78399  
ID ABS78399 standard; DNA; 24 BP.  
XX  
XX  
AC ABS78399;  
XX  
XX  
DT 13-DEC-2002 (first entry)  
DE  
DE Angiogenesis inhibitory oligonucleotide #883.  
XX  
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX  
XX Synthetic.  
OS  
XX WO200253141-A2.  
PN  
XX 11-JUL-2002.  
PD  
XX  
PF 14-DEC-2001; 2001WO-US048458.  
XX  
PR 14-DEC-2000; 2000US-0255534P.  
XX  
XX (COLE-) COLEY PHARM GROUP INC.  
XX  
XX Bratzler RL;  
PI

XX WPI; 2002-566690/60.  
XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.  
XX Claim 2; Page 35; 276pp; English.  
XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
SQ Sequence 24 BP; 0 A; 2 C; 8 G; 14 T; 0 U; 0 Other;  
Query Match 74.0%; Score 14.8; DB 6; Length 24;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGTTT 18  
DB 7 TTTTGGGTTTGGGTTT 24  
RESULT 49  
ABS78210  
ID ABS78210 standard; DNA; 24 BP.  
XX  
AC ABS78210;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Angiogenesis inhibitory oligonucleotide #694.  
XX  
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX  
OS Synthetic.  
XX  
XX WO200253141-A2.  
XX  
PN 11-JUL-2002.  
XX  
PD 14-DEC-2001; 2001WO-US048458.  
XX  
PF 14-DEC-2000; 2000US-0255534P.  
XX  
PR (COLE-) COLEY PHARM GROUP INC.  
XX  
PA Bratzler RL;  
XX  
PI WPI; 2002-566690/60.  
XX  
DR Inhibiting angiogenesis in a subject, involves administering at least one  
XX antiangiogenic nucleic acid molecule to the subject.  
PT Claim 2; Page 31; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
SQ Sequence 24 BP; 0 A; 0 C; 7 G; 17 T; 0 U; 0 Other;  
Query Match 74.0%; Score 14.8; DB 6; Length 24;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGTTT 18  
DB 7 TTTTGGGTTTGGGTTT 24  
RESULT 50  
ABL39306  
ID ABL39306 standard; DNA; 24 BP.  
XX  
AC ABL39306;  
XX  
DT 16-APR-2002 (first entry)  
XX  
DE Immunostimulatory nucleic acid SEQ ID NO: 735.  
XX  
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..24  
FT /\*tag= a  
FT /mcd\_base= OTHER  
FT /note= "phosphorothioate backbone"  
XX WO200197843-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 22-JUN-2001; 2001WO-US020154.  
XX  
PR 22-JUN-2000; 2000US-0213346P.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Weiner G, Hartmann G;  
XX  
DR WPI; 2002-154611/20.  
XX  
PT Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.  
XX  
PS Disclosure; Page 283; 312pp; English.  
XX  
CC The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for

CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention  
XX  
SQ Sequence 24 BP; 0 A; 2 C; 8 G; 14 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 6; Length 24;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTTT 18  
      |||||  
Db 7 TTTTGGGTTTGGGTTT 24

Search completed: February 15, 2006, 18:06:46  
Job time : 161.744 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:07:43 ; Search time 1330.25 Seconds  
(without alignments)  
703.434 Million cell updates/sec

Title: US-09-669-187A-73

Perfect score: 20

Sequence: 1 ttttggggtttgggggtttt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_est4:\*

5: gb\_est5:\*

6: gb\_est6:\*

7: gb\_est7:\*

8: gb\_est8:\*

9: gb\_est9:\*

10: gb\_est10:\*

11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 16.8  | 84.0        | 37     | 6  | CF301952 7LEAF--07 |
| 2          | 16    | 80.0        | 37     | 1  | AA916364 OG29B09.5 |
| 3          | 16    | 80.0        | 43     | 1  | AI813791 WK79F07.X |
| 4          | 15.2  | 76.0        | 31     | 1  | AI468834 t142d08.x |
| 5          | 14.8  | 74.0        | 31     | 10 | AL756692 Arabidops |
| 6          | 14.8  | 74.0        | 32     | 9  | AZ794869 2M0048017 |
| 7          | 14.4  | 72.0        | 27     | 9  | AZ807733 2M0070H16 |
| 8          | 14.4  | 72.0        | 39     | 10 | AJ590961 Arabidops |
| 9          | 14.4  | 72.0        | 40     | 1  | AI671079 t217H03.X |
| 10         | 14.4  | 72.0        | 46     | 1  | AI264859 gx66h12.x |
| 11         | 14.4  | 72.0        | 46     | 1  | AI564592 tp98d09.x |
| 12         | 14.4  | 72.0        | 48     | 10 | CZ918128 4021008B1 |
| 13         | 14.4  | 72.0        | 49     | 1  | AI475390 t182g01.x |
| 14         | 14.4  | 72.0        | 49     | 10 | AL943577 Arabidops |
| 15         | 14.4  | 72.0        | 50     | 10 | CZ559680 PL00447-5 |
| 16         | 14.2  | 71.0        | 33     | 10 | BX535866 Arabidops |
| 17         | 14.2  | 71.0        | 37     | 11 | DR63F21T           |
| 18         | 14.2  | 71.0        | 43     | 10 | CG722753 1119073D0 |
| 19         | 14.2  | 71.0        | 50     | 10 | CZ470781 C06535-5D |
| 20         | 14.2  | 71.0        | 50     | 10 | CG729919 111911E50 |
| 21         | 13.8  | 69.0        | 31     | 10 | AL940076 Arabidops |
| 22         | 13.8  | 69.0        | 46     | 8  | H71330 yu55d08.s1  |

|          |            |    |    |           |      |      |    |      |      |    |    |           |
|----------|------------|----|----|-----------|------|------|----|------|------|----|----|-----------|
| AZ774479 | 2M0004A05  | 33 | 9  | AZ774479  | 68.0 | 13.6 | 23 | 13.6 | 68.0 | 33 | 9  | AZ774479  |
| AI018534 | ou24h12.x  | 37 | 1  | AI018534  | 68.0 | 13.6 | 24 | 13.6 | 68.0 | 37 | 1  | AI018534  |
| AI446151 | tj07e11.x  | 37 | 1  | AI446151  | 68.0 | 13.6 | 25 | 13.6 | 68.0 | 37 | 1  | AI446151  |
| BE974781 | 601680831  | 38 | 2  | BE974781  | 68.0 | 13.6 | 26 | 13.6 | 68.0 | 38 | 2  | BE974781  |
| CF295607 | 30DGS--05  | 39 | 6  | CF295607  | 68.0 | 13.6 | 27 | 13.6 | 68.0 | 39 | 6  | CF295607  |
| AZ579518 | 1M0367G03  | 42 | 9  | AZ579518  | 68.0 | 13.6 | 28 | 13.6 | 68.0 | 42 | 9  | AZ579518  |
| BX946019 | Arabidops  | 42 | 10 | BX946019  | 68.0 | 13.6 | 29 | 13.6 | 68.0 | 42 | 10 | BX946019  |
| AI442438 | sa26h06.Y  | 43 | 1  | AI442438  | 68.0 | 13.6 | 30 | 13.6 | 68.0 | 43 | 1  | AI442438  |
| AZ634906 | 1M0490P20  | 43 | 9  | AZ634906  | 68.0 | 13.6 | 31 | 13.6 | 68.0 | 43 | 9  | AZ634906  |
| CZ472331 | d01604-3P  | 43 | 10 | CZ472331  | 68.0 | 13.6 | 32 | 13.6 | 68.0 | 43 | 10 | CZ472331  |
| CF300934 | 7LEAF--05  | 44 | 6  | CF300934  | 68.0 | 13.6 | 33 | 13.6 | 68.0 | 44 | 6  | CF300934  |
| AZ476389 | 1M0295E09  | 44 | 9  | AZ476389  | 68.0 | 13.6 | 34 | 13.6 | 68.0 | 44 | 9  | AZ476389  |
| CF298361 | 7LEAF--01  | 45 | 6  | CF298361  | 68.0 | 13.6 | 35 | 13.6 | 68.0 | 45 | 6  | CF298361  |
| AZ751963 | APHL3SD-X  | 45 | 7  | CN751963  | 68.0 | 13.6 | 36 | 13.6 | 68.0 | 45 | 7  | CN751963  |
| AZ786064 | 2M0030G22  | 46 | 9  | AZ786064  | 68.0 | 13.6 | 37 | 13.6 | 68.0 | 46 | 9  | AZ786064  |
| AA959573 | ub54h01.s  | 49 | 1  | AA959573  | 68.0 | 13.6 | 39 | 13.6 | 68.0 | 49 | 1  | AA959573  |
| BX171071 | Danio rer  | 50 | 10 | BX171071  | 68.0 | 13.6 | 40 | 13.6 | 68.0 | 50 | 10 | BX171071  |
| AL465643 | T. brucei  | 24 | 11 | TX131805Q | 67.0 | 13.4 | 41 | 13.4 | 67.0 | 24 | 11 | TX131805Q |
| CZ916406 | 4021001C1  | 30 | 10 | CZ916406  | 67.0 | 13.4 | 42 | 13.4 | 67.0 | 30 | 10 | CZ916406  |
| AI439312 | t159e12.x  | 34 | 1  | AI439312  | 67.0 | 13.4 | 43 | 13.4 | 67.0 | 34 | 1  | AI439312  |
| AI280814 | qw11e03.x  | 37 | 1  | AI280814  | 67.0 | 13.4 | 44 | 13.4 | 67.0 | 37 | 1  | AI280814  |
| AI865173 | wk09b01.x  | 49 | 1  | AI865173  | 67.0 | 13.4 | 45 | 13.4 | 67.0 | 49 | 1  | AI865173  |
| AZ761211 | 1M0553I22  | 22 | 9  | AZ761211  | 66.0 | 13.2 | 46 | 13.2 | 66.0 | 22 | 9  | AZ761211  |
| AJ590891 | Arabidops  | 24 | 10 | AJ590891  | 66.0 | 13.2 | 47 | 13.2 | 66.0 | 24 | 10 | AJ590891  |
| AZ59683  | 1M0352C18  | 37 | 9  | AZ59683   | 66.0 | 13.2 | 48 | 13.2 | 66.0 | 37 | 9  | AZ59683   |
| BX120037 | Danio rer  | 40 | 10 | BX120037  | 66.0 | 13.2 | 49 | 13.2 | 66.0 | 40 | 10 | BX120037  |
| AL944738 | Arabidops  | 41 | 10 | AL944738  | 66.0 | 13.2 | 50 | 13.2 | 66.0 | 41 | 10 | AL944738  |
| AA903096 | ok46f02.s  | 43 | 1  | AA903096  | 66.0 | 13.2 | 51 | 13.2 | 66.0 | 43 | 1  | AA903096  |
| AQ074129 | EP(X)1612  | 44 | 9  | AQ074129  | 66.0 | 13.2 | 52 | 13.2 | 66.0 | 44 | 9  | AQ074129  |
| CD534193 | 36C18 Ara  | 50 | 6  | CD534193  | 66.0 | 13.2 | 53 | 13.2 | 66.0 | 50 | 6  | CD534193  |
| AU012010 | AU012010   | 38 | 1  | AU012010  | 65.0 | 13   | 54 | 13.2 | 66.0 | 38 | 1  | AU012010  |
| AI473924 | tm04a11.x  | 40 | 1  | AI473924  | 65.0 | 13   | 55 | 13   | 65.0 | 40 | 1  | AI473924  |
| AI442798 | sa26f09.x  | 25 | 1  | AI442798  | 64.0 | 12.8 | 56 | 12.8 | 64.0 | 25 | 1  | AI442798  |
| AA910220 | oj29e06.s  | 34 | 1  | AA910220  | 64.0 | 12.8 | 57 | 12.8 | 64.0 | 34 | 1  | AA910220  |
| AZ787308 | 2M0033B21  | 35 | 6  | AZ787308  | 64.0 | 12.8 | 58 | 12.8 | 64.0 | 35 | 6  | AZ787308  |
| CF298926 | 7LEAF--02  | 37 | 1  | AI803262  | 64.0 | 12.8 | 59 | 12.8 | 64.0 | 37 | 1  | AI803262  |
| AI803262 | tc38h12.x  | 37 | 1  | AI803262  | 64.0 | 12.8 | 60 | 12.8 | 64.0 | 37 | 1  | AI803262  |
| AI184834 | wk67e06.x  | 37 | 10 | AJ587236  | 64.0 | 12.8 | 61 | 12.8 | 64.0 | 37 | 10 | AJ587236  |
| AJ587236 | Arabidops  | 37 | 10 | AJ587236  | 64.0 | 12.8 | 62 | 12.8 | 64.0 | 37 | 10 | AJ587236  |
| AI678633 | tu84h12.x  | 40 | 1  | AI678633  | 64.0 | 12.8 | 63 | 12.8 | 64.0 | 40 | 1  | AI678633  |
| AI188640 | qd15f04.x  | 43 | 1  | AI188640  | 64.0 | 12.8 | 64 | 12.8 | 64.0 | 43 | 1  | AI188640  |
| AZ637149 | 1M0496F19  | 43 | 9  | AZ637149  | 64.0 | 12.8 | 65 | 12.8 | 64.0 | 43 | 9  | AZ637149  |
| AL451639 | T. brucei  | 43 | 11 | TA11A10P  | 64.0 | 12.8 | 66 | 12.8 | 64.0 | 43 | 11 | TA11A10P  |
| AI654317 | tg90c04.x  | 49 | 1  | AI654317  | 64.0 | 12.8 | 67 | 12.8 | 64.0 | 49 | 1  | AI654317  |
| BH814653 | SALK 0667  | 49 | 9  | BH814653  | 64.0 | 12.8 | 68 | 12.8 | 64.0 | 49 | 9  | BH814653  |
| AI215622 | ql18G09.x  | 50 | 1  | AI215622  | 64.0 | 12.8 | 69 | 12.8 | 64.0 | 50 | 1  | AI215622  |
| CF319590 | HD--10-C1  | 21 | 6  | CF319590  | 63.0 | 12.6 | 70 | 12.6 | 63.0 | 21 | 6  | CF319590  |
| AZ452777 | 1M0252N14  | 22 | 9  | AZ452777  | 63.0 | 12.6 | 71 | 12.6 | 63.0 | 22 | 9  | AZ452777  |
| AZ830405 | 2M0109F12  | 25 | 9  | AZ830405  | 63.0 | 12.6 | 72 | 12.6 | 63.0 | 25 | 9  | AZ830405  |
| AZ345475 | 1M0080P10  | 26 | 9  | AZ345475  | 63.0 | 12.6 | 73 | 12.6 | 63.0 | 26 | 9  | AZ345475  |
| AZ599962 | 1M0416N01  | 29 | 9  | AZ599962  | 63.0 | 12.6 | 74 | 12.6 | 63.0 | 29 | 9  | AZ599962  |
| AZ761587 | 1M0556B04  | 29 | 10 | AZ761587  | 63.0 | 12.6 | 75 | 12.6 | 63.0 | 29 | 10 | AZ761587  |
| CZ907959 | 4018001C0  | 29 | 10 | CZ907959  | 63.0 | 12.6 | 76 | 12.6 | 63.0 | 29 | 10 | CZ907959  |
| AZ505954 | 1M0346E24  | 31 | 9  | AZ505954  | 63.0 | 12.6 | 77 | 12.6 | 63.0 | 31 | 9  | AZ505954  |
| AU258912 | AU258912   | 33 | 1  | AU258912  | 63.0 | 12.6 | 78 | 12.6 | 63.0 | 33 | 1  | AU258912  |
| AA907684 | om11e03.s  | 34 | 1  | AA907684  | 63.0 | 12.6 | 79 | 12.6 | 63.0 | 34 | 1  | AA907684  |
| AV963838 | AV963838   | 34 | 1  | AV963838  | 63.0 | 12.6 | 80 | 12.6 | 63.0 | 34 | 1  | AV963838  |
| AZ834104 | 2M0116G09  | 35 | 9  | AZ834104  | 63.0 | 12.6 | 81 | 12.6 | 63.0 | 35 | 9  | AZ834104  |
| AJ587667 | Arabidops  | 36 | 10 | AJ587667  | 63.0 | 12.6 | 82 | 12.6 | 63.0 | 36 | 10 | AJ587667  |
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| AI367571 | ty99g08.x  | 37 | 1  | AI367571  | 63.0 | 12.6 | 84 | 12.6 | 63.0 | 37 | 1  | AI367571  |
| AZ813933 | 2M0081J23  | 37 | 9  | AZ813933  | 63.0 | 12.6 | 85 | 12.6 | 63.0 | 37 | 9  | AZ813933  |
| AV965852 | AV965852   | 38 | 1  | AV965852  | 63.0 | 12.6 | 86 | 12.6 | 63.0 | 38 | 1  | AV965852  |
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| AL985601 | Danio rer  | 40 | 11 | DR43017S  | 63.0 | 12.6 | 89 | 12.6 | 63.0 | 40 | 11 | DR43017S  |
| AZ620116 | tu92g02.x  | 43 | 9  | AZ620116  | 63.0 | 12.6 | 90 | 12.6 | 63.0 | 43 | 9  | AZ620116  |
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| 96    | 12.6 | 63.0 | 46 | 1  | AV966826  | AV966826  | AV966826    | 169   | 12   | 60.0 | 39 | 1  | AL041218 | AL041218   | DKF2p434J |
| c 97  | 12.6 | 63.0 | 47 | 9  | CC897341  | CC897341  | SALK_1500   | 170   | 12   | 60.0 | 39 | 1  | AV949716 | AV949716   | AV949716  |
| c 98  | 12.6 | 63.0 | 48 | 3  | BJ040279  | BJ040279  | BJ040279    | 171   | 12   | 60.0 | 39 | 1  | AV767935 | AV767935   | IM0567B12 |
| c 99  | 12.6 | 63.0 | 49 | 8  | D20657    | D20657    | HUMGS01633  | c 172 | 12   | 60.0 | 39 | 11 | DR42B18T | DR42B18T   | AL974899  |
| c 100 | 12.6 | 63.0 | 49 | 9  | BH855874  | BH855874  | SALK_0844   | c 173 | 12   | 60.0 | 40 | 1  | AI362383 | qu55h04.x  | Danio rer |
| c 101 | 12.6 | 63.0 | 50 | 1  | AU107052  | AU107052  | AU107052    | c 174 | 12   | 60.0 | 40 | 1  | AI362383 | qu55h04.x  | AI362383  |
| c 102 | 12.6 | 63.0 | 50 | 1  | AU107060  | AU107060  | AU107060    | c 175 | 12   | 60.0 | 40 | 9  | BH146179 | BG02782-5  | BH146179  |
| c 103 | 12.6 | 63.0 | 50 | 3  | BM069725  | BM069725  | ie88d07.y   | c 176 | 12   | 60.0 | 40 | 10 | C2484867 | f02361-5p  | C2484867  |
| c 104 | 12.6 | 63.0 | 50 | 6  | CA339922  | CA339922  | NISC_ly09   | c 177 | 12   | 60.0 | 40 | 10 | BX127424 | Danio rer  | BX127424  |
| c 105 | 12.4 | 62.0 | 19 | 1  | AI641650  | AI641650  | fc228d01.x  | c 178 | 12   | 60.0 | 41 | 9  | AZ655083 | IM0529C19  | AZ655083  |
| c 106 | 12.4 | 62.0 | 25 | 9  | AZ377955  | AZ377955  | IM0132F05   | c 179 | 12   | 60.0 | 41 | 10 | BX242916 | Danio rer  | BX242916  |
| c 107 | 12.4 | 62.0 | 34 | 1  | AA932536  | AA932536  | co64e08.s   | c 180 | 12   | 60.0 | 42 | 9  | AZ625468 | IM0464N22  | AZ625468  |
| c 108 | 12.4 | 62.0 | 42 | 8  | DN955340  | DN955340  | ie86b08.g   | c 181 | 12   | 60.0 | 42 | 10 | BX163193 | Danio rer  | BX163193  |
| c 109 | 12.4 | 62.0 | 46 | 1  | AI719194  | AI719194  | at06h08.x   | c 182 | 12   | 60.0 | 43 | 1  | AA878752 | of85d03.s  | AA878752  |
| c 110 | 12.4 | 62.0 | 49 | 9  | AZ579577  | AZ579577  | IM0357M09   | c 183 | 12   | 60.0 | 43 | 7  | CN546803 | EST_18574  | CN546803  |
| c 111 | 12.2 | 61.0 | 23 | 9  | AZ779474  | AZ779474  | 2M0015N19   | c 184 | 12   | 60.0 | 44 | 9  | AZ433032 | IM0218M12  | AZ433032  |
| c 112 | 12.2 | 61.0 | 26 | 5  | C21526    | C21526    | HUMGS001052 | c 185 | 12   | 60.0 | 44 | 9  | AZ504238 | IM0344A23  | AZ504238  |
| c 113 | 12.2 | 61.0 | 29 | 9  | AZ414397  | AZ414397  | IM0188L15   | c 186 | 12   | 60.0 | 45 | 2  | BE336369 | 601086943  | BE336369  |
| c 114 | 12.2 | 61.0 | 30 | 9  | AZ513419  | AZ513419  | IM0359E24   | c 187 | 12   | 60.0 | 45 | 9  | BH853498 | SALK_0770  | BH853498  |
| c 115 | 12.2 | 61.0 | 30 | 10 | CZ489705  | CZ489705  | f06962-5p   | c 188 | 12   | 60.0 | 45 | 10 | AJ598952 | Arabidops  | AJ598952  |
| c 116 | 12.2 | 61.0 | 31 | 1  | AA937745  | AA937745  | o101e10.s   | c 189 | 12   | 60.0 | 45 | 10 | BX219077 | Danio rer  | BX219077  |
| c 117 | 12.2 | 61.0 | 31 | 1  | AI768947  | AI768947  | WG03909.x   | c 190 | 12   | 60.0 | 46 | 1  | AI223398 | qx12h07.x  | AI223398  |
| c 118 | 12.2 | 61.0 | 33 | 9  | AZ320037  | AZ320037  | IM0039G22   | c 191 | 12   | 60.0 | 46 | 1  | AI471447 | Em11F04.x  | AI471447  |
| c 119 | 12.2 | 61.0 | 38 | 9  | BZ291479  | BZ291479  | SALK_1208   | c 192 | 12   | 60.0 | 46 | 1  | AI749628 | at25d10.x  | AI749628  |
| c 120 | 12.2 | 61.0 | 39 | 9  | CC057363  | CC057363  | SALK_1408   | c 193 | 12   | 60.0 | 46 | 9  | AZ767539 | IM0566H17  | AZ767539  |
| c 121 | 12.2 | 61.0 | 40 | 1  | AA876140  | AA876140  | ob93H05.s   | c 194 | 12   | 60.0 | 47 | 9  | AZ639767 | IM0501K24  | AZ639767  |
| c 122 | 12.2 | 61.0 | 40 | 10 | BX227306  | BX227306  | Danio rer   | c 195 | 12   | 60.0 | 47 | 10 | BX121950 | Danio rer  | BX121950  |
| c 123 | 12.2 | 61.0 | 41 | 9  | BH861613  | BH861613  | SALK_0876   | c 196 | 12   | 60.0 | 48 | 1  | AJ663146 | AJ663146   | AJ663146  |
| c 124 | 12.2 | 61.0 | 42 | 9  | BH791460  | BH791460  | SALK_0599   | c 197 | 12   | 60.0 | 48 | 9  | AZ514368 | IM0361D04  | AZ514368  |
| c 125 | 12.2 | 61.0 | 43 | 9  | AZ860401  | AZ860401  | 2M0166E22   | c 198 | 12   | 60.0 | 48 | 9  | BZ354073 | SALK_1225  | BZ354073  |
| c 126 | 12.2 | 61.0 | 45 | 10 | CZ469757  | CZ469757  | co5130-3p   | c 199 | 12   | 60.0 | 49 | 1  | AA954745 | on56804.s  | AA954745  |
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| c 128 | 12.2 | 61.0 | 48 | 9  | AZ949234  | AZ949234  | 2M0212D07   | c 201 | 12   | 60.0 | 49 | 1  | AI587491 | tr51d10.x  | AI587491  |
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| c 131 | 12.2 | 61.0 | 50 | 1  | AU104045  | AU104045  | IM0104045   | c 204 | 12   | 60.0 | 49 | 10 | CZ490512 | f07777-5p  | CZ490512  |
| c 132 | 12.2 | 61.0 | 50 | 1  | AW643187  | AW643187  | cm27a03.w   | c 205 | 12   | 60.0 | 50 | 1  | AU103941 | AU103941   | AU103941  |
| c 133 | 12   | 60.0 | 19 | 1  | AA9248820 | AA9248820 | 2821008.3   | c 206 | 12   | 60.0 | 50 | 1  | AU107056 | AU107056   | AU107056  |
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| c 135 | 12   | 60.0 | 22 | 9  | AZ844290  | AZ844290  | 2M0143A10   | c 208 | 12   | 60.0 | 50 | 2  | BE887296 | 601510120  | BE887296  |
| c 136 | 12   | 60.0 | 25 | 2  | BG24523   | BG24523   | HNC27-1-G   | c 209 | 12   | 60.0 | 50 | 3  | BQ125541 | ec69f06.y  | BQ125541  |
| c 137 | 12   | 60.0 | 25 | 10 | AJ590986  | AJ590986  | Arabidops   | c 210 | 12   | 60.0 | 50 | 5  | BX274604 | BX274604   | BX274604  |
| c 138 | 12   | 60.0 | 26 | 1  | AI288386  | AI288386  | gv85c01.x   | c 211 | 12   | 60.0 | 50 | 3  | BZ378836 | SALK_1120  | BZ378836  |
| c 139 | 12   | 60.0 | 28 | 1  | AI288386  | AI288386  | fv85c01.x   | c 212 | 12   | 60.0 | 50 | 10 | AL948306 | Arabidops  | AL948306  |
| c 140 | 12   | 60.0 | 28 | 1  | AI376644  | AI376644  | te63b01.x   | c 213 | 12   | 60.0 | 50 | 10 | BX198108 | Danio rer  | BX198108  |
| c 141 | 12   | 60.0 | 28 | 11 | T3236A02P | T3236A02P | T_brucei    | c 214 | 12   | 60.0 | 50 | 11 | CF155014 | Forward s  | CF155014  |
| c 142 | 12   | 60.0 | 29 | 10 | AJ589262  | AJ589262  | Arabidops   | c 215 | 11.8 | 59.0 | 21 | 9  | AZ447989 | IM0245J19  | AZ447989  |
| c 143 | 12   | 60.0 | 30 | 5  | BX569324  | BX569324  | EX569324    | c 216 | 11.8 | 59.0 | 21 | 9  | AZ991107 | 2M0275E08  | AZ991107  |
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| c 148 | 12   | 60.0 | 32 | 1  | AV959908  | AV959908  | AV959908    | c 221 | 11.8 | 59.0 | 31 | 1  | AI560864 | tq4aa06.x  | AI560864  |
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| c 152 | 12   | 60.0 | 33 | 10 | CG711881  | CG711881  | 1119023B0   | c 225 | 11.8 | 59.0 | 37 | 1  | AI401219 | tf60g11.x  | AI401219  |
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| c 154 | 12   | 60.0 | 34 | 1  | AI174461  | AI174461  | an46f02.s   | c 227 | 11.8 | 59.0 | 37 | 2  | BG569157 | 602588418  | BG569157  |
| c 155 | 12   | 60.0 | 34 | 9  | CC053791  | CC053791  | SALK_0485   | c 228 | 11.8 | 59.0 | 37 | 10 | AL751513 | Arabidops  | AL751513  |
| c 156 | 12   | 60.0 | 35 | 9  | AZ308581  | AZ308581  | IM0011011   | c 229 | 11.8 | 59.0 | 37 | 10 | BX662468 | Arabidops  | BX662468  |
| c 157 | 12   | 60.0 | 35 | 9  | BZ664505  | BZ664505  | SALK_0757   | c 230 | 11.8 | 59.0 | 38 | 9  | AZ504168 | IM0344E13  | AZ504168  |
| c 158 | 12   | 60.0 | 35 | 10 | CZ484272  | CZ484272  | f01797-3p   | c 231 | 11.8 | 59.0 | 40 | 10 | BX200119 | Danio rer  | BX200119  |
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| c 162 | 12   | 60.0 | 37 | 1  | AI440016  | AI440016  | tk19e08.x   | c 235 | 11.8 | 59.0 | 45 | 1  | AU256617 | AU256617   | AU256617  |
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| c 164 | 12   | 60.0 | 37 | 8  | DR907951  | DR907951  | CCSEN05F0   | c 237 | 11.8 | 59.0 | 45 | 9  | CC796721 | SALK_1369  | CC796721  |
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ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)  
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
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Location/Qualifiers  
1..37  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="7LEAF--07-A07"  
/issue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 84.0%; Score 16.8; DB 6; Length 37;  
Best Local Similarity 90.0%; Pred. No. 1.4e+04;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 TTTTGGGTTTGGGTTT 20  
|||||  
12 TTTTGGGTTTGGGTTT 31

AA916364 37 bp mRNA linear EST 29-APR-1998  
cg29b09.s1 NCI CGAP Br7 Homo sapiens cDNA clone IMAGE:1441241.3,  
similar to TR:Q29427 Q29427 PROLINE-RICH PROTEIN.; mRNA sequence.

AA916364 1 GI:3055756  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 37)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
Trace considered overall poor quality  
Insert Length: 1205 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..37  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1441241"

RESULT 1  
CF301952  
LOCUS  
DEFINITION  
CF301952.1 GI:33673713  
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-A07, mRNA  
sequence.  
ACCESSION  
VERSION  
KEYWORDS

ALIGNMENTS

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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Bx7"
/notes="Organ: breast; Vector: pCMV-SPORT4; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.2 kb. Life Technologies catalog
#:10985-018"

ORIGIN

Query Match      80.0%; Score 16; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGGTTTGGGGTTT 20
    |||||
Db 34 GGGGTTTGGGGTTT 19
    |||||

RESULT 3
AI813791/c
LOCUS
DEFINITION
wk79f07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2421637.3.
similar to TR:000599 000599 CON1.; contains element MSRI repetitive
element ;, mRNA sequence.
ACCESSION      AI813791
VERSION        AI813791.1 GI:5425006
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 43)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 831 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2421637"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pan1"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN

Query Match      80.0%; Score 16; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGGTTTGGGGTTT 20
    |||||
Db 34 GGGGTTTGGGGTTT 19
    |||||

RESULT 4
AI813791/c
LOCUS
DEFINITION
wk79f07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2421637.3.
similar to TR:000599 000599 CON1.; contains element MSRI repetitive
element ;, mRNA sequence.
ACCESSION      AI813791
VERSION        AI813791.1 GI:5425006
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 43)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 831 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2421637"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pan1"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN

Query Match      76.0%; Score 15.2; DB 1; Length 31;
Best Local Similarity 85.0%; Pred. No. 5.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
    |||||
Db 21 TTTTGGGGTTTGGGGTTT 2
    |||||

RESULT 5
AL756692
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-111H11-012331,
genomic survey sequence.
ACCESSION      AL756692
VERSION        AL756692.1 GI:21489190
KEYWORDS
SOURCE
ORGANISM      Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1
AUTHORS
Li Y., Rosso M.G., Strizhov N., Viehoever P. and Weisshaar B.
TITLE
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
```



```

JOURNAL      Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED      12874060
REFERENCE
AUTHORS      Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
              Weisshaar, B.
TITLE        An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
              flanking sequence tag-based reverse genetics
JOURNAL      Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED      14756321
REFERENCE
AUTHORS      Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
              Weisshaar, B.
TITLE        High-throughput generation of sequence indexes from T-DNA
              mutagenized Arabidopsis thaliana lines
JOURNAL      Biotechniques 35 (6), 1164-1168 (2003)
PUBMED      14682050
REFERENCE
AUTHORS      Rosso, M.G., Li, Y., Strizhov, N. and Weisshaar, B.
TITLE        Direct Submission
COMMENT      Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
              Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
              This sequence has been recovered from the right border of the
              T-DNA. It indicates an insertion close to or within gene At1g17190.
              Details on the protocols used for generation of the sequence are
              described in References 1-3. The sequences are generated at the MPI
              for Plant Breeding Research in the context of the GABI-Kat project.
              GABI-Kat is part of the German Plant Genomics program designated
              'GABI'. Information on line availability can be found at:
              http://www.mpiz-koeln.mpg.de/GABI-Kat/.
              Location/Qualifiers
FEATURES
    source
        1..31
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /db_xref="taxon:3702"
            /clone="GK-111H1-012331"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            /ecotype="Col-0"
            /notes="PCR was performed on DNA from Arabidopsis thaliana
            plants (rt) which were transformed with the T-DNA from
            vector pAC161 (Genbank accession number: AJ537514). The
            lines contain one or more T-DNA insertions. The DNA
            fragment(s) resulting from the PCR were directly sequenced
            to determine the genomic sequence flanking the insertion.
            T-DNA derived sequences were removed."
ORIGIN
Query Match      74.0%; Score 14.8; DB 10; Length 31;
Best Local Similarity 88.9%; Pred. No. 8.3e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 TTGGGGTTTGGGGTTT 20
Db      11 TTAGGGTTTAGGGTTT 28

RESULT 6
AZ794869
LOCUS      2M0048017R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0048017 R, genomic survey sequence.
ACCESSION  AZ794869
VERSION     AZ794869.1 GI:12941283
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 32)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.

JOURNAL      Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED      12874060
REFERENCE
AUTHORS      Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
              Weisshaar, B.
TITLE        An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
              flanking sequence tag-based reverse genetics
JOURNAL      Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED      14756321
REFERENCE
AUTHORS      Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
              Weisshaar, B.
TITLE        High-throughput generation of sequence indexes from T-DNA
              mutagenized Arabidopsis thaliana lines
JOURNAL      Biotechniques 35 (6), 1164-1168 (2003)
PUBMED      14682050
REFERENCE
AUTHORS      Rosso, M.G., Li, Y., Strizhov, N. and Weisshaar, B.
TITLE        Direct Submission
COMMENT      Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
              Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
              This sequence has been recovered from the right border of the
              T-DNA. It indicates an insertion close to or within gene At1g17190.
              Details on the protocols used for generation of the sequence are
              described in References 1-3. The sequences are generated at the MPI
              for Plant Breeding Research in the context of the GABI-Kat project.
              GABI-Kat is part of the German Plant Genomics program designated
              'GABI'. Information on line availability can be found at:
              http://www.mpiz-koeln.mpg.de/GABI-Kat/.
              Location/Qualifiers
FEATURES
    source
        1..32
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0048017"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /notes="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
ORIGIN
Query Match      74.0%; Score 14.8; DB 9; Length 32;
Best Local Similarity 88.9%; Pred. No. 8.3e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TTTTGGGGTTTGGGGTTT 18
Db      7 TTTTGGGGTTTGGGGTTT 24

RESULT 7
AZ807733
LOCUS      2M0070H16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0070H16 R, genomic survey sequence.
ACCESSION  AZ807733
VERSION     AZ807733.1 GI:12972374
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 27)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.

```

**TITLE**  
Niederhausern,A. and Wright,D.,Weiss,P.  
Mouse whole genome scaffolding with paired end reads from 10kb  
Plasmid inserts  
Unpublished (2000)  
**JOURNAL**  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0070 row: H column: 16  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.

**FEATURES**  
source  
1. .27  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0070H16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Cold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb Plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|3732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

**ORIGIN**  
Query Match 72.0%; Score 14.4; DB 9; Length 27;  
Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 1 TTTTGGGTTTGGGG 16  
|||||  
**Db** 12 TTTTGGGTTTGGGG 27  
|||||

**RESULT 8**  
AJ590961  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
577E03, genomic survey sequence.  
ACCESSION  
AJ590961.1 GI:37940585  
VERSION  
GSS; left border; T-DNA flanking sequence.  
KEYWORDS  
Arabidopsis thaliana (thale cress)  
SOURCE  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
1 Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,

Lepiniec,L., Caboche,M. and Lecharny,A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)  
12446565  
**REFERENCE**  
2 (bases 1 to 39)  
Balzergue,S.  
**AUTHORS**  
Direct Submission  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
http://dbgap.versailles.inra.fr/publiclines/. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.inbiolegen.fr).  
**FEATURES**  
source  
1. .39  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="577E03"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Wassilewskija"  
misc\_feature 1. .39  
/note="T-DNA flanking sequence  
left border"

**ORIGIN**  
Query Match 72.0%; Score 14.4; DB 10; Length 39;  
Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 5 GGGGTTTTGGGTTTT 20  
|||||  
**Db** 4 GAGGTTTTGGGTTTT 19  
|||||

**RESULT 9**  
AI671079  
LOCUS  
DEFINITION  
tzi17h03.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:228885 3,  
similar to TR:000599 000599 CON1.; contains element MER22  
repetitive element ;, mRNA sequence.  
ACCESSION  
AI671079  
VERSION  
AI671079.1 GI:4850810  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarctontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 40)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
**AUTHORS**  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
**TITLE**  
Unpublished (1997)  
**JOURNAL**  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Insert Length: 1514 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

#### FEATURES

source  
 1. .40  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:228885"  
 /tissue\_type="moderately-differentiated endometrial  
 adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.85 kb. Life Technologies catalog #:  
 11539-012"

#### ORIGIN

Query Match 72.0%; Score 14.4; DB 1; Length 40;  
 Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGG 16  
 ||||| |||||  
 Db 38 TTTTGGGTTTGGGG 23

#### RESULT 10

AI264859  
 LOCUS  
 DEFINITION  
 QX66h12.x1 NCI CGAP Ov36 Homo sapiens cDNA clone IMAGE:2006375 3'  
 similar to SW:NPX\_HUMAN P55769 NHP2/RS6 FAMILY PROTEIN YEL026W  
 HOMOLOG ;, mRNA sequence.

#### ACCESSION

AI264859  
 VERSION  
 AI264859.1 GI:3873062  
 EST.

#### KEYWORDS

SOURCE  
 Homo sapiens (human)

#### ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.

#### REFERENCE

1 (bases 1 to 46)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

#### JOURNAL

COMMENT  
 Unpublished (1997)

Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb@mail.nih.gov  
 CDNA Library Preparation: David B. Krizman, Ph.D.  
 CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Insert Length: 200 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

#### FEATURES

source  
 1. .46  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2006375"  
 /sex="female"  
 /tissue\_type="borderline ovarian carcinoma"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ov36"  
 /note="Organ: ovary; Vector: pAMP1; mRNA made from

#### ORIGIN

Query Match 72.0%; Score 14.4; DB 1; Length 46;  
 Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGG 16  
 ||||| |||||  
 Db 29 TTTTGGGTTTGGGG 44

#### RESULT 11

AI564592/c  
 LOCUS  
 DEFINITION  
 tp98d09.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2207345 3'  
 similar to SW:PRP3\_MOUSE P05143 PROLINE-RICH PROTEIN MP-3 ;, mRNA  
 sequence.

#### ACCESSION

AI564592  
 VERSION  
 AI564592.1 GI:4523049  
 EST.

#### KEYWORDS

SOURCE  
 Homo sapiens (human)

#### ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.

#### REFERENCE

1 (bases 1 to 46)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

#### JOURNAL

COMMENT  
 Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 2382 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

#### FEATURES

source

1. .46  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2207345"  
 /tissue\_type="poorly-differentiated endometrial  
 adenocarcinoma 2 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut3"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.45 kb. Life Technologies catalog #:  
 11541-018"

#### ORIGIN

Query Match 72.0%; Score 14.4; DB 1; Length 46;  
 Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGG 16  
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 Db 20 TTTTGGGTTTGGGG 5

|                       |   |         |                        |                   |       |      |        |     |             |
|-----------------------|---|---------|------------------------|-------------------|-------|------|--------|-----|-------------|
| RESULT 12             | CZ918128  | LOCUS   | 4021008B10.1EL.Y1 4021 | - RescueMu Grid V | 48 bp | DNA  | linear | GSS | 08-AUG-2005 |
| DEFINITION            | survey sequence.  |         |                        |                   |       |      |        |     |             |
| ACCESSION             | CZ918128  | VERSION | CZ918128.1             | GI:71937386       |       |      |        |     |             |
| KEYWORDS              | GSS.  |         |                        |                   |       |      |        |     |             |
| SOURCE                | Zea mays  |         |                        |                   |       |      |        |     |             |
| ORGANISM              | Zea mays  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Walbot,V.   |         |                        |                   |       |      |        |     |             |
| TITLE                 | Maize genomic sequences found using engineered RescueMu transposon  |         |                        |                   |       |      |        |     |             |
| JOURNAL               | Unpublished (2001)  |         |                        |                   |       |      |        |     |             |
| COMMENT               | Contact: Walbot V<br>Department of Biological Sciences<br>Stanford University<br>855 California Ave, Palo Alto, CA 94304, USA<br>Tel: 650 723 2227<br>Fax: 650 725 8221<br>Email: walbot@stanford.edu<br>Very probable ligation site of ends cut by single endonuclease.<br>Reverse complemented post-ligation sequence from source sequence.<br>Plate: 4021008 row: 1<br>Class: transposon-tagged.   |         |                        |                   |       |      |        |     |             |
| FEATURES              | Location/Qualifiers   |         |                        |                   |       |      |        |     |             |
| Source                | 1..48   |         |                        |                   |       |      |        |     |             |
|                       | /organism="Zea mays"  |         |                        |                   |       |      |        |     |             |
|                       | /mol_type="genomic DNA"   |         |                        |                   |       |      |        |     |             |
|                       | /cultivar="mixed background W23/A188/B73/K55"   |         |                        |                   |       |      |        |     |             |
|                       | /db_xref="taxon:4577"   |         |                        |                   |       |      |        |     |             |
|                       | /tissue_type="leaf"   |         |                        |                   |       |      |        |     |             |
|                       | /dev_stage="adult"  |         |                        |                   |       |      |        |     |             |
|                       | /lab_host="DH10B"   |         |                        |                   |       |      |        |     |             |
|                       | /clone_lib="4021 - RescueMu Grid V"   |         |                        |                   |       |      |        |     |             |
|                       | /note="Organ: leaf; Vector: RescueMu (engineered from plasmidScript backbone); Site.1: BamHI, Site.2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin." |         |                        |                   |       |      |        |     |             |
| ORIGIN                |   |         |                        |                   |       |      |        |     |             |
| Query Match           | 72.0%; Score 14.4; DB 10; Length 48;  |         |                        |                   |       |      |        |     |             |
| Best Local Similarity | 93.8%; Pred. No. 1.2e+05;   |         |                        |                   |       |      |        |     |             |
| Matches               | 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;   |         |                        |                   |       |      |        |     |             |
| QY                    | 5 GGGGTTTGGGGTTT 20   |         |                        |                   |       |      |        |     |             |
|                       |   |         |                        |                   |       |      |        |     |             |
| Db                    | 6 GGGTTTGGGGTTT 21  |         |                        |                   |       |      |        |     |             |
|                       |   |         |                        |                   |       |      |        |     |             |
| RESULT 13             | AI475390/c  | LOCUS   | AI475390.1             | NCI CGAP Col4     | 49 bp | mRNA | linear | EST | 14-APR-1999 |
| DEFINITION            | t182g01.x1 similar to SW:PRPM HUMAN P10161 SALIVARY PROLINE-RICH PROTEIN PO ;contains element MSR1 repetitive element ; mRNA sequence.  |         |                        |                   |       |      |        |     |             |
| ACCESSION             | AI475390  | VERSION | AI475390.1             | GI:4328435        |       |      |        |     |             |
| KEYWORDS              | EST.  |         |                        |                   |       |      |        |     |             |
| SOURCE                | Homo sapiens (human)  |         |                        |                   |       |      |        |     |             |
| ORGANISM              | Homo sapiens  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | 2   |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| ORGANISM              | Homo sapiens  |         |                        |                   |       |      |        |     |             |
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| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
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| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | 2   |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| ORGANISM              | Homo sapiens  |         |                        |                   |       |      |        |     |             |
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| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | 2   |         |                        |                   |       |      |        |     |             |
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| ORGANISM              | Homo sapiens  |         |                        |                   |       |      |        |     |             |
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| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
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| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
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| ORGANISM              | Homo sapiens  |         |                        |                   |       |      |        |     |             |
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| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
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| REFERENCE             | 2   |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| ORGANISM              | Homo sapiens  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  |         |                        |                   |       |      |        |     |             |
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| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | 2   |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
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| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
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| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
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| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
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| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
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| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
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| ORGANISM              | Homo sapiens  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | 2   |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| ORGANISM              | Homo sapiens  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | 2   |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| ORGANISM              | Homo sapiens  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
| JOURNAL               | Bioinformatics 19 (11), 1441-1442 (2003)  |         |                        |                   |       |      |        |     |             |
| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
| REFERENCE             | 2   |         |                        |                   |       |      |        |     |             |
| AUTHORS               | Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  |         |                        |                   |       |      |        |     |             |
| TITLE                 | An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  |         |                        |                   |       |      |        |     |             |
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| PUBMED                | 12874060  |         |                        |                   |       |      |        |     |             |
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| TITLE                 | An Arabid   |         |                        |                   |       |      |        |     |             |

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
14756321

3  
Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and  
Weishaar,B.

TITLE  
High-throughput generation of sequence indexes from T-DNA  
mutagenized Arabidopsis thaliana lines

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Biotechniques 35 (6), 1164-1168 (2003)  
14682050

4 (bases 1 to 49)  
Li,Y., Rosso,M.G., Strizhov,N. and Weishaar,B.

TITLE  
Direct Submission

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer  
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA.  
It indicates an insertion close to or within gene At5g11660.  
Details on the protocols used for generation of the sequence are  
described in References 1-3. The sequences are generated at the MPI  
for Plant Breeding Research in the context of the GABI-kat project.  
GABI-kat is part of the German Plant Genomics program designated  
'GABI'. Information on line availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES  
source  
Location/Qualifiers  
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/organism="Arabidopsis thaliana"  
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/db\_xref="taxon:3702"  
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plants (T1) which were transformed with the T-DNA from  
vector pAC161 (GenBank accession number: AJ537514). The  
lines contain one or more T-DNA insertions. The DNA  
fragment(s) resulting from the PCR were directly sequenced  
to determine the genomic sequence flanking the insertion.  
T-DNA derived sequences were removed."

ORIGIN

Query Match 72.0%; Score 14.4; DB 10; Length 49;  
Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TGGGGTTTGGGGTTT 19  
|||||  
Db 20 TGGAGTTTGGGGTTT 35  
|||||

RESULT 15  
CZ559680/c  
LOCUS  
DEFINITION

50 bp DNA linear GSS 10-JUN-2005  
PL00447-5prime Drosophila melanogaster PL strains, transposon  
insertion flanking sequences Drosophila melanogaster genomic  
sequence recovered from 5' end of piggyBAC, genomic survey  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CZ559680  
CZ559680.1 GI:67486434  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 50)  
Levis,R., Hoskins,R., Liao,G., Mozdén,N., Tsang,G., He,Y.,  
Karpen,G., Bellen,H., Rubin,G. and Spradling,A.  
The Berkeley Drosophila Genome Project Gene Disruption Project  
Unpublished (2001)  
Contact: Roger A Hoskins  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory  
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA  
Tel: 510 486 4015

Fax: 510 486 6798  
Email: RHoskins@lbl.gov  
Sequence recovery method was inverse PCR.  
Sequence orientation is forward strand relative to 5' end of  
piggyBAC.  
The piggyBAC insertion position is 47 in the 50 bases. This  
insertion position refers to the first base of the 4 base target  
recognition sequence.  
Class: transposon-tagged.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
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/clone\_lib="Drosophila melanogaster PL strains, transposon  
insertion flanking sequences"  
/notes="Drosophila melanogaster was mutagenized by  
remobilization of the piggyBAC vector pBac(CAL4D,EFPP)  
(Horn et al. 2003 Genetics 163: 647-661) (FlyBase ID  
FBtp0017476) as described by Hacker et al. 2003 (Proc Natl  
Acad Sci USA 100: 7720-7725). Each strain in the  
collection has an independent insertion of the mutator  
transposon and the name of each strain begins with the  
letters PL. Genomic DNA was prepared from samples from  
each PL strain, DNA segments flanking the transposon  
insertion sites were amplified by inverse PCR, and the  
inverse PCR products were sequenced as described by Bellen  
et al. 2004 (Genetics 167: 761-781)."

ORIGIN

Query Match 72.0%; Score 14.4; DB 10; Length 50;  
Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGG 16  
|||||  
Db 16 TTTTGGGGTTTGGGG 1  
|||||

RESULT 16  
BX535866/c  
LOCUS  
DEFINITION

33 bp DNA linear GSS 04-APR-2004  
Arabidopsis thaliana T-DNA flanking sequence GK-521H07-020048,  
genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BX535866  
BX535866.1 GI:31412996  
GSS.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE  
AUTHORS  
TITLE

Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weishaar,B.  
GABI-Kat Simplesearch: a flanking sequence tag (fST) database for  
the identification of T-DNA insertion mutants in Arabidopsis  
thaliana  
Bioinformatics 19 (11), 1441-1442 (2003)  
12874060

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

2  
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and  
Weishaar,B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
14756321

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

3  
Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and  
Weishaar,B.  
High-throughput generation of sequence indexes from T-DNA  
mutagenized Arabidopsis thaliana lines  
Biotechniques 35 (6), 1164-1168 (2003)  
14682050

```

REFERENCE
AUTHORS      4 (bases 1 to 33)
TITLE        Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.
JOURNAL      Direct Submission
COMMENT      Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
              Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
              This sequence has been recovered from the left border of the T-DNA.
              It indicates an insertion within the locus defined by BAC clone
              t5e7. Details on the protocols used for generation of the sequence
              are described in References 1-3. The sequences are generated at the
              MPI for Plant Breeding Research in the context of the GABI-Kat
              project. GABI-Kat is part of the German Plant Genomics program
              designated 'GABI'. Information on line availability can be found
              at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source
  Location/Qualifiers
    1..33
      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
      /db_xref="taxon:3702"
      /clone="GK-521H07-020048"
      /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
      /ecotypes="Col-0"
      /note="PCR was performed on DNA from Arabidopsis thaliana
      plants (T1) which were transformed with the T-DNA from
      vector pAC161 (GenBank accession number: AJ537514). The
      lines contain one or more T-DNA insertions. The DNA
      fragment(s) resulting from the PCR were directly sequenced
      to determine the genomic sequence flanking the insertion.
      T-DNA derived sequences were removed."

ORIGIN
Query Match      71.0%; Score 14.2; DB 10; Length 33;
Best Local Similarity 84.2%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TTTGGGGTTTGGGGTTT 20
        ||||| ||||| |||||
DB      22 TTTGGGCTCTGGAGTGT 4

RESULT 17
DR63F21T/c      37 bp DNA linear GSS 22-NOV-2002
LOCUS           Danio rerio genomic clone DKEY-63F21, genomic survey sequence.
DEFINITION
ACCESSION      AL981876
VERSION        AL981876.1 GI:25187365
KEYWORDS
SOURCE
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
  Cypriniformes; Cyprinidae; Danio.
  1 (bases 1 to 37)
  Humphray,S.J., Huckle,E. and Hunt,S.E.
  Direct Submission
  Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
  Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
  humquery@sanger.ac.uk Unpublished
  This sequence was generated from the T7 end of BAC 63F21. 63F21 is
  part of the Daniokey BAC Library created by R. Plasterk and N.V.
  Keygene.
  Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
source
  Location/Qualifiers
    1..37
      /organism="Danio rerio"
      /mol_type="genomic DNA"
      /db_xref="taxon:7955"
      /clone="DKEY-63F21"
      /tissue_type="Testis"
      /note="vector pindigoBAC-536"

ORIGIN
Query Match      71.0%; Score 14.2; DB 11; Length 37;
Best Local Similarity 84.2%; Pred. No. 1.4e+05;

MATCHES 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TTTTGGGGTTTGGGGTTT 19
        ||||| ||||| |||||
DB      37 TTTTGGGGTTTAGAGGTGT 19

RESULT 18
CG722753      43 bp DNA linear GSS 20-OCT-2003
LOCUS           1119073D02.2EL_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
DEFINITION      survey sequence.
ACCESSION      CG722753
VERSION        CG722753.1 GI:37757925
KEYWORDS
SOURCE
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 43)
  Walbot,V.
  Maize genomic sequences found using engineered RescueMu transposon
  Unpublished (2001)
  Contact: Walbot V
  Department of Biological Sciences
  Stanford University
  855 California Ave, Palo Alto, CA 94304, USA
  Tel: 650 723 2227
  Fax: 650 725 8221
  Email: walbot@stanford.edu
  Possible ligation site of ends cut by 2 different endonucleases.
  Reverse complemented post-ligation sequence from source sequence.
  Plate: 1119073 row: 35
  Class: transposon-tagged
  Location/Qualifiers
    1..43
      /organism="Zea mays"
      /mol_type="genomic DNA"
      /cultivar="mixed background W23/A188/B73/K55"
      /db_xref="taxon:4577"
      /tissue_type="leaf"
      /dev_stage="adult"
      /lab_host="DH10B"
      /clone_lib="1119 - RescueMu Grid AA"
      /note="Organ: leaf; Vector: RescueMu (engineered from
      pBluescript backbone); Site 1: BamHI; Site 2: BglII;
      RescueMu is a 4.9 kb, modified maize Mu transposon
      designed to allow plasmid rescue from total genomic DNA.
      Mu elements insert preferentially into transcription
      units. For more information on RescueMu, go to the web
      site 'www.zmldb.iastate.edu' and follow the links for
      'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
      was extracted from leaf strips, double digested using
      BamHI and BglII, and ligated to form circular plasmids.
      DH10B cells were transformed and then screened on LB
      plates with ampicillin."

ORIGIN
Query Match      71.0%; Score 14.2; DB 10; Length 43;
Best Local Similarity 84.2%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TTTGGGGTTTGGGGTTT 20
        ||||| ||||| |||||
DB      19 TTGGGCTTTGGGGTTT 37

RESULT 19
CZ470781      50 bp DNA linear GSS 29-APR-2005
LOCUS           c06535-5prime Exelixis piggyBac PB insertions Drosophila
DEFINITION      melanogaster genomic Sequence recovered from 5' end of piggyBac,

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genomic survey sequence.
CZ470781
VERSION CZ470781.1 GI:62964794
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 50)
AUTHORS Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
Greer,K., Hartouni,S.R., Howie,B., Jakkula,L., Joo,D., Killpack,K.,
Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.
TITLE A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
JOURNAL Nat. Genet. 36 (3), 283-287 (2004)
PUBMED 14981521
COMMENT Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
piggyBac element.
The piggyBac insertion position is 47 in the 50 bases. This
insertion position refers to the first base of the 4 base TTA
target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
1..50
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac PB insertions"
/notes="Vector: piggyBac PB (Genbank accession number
AY515146); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the PB element using
Hap70.piggyBac transposase from a single ammunition
element on either the X or third chromosome. We induced
transposase expression by immersing bottles in a
circulating 37°C water bath for a daily (days 3-10 after
egg-laying) 1-h heat shock. We outcrossed the resulting
dysgenic males to an isogenic w- strain. New insertions
were identified on the basis of a change in eye color
(third chromosome ammunition) or the appearance of w+ male
progeny (X chromosome ammunition). All lines were mapped
to a chromosome by standard genetic methods, examined for
homozygous viability, and used for recovery of flanking
genomic sequence by inverse PCR."

ORIGIN
Query Match 71.0%; Score 14.2; DB 10; Length 50;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTCGGGTTTGGGGTTTT 20
||| ||||| |||||
DB 5 TTTCGGGTTTGGGGTTTT 23

RESULT 20
CG729919
LOCUS 50 bp DNA linear GSS 20-OCT-2003
DEFINITION 1119116E01.2EL_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic

genomic survey sequence.
CG729919
VERSION CG729919.1 GI:37772091
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 50)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
JOURNAL Contact: Walbot V
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119116 row: 36
Class: transposon-tagged.
Location/Qualifiers
1..50
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/dev_stage="adult"
/tissue_type="leaf"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 Kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match 71.0%; Score 14.2; DB 10; Length 50;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTCGGGTTTGGGGTTTT 20
||| ||||| |||||
DB 19 TTTCGGCCTTTGGGGTTTT 37

RESULT 21
AL940076/c
LOCUS 31 bp DNA linear GSS 01-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-244B11-014397,
genomic survey sequence.
ACCESSION AL940076
VERSION AL940076.1 GI:24396525
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Vichosover,P. and Weisshaar,B.
TITLE GABI-Kat Simplesearch: a flanking sequence tag (FST) database for

```

the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 bioinformatics 19 (11), 1441-1442 (2003)  
 12874060  
 2  
 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.  
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 14756321  
 3  
 Strizhov,N., Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.  
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 Biotechniques 35 (6), 1164-1168 (2003)  
 14682050  
 4 (bases 1 to 31)  
 Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.  
 Direct Submission  
 Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone f26h11. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

#### FEATURES

Location/Qualifiers

1..31  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="GK-244B11-014397"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /scotYPE="Col-0"  
 /notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

#### ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 31;  
 Best Local Similarity 88.2%; Pred. No. 2.1e+05;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGCTTTGGGCT 17  
 |||||  
 Db 17 TGTGGGCTTTGGGCT 1

#### RESULT 22

H71330  
 LOCUS  
 YU55D08.s1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone IMAGE:230031.3' similar to SP:JC2012 JC2012 RIBOSOMAL PROTEIN 17K - i, mRNA sequence.  
 H71330  
 ACCESSION H71330.1 GI:1043146  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 46)  
 Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags  
 Genome Res. 6 (9), 807-828 (1996)

#### TITLE

JOURNAL

PUBMED

#### COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)

Insert Size: 356

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert Length: 356 Std Error: 0.00

Seq primer: Promega -21m13

High quality sequence stop: 1.

#### FEATURES

Location/Qualifiers

1..46

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3781127"

/db\_xref="taxon:9606"

/clone="IMAGE:230031"

/sex="male"

/dev\_stage="20 week-post conception fetus"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal liver spleen INFUS"

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer

15' AACGGAAGATTAATTAAGATCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

#### ORIGIN

Query Match 69.0%; Score 13.8; DB 8; Length 46;  
 Best Local Similarity 88.2%; Pred. No. 2.1e+05;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTGGGCTTTGGGCTT 18  
 |||||  
 Db 3 TTTGGGCTTTGGGCTT 19

#### RESULT 23

AZ774479  
 LOCUS  
 2M0004A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004A05 F, genomic survey sequence.  
 AZ774479  
 ACCESSION AZ774479.1 GI:12899972  
 VERSION  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 33)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,





Trace considered overall poor quality  
Insert Length: 1210 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

**FEATURES**  
**source**

```

1. 37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2140844"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Gas4"
/notes="Organ: Stomach; Vector: pCMV-SPORT6; Site 1: Salt;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

```

## ORIGIN

|                       |                 |                      |           |            |
|-----------------------|-----------------|----------------------|-----------|------------|
| Query Match           | 68.0%;          | Score 13.6;          | DB 1;     | Length 37; |
| Best Local Similarity | 80.0%;          | Pred.No. 2.5e+05;    |           |            |
| Matches 16;           | Conservative 0; | Mismatches 4;        | Indels 0; | Gaps 0;    |
| Qy                    | 1               | TTTTGGGGTTTGGGCTTT   | 20        |            |
| Dd                    | 29              | TTTTTGGGGGTtTGCGCTTT | 10        |            |

RESULT 26  
BE974781

BE974781 38 bp mRNA linear EST 04-OCT-20  
601680831R2 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:3951175 3',  
mRNA sequence.  
BE974781  
BE974781.1 GI:10588117  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 38)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: CLONETECH Laboratories, Inc.  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

## ORIGIN

```

Query Match      68.0%; Score 13.6; DB 6; Length 39;
Best Local Similarity 80.0%; Pred. No. 2.Se+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTTGGGGTTTT 20
    |||||
Db 24 TTTTGGGGGGGGGGGGTTTT 5

```

RESULT 28  
A7579518/C

|            |                        |                    |                |                      |
|------------|------------------------|--------------------|----------------|----------------------|
| AZ579518   | 42 bp                  | DNA                | linear         | GSS 13-DEC-2000      |
| LOCUS      | 1M0367G03F             | Mouse 10kb plasmid | UUGC1M library | Mus musculus genomic |
| DEFINITION | clone UUGC1M0367G03 F, | genomic survey     | sequence.      |                      |
| ACCESSION  | AZ579518               |                    |                |                      |
| VERSION    | AZ579518.1             | GI:11693947        |                |                      |
| KEYWORDS   | GSS.                   |                    |                |                      |

**SOURCE**  
ORGANISM  
Mus musculus (house mouse)

**REFERENCE**  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ismail,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Tilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

**JOURNAL**  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0367 row: G column: 03  
Seq primer: CGTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 42.

**FEATURES**  
source  
1..42  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0367G03"  
/sex="Male"  
/lab-host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**ORIGIN**  
Query Match 68.0%; Score 13.6; DB 9; Length 42;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 23 TTTTGGGTTTGGGGTTTT 4  
|||||

**RESULT** 29  
BX946019  
LOCUS  
DEFINITION  
Arabisopsis thaliana T-DNA flanking sequence GK-747F04-024638, genomic survey sequence.  
BX946019  
ACCESSION  
VERSION  
BX946019.1 GI:42595705

**RESULT** 30  
AI442438/c  
LOCUS  
DEFINITION  
Arabisopsis thaliana T-DNA flanking sequence GK-747F04-024638, genomic survey sequence.  
AI442438

**RESULT** 30  
AI442438  
LOCUS  
DEFINITION  
Arabisopsis thaliana T-DNA flanking sequence GK-747F04-024638, genomic survey sequence.  
AI442438

**ORIGIN**  
Query Match 68.0%; Score 13.6; DB 10; Length 42;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 11 TTTTGGGTTTCTGGTTTT 30  
|||||

**FEATURES**  
source  
1..42  
/organism="Arabisopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-747F04-024638"  
/clone\_lib="Arabisopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

**ORIGIN**  
Query Match 68.0%; Score 13.6; DB 10; Length 42;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 11 TTTTGGGTTTCTGGTTTT 30  
|||||

**REFERENCE**  
AUTHORS  
Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.  
GABI-Kat SimpleSearch: a flanking sequence tag (fST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
Bioinformatics 19 (11), 1441-1442 (2003)

**JOURNAL**  
PUBMED  
12874060

**REFERENCE**  
AUTHORS  
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

**JOURNAL**  
PUBMED  
14756321

**REFERENCE**  
AUTHORS  
Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.  
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
Biotechniques 35 (6), 1164-1168 (2003)

**JOURNAL**  
PUBMED  
14682050

**REFERENCE**  
AUTHORS  
Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.  
Direct Submission  
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g10360.  
Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German plant genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

**FEATURES**  
Location/Qualifiers  
1..42  
/organism="Arabisopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-747F04-024638"  
/clone\_lib="Arabisopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

**KEYWORDS**  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

**REFERENCE**  
AUTHORS  
Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.  
GABI-Kat SimpleSearch: a flanking sequence tag (fST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
Bioinformatics 19 (11), 1441-1442 (2003)

**JOURNAL**  
PUBMED  
12874060

**REFERENCE**  
AUTHORS  
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

**JOURNAL**  
PUBMED  
14756321

**REFERENCE**  
AUTHORS  
Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.  
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
Biotechniques 35 (6), 1164-1168 (2003)

**JOURNAL**  
PUBMED  
14682050

**REFERENCE**  
AUTHORS  
Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.  
Direct Submission  
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g10360.  
Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German plant genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

**FEATURES**  
source  
1..42  
/organism="Arabisopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-747F04-024638"  
/clone\_lib="Arabisopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

**ORIGIN**  
Query Match 68.0%; Score 13.6; DB 10; Length 42;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 11 TTTTGGGTTTCTGGTTTT 30  
|||||

**RESULT** 30  
AI442438  
LOCUS  
DEFINITION  
Arabisopsis thaliana T-DNA flanking sequence GK-747F04-024638, genomic survey sequence.  
AI442438

**RESULT** 30  
AI442438/c  
LOCUS  
DEFINITION  
Arabisopsis thaliana T-DNA flanking sequence GK-747F04-024638, genomic survey sequence.  
AI442438

**ORIGIN**  
Query Match 68.0%; Score 13.6; DB 10; Length 42;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 11 TTTTGGGTTTCTGGTTTT 30  
|||||



## ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 43;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTTT 20  
 ||||| ||||| |||||  
 Db 21 TTTTGGTGTTCGTCTTT 2

## RESULT 32

CZ472331

## LOCUS

DEFINITION CZ472331 43 bp DNA linear GSS 29-APR-2005  
 d01604-3prime Exelixis P element XP insertions Drosophila  
 melanogaster genomic Sequence recovered from 3' end of P element,  
 genomic survey sequence.

## ACCESSION

CZ472331

## VERSION

GSS.

## SOURCE

Drosophila melanogaster (fruit fly)

## ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

1 (bases 1 to 43)

Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,  
 Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,  
 Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,  
 Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Kilpack, K.,  
 Laufer, A., Mazotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,  
 Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,  
 Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.A complementary transposon tool kit for Drosophila melanogaster  
 using P and piggyBac

Nat. Genet. 36 (3), 283-287 (2004)

14981521

## TITLE

Contact: Roger A Hoskins

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory

Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA

Tel: 510 486 4015

Fax: 510 486 6798

Email: RHoskins@lbl.gov

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P  
 element.The P element insertion position is 1 in the 43 bases. This  
 insertion position refers to the first base of the 8 base target  
 recognition sequence.

Class: transposon insertion site.

Location/Qualifiers

1..43

/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

/strain="isogenic w- strain"

/db\_xref="taxon:7227"

/clone\_lib="Exelixis P element XP insertions"

/note="Vector: P element XP (GenBank accession number  
 AF15149); An isogenic w- Drosophila melanogaster strain  
 was mutagenized by remobilization of transposable  
 elements. For the P element XP, we selected an easily  
 mobilized ammunition element among inserts hopped into the  
 Binsyncy balancer. New insertions were collected in vials  
 from dysgenic females using the standard chromosomal  
 source of transposase, delta2-3. All lines were mapped to  
 a chromosome by standard genetic methods, examined for  
 homozygous viability and used for recovery of flanking  
 genomic sequence by inverse PCR."

ORIGIN

Query Match 68.0%; Score 13.6; DB 10; Length 43;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;

## Matches

16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TTTTGGGTTTGGGTTT 20  
 ||||| ||||| |||||  
 Db 20 TGTGGGCTTTGGAGCTTT 39

## RESULT 33

CF300934/c

## LOCUS

DEFINITION CF300934 44 bp mRNA linear EST 15-AUG-2003  
 7LEAF--05-J13.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa (japonica cultivar-group) cDNA clone 7LEAF--05-J13, mRNA  
 sequence.

## ACCESSION

CF300934

## VERSION

EST.

## KEYWORDS

Oryza sativa (japonica cultivar-group)

## SOURCE

Oryza sativa (japonica cultivar-group)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzae; Oryza.

## REFERENCE

1 (bases 1 to 44)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

## TITLE

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..44

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="7LEAF--05-J13"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

## ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 44;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;QY 1 TTTTGGGTTTGGGTTT 20  
 ||||| ||||| |||||  
 Db 34 TTTTGTGTTTGGGATTT 15

## RESULT 34

AZ476389/c

## LOCUS

DEFINITION AZ476389 44 bp DNA linear GSS 04-OCT-2000  
 1M0295E09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
 clone UUGCIM0295E09 F, genomic survey sequence.

## ACCESSION

AZ476389

## VERSION

GSS.

## KEYWORDS

Mus musculus (house mouse)

## SOURCE

Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 44)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausen,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
**JOURNAL**  
**COMMENT**

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0295 row: E column: 09  
 Seq primer: CCGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 44.  
**FEATURES**  
 source  
 1..44  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0295E09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, P-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

**ORIGIN**  
 Query Match 68.0%; Score 13.6; DB 9; Length 44;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TTTTGGGTTTGGGTTT 20  
 Db 22 TTTTGGTTTGGGTTT 11

**RESULT 35**  
 CF298361/c  
**LOCUS**  
 DEFINITION  
 CF298361 45 bp mRNA linear EST 15-AUG-2003  
 sativa (japonica cultivar-group) cDNA clone 7LEAF--01-L10, mRNA  
 sequence.  
**ACCESSION**  
**VERSION**  
**KEYWORDS**  
**SOURCE**  
**ORGANISM**  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

**REFERENCE**  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Query Match 68.0%; Score 13.6; DB 9; Length 44;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TTTTGGGTTTGGGTTT 20  
 Db 30 TTTTGGTTTGGGTTT 11

**RESULT 35**  
 CF298361/c  
**LOCUS**  
 DEFINITION  
 CF298361 45 bp mRNA linear EST 15-AUG-2003  
 sativa (japonica cultivar-group) cDNA clone 7LEAF--01-L10, mRNA  
 sequence.  
**ACCESSION**  
**VERSION**  
**KEYWORDS**  
**SOURCE**  
**ORGANISM**  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 45)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
**JOURNAL**  
**COMMENT**

Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
**FEATURES**  
 source  
 1..45  
 Location/Qualifiers  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="7LEAF--01-L10"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

**ORIGIN**  
 Query Match 68.0%; Score 13.6; DB 6; Length 45;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 TTTTGGGTTTGGGTTT 20  
 Db 22 TTTTGTGTTTGGGATTT 3

**RESULT 36**  
 CN751963/c  
**LOCUS**  
 DEFINITION  
 CN751963 45 bp mRNA linear EST 19-MAY-2004  
 APhL3SD-XXI-A6 APhL3SD Acyrthosiphon pisum cDNA clone APhL3SDXXIA6  
 5', mRNA sequence.  
**ACCESSION**  
**VERSION**  
**KEYWORDS**  
**SOURCE**  
**ORGANISM**  
 Acyrthosiphon pisum (pea aphid)  
 Acyrthosiphon pisum  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
 Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.  
 Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,  
 Stern,D., Tagu,D. and Wincker,P.  
 An expressed sequence tags database for the pea aphid Acyrthosiphon  
 pisum  
 Unpublished (2004)  
 Contact: D. Tagu  
 INRA Rennes  
 UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France  
 Tel: +33.2.23.48.51.65  
 Fax: +33.2.23.48.51.50  
 Risk of contamination by bacterial sequences from obligatory  
 (Buchnera) or facultative endosymbionts.  
 PCR Primers  
 FORWARD: GCCGATAACTTCGTATAGCA  
 Plate: XXI row: A column: 6.  
 Location/Qualifiers  
 1..45  
 /organism="Acyrthosiphon pisum"  
 /mol\_type="mRNA"  
 /cultivar="yr2"  
 /db\_xref="taxon:7029"  
 /clone="APHL3SDXXIA6"

/tissue\_type="head"  
/dev\_stage="third instar nymph (L3)"  
/lab\_host="TOP10"

/clone\_lib="AphL3SD"  
/note="Vector: PDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;  
Sample name: AphL3SD ; Plant growth place: INRA-Rennes,  
UMR BIO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil  
conditions: peat ; Sowing date: 20/03/2003 ; Harvesting  
date: 10/04/2003 ; Stress date: no stress ; Description:  
aphids inoculated on one-week old Vicia faba germinations  
under non sterile conditions. ; experimental condition:  
short photoperiod (12-hr light/12-hr dark at 18 c)"

## ORIGIN

Query Match 68.0%; Score 13.6; DB 7; Length 45;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
||||| ||||| ||||| |||||  
Db 45 TTTTGGGGTTTGGGGTTTT 26

## RESULT 37

AZ793049/c

LOCUS

DEFINITION 2M0045M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0045M14 R, genomic survey sequence.

ACCESSION

AZ793049

VERSION

AZ793049.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 46)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: M column: 14

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 46.

Location/Qualifiers

1. .46

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0045M14"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

## ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 46;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
||||| ||||| ||||| |||||  
Db 26 TTTTGGGGTTTGGGGTTTT 7

## RESULT 38

AZ786064

LOCUS

DEFINITION

2M0030G22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0030G22 R, genomic survey sequence.

ACCESSION

AZ786064

VERSION

AZ786064.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 47)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0030 row: G column: 22

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 47.

Location/Qualifiers

1. .47

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0030G22"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## FEATURES

source

1. .47

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0030G22"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 47;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20  
||||| ||||| |||||  
Db 2 TTTTGGGTTTGGGGTTT 21

## RESULT 39

AA959573 49 bp mRNA linear EST 08-MAY-1998  
LOCUS ub54h01.s1 Soares mammary gland NMLMG Mus musculus cDNA clone  
DEFINITION IMAGE:1381585 3', similar to gb:J03464 PROCOLLAGEN ALPHA 2(I) CHAIN  
PRECUSOR (HUMAN); gb:X59251 Mouse COL1A2 mRNA for pro-alpha-2(I)  
collagen (HUMAN); mRNA sequence.

ACCESSION AA959573 GI:3125473  
VERSION  
KEYWORDS  
SOURCE

## ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 49)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.

## TITLE

The WashU-HMI Mouse EST Project

## JOURNAL

Unpublished (1996)

## COMMENT

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.lml.gov) for further information.

MGI:904053

## FEATURES

## source

1. .49  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1381585"  
/sex="female (lactating)"  
/tissue type="mammary gland"  
/lab\_host="DH10B"  
/clone lib="Soares mammary gland NMLMG"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 68.0%; Score 13.6; DB 1; Length 49;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20  
||||| ||||| |||||  
Db 28 TTCAGGGGTTTGGGGTTT 47

## RESULT 40

EX171071/c 50 bp DNA linear GSS 28-JAN-2003  
LOCUS BX171071  
DEFINITION Danio rerio genomic clone DKEY-174L12, genomic survey sequence.  
ACCESSION BX171071  
VERSION BX171071.1 GI:28002776  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)

## ORGANISM

Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 50)  
Humphray, S.J., Huckle, E. and Durham, J.L.  
Direct Submission  
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquerry@sanger.ac.uk Unpublished  
This sequence was generated from the T7 end of BAC 174L12. 174L12  
is part of the Daniokey BAC Library created by R. Plasterk and N.V.  
KeyGene. Further details:  
http://www.sanger.ac.uk/Projects/D\_rerio/.

## FEATURES

## source

1. .50  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEY-174L12"  
/tissue\_type="Testis"  
/note="vector pindigoBAC-536"

## ORIGIN

Query Match 68.0%; Score 13.6; DB 10; Length 50;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20  
||||| ||||| |||||  
Db 20 TTTTGGGTTTGGGGTTT 1

## RESULT 41

TA131B05Q/c 24 bp DNA linear GSS 13-DEC-2000  
LOCUS T. brucei sheared genomic DNA clone 131b05, reverse sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AL465643  
VERSION AL465643.1 GI:11834938  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei

## ORGANISM

Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 24)  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,



```

Melville,S.B., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
mhi@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nrelayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
    source
        1. .24
            /location/Qualifiers
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="131b05"
ORIGIN
    Query Match          67.0%; Score 13.4; DB 11; Length 24;
    Best Local Similarity 93.3%; Pred. No. 2.9e+05;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TGGGGTTTGGGGTTT 18
      ||| ||||| |||
Db      24 TGGCGTTTGGGGTT 10

RESULT 42
CZ916406/c
LOCUS
DEFINITION
    4021001C10.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
    survey sequence.
ACCESSION
CZ916406
VERSION
CZ916406.1 GI:71934408
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 30)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021001 row: C column: 10
Class: transposon-tagged
FEATURES
    source
        1. .30
            /location/Qualifiers
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="mixed background w23/A188/B73/K55"
            /db_xref="taxon:4577"
            /tissue_type="leaf"
            /dev_stage="adult"
            /lab_host="DH10B"

Melville,S.B., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
mhi@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nrelayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
    source
        1. .24
            /location/Qualifiers
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="131b05"
ORIGIN
    Query Match          67.0%; Score 13.4; DB 11; Length 24;
    Best Local Similarity 93.3%; Pred. No. 2.9e+05;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TGGGGTTTGGGGTTT 18
      ||| ||||| |||
Db      24 TGGCGTTTGGGGTT 10

RESULT 42
CZ916406/c
LOCUS
DEFINITION
    4021001C10.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
    survey sequence.
ACCESSION
CZ916406
VERSION
CZ916406.1 GI:71934408
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 30)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021001 row: C column: 10
Class: transposon-tagged
FEATURES
    source
        1. .30
            /location/Qualifiers
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="mixed background w23/A188/B73/K55"
            /db_xref="taxon:4577"
            /tissue_type="leaf"
            /dev_stage="adult"
            /lab_host="DH10B"

/clone_lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
ORIGIN
    Query Match          67.0%; Score 13.4; DB 10; Length 30;
    Best Local Similarity 93.3%; Pred. No. 2.9e+05;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TTTGGGGTTTGGGG 16
      ||| ||||| |||
Db      15 TTTTGGGTTTGGGG 1

RESULT 43
AI439312/c
LOCUS
DEFINITION
    ti59e12.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134798 3'
    similar to SW:PRP2 HUMAN P02812 SALIVARY PROLINS-RICH PROTEIN
    PRECURSOR ;contains MER22.B2 TAR1 repetitive element ;, mRNA
    sequence.
ACCESSION
AI439312
VERSION
AI439312.1 GI:4303441
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 34)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 861 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
    Location/Qualifiers
        1. .34
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2134798"
            /tissue_type="lymphoma, follicular mixed small and large
            cell"
            /lab_host="DH10B"
            /clone_lib="NCI_CGAP_Lym12"
            /note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1:
            SalI; Site 2: NotI; Cloned unidirectionally. Primer:
            Oligo dT. Average insert size 1.25 kb. Life Technologies
            catalog #: 11547-015"
ORIGIN
    Query Match          67.0%; Score 13.4; DB 1; Length 34;

```

```

Best Local Similarity 93.3%; Pred. No. 3e+05; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 1;

Qy 5 GGGGTTTTGGGTTT 19
Db 34 GGGGTTTTGGGTTT 20

RESULT 44
AI280814/c
LOCUS
DEFINITION
  qw11603.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:1990780 3',
  similar to SW:RP1_HUMAN P04280 SALIVARY PROLINE-RICH PROTEIN
  PRECURSOR ;contains element MSRI repetitive element ;, mRNA
  sequence.
ACCESSION
  AI280814
  AI280814.1 GI:3919047
  EST.
  Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  1 (bases 1 to 37)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 890 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
  1. .37
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:1990780"
  /tissue_type="poorly-differentiated endometrial
  adenocarcinoma, 2 pooled tumors"
  /lab_host="DH10B"
  /clone_lib="NCI CGAP Ut3"
  /note="Organ: uterus; Vector: pCMV-SPORT6; Site.1: SalI;
  Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
  Average insert size 1.45 kb. Life Technologies catalog #:
  11541-018"

ORIGIN
  Query Match 67.0%; Score 13.4; DB 1; Length 37;
  Best Local Similarity 93.3%; Pred. No. 3e+05;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTTGGG 15
Db 15 TTATGGGGTTTTGGG 1

RESULT 45
AI865173/c
LOCUS
DEFINITION
  wk09b01.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2411785 3',
  similar to WP:R148.5 CE12856 ;, mRNA sequence.
  sequence.
ACCESSION
  AI865173
  AI865173.1 GI:5529280
  EST.
  Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  1 (bases 1 to 49)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Life Technologies catalog #: 11547-015
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 808 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
  1. .49
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:2411785"
  /tissue_type="lymphoma, follicular mixed small and large
  cell"
  /lab_host="DH10B"
  /clone_lib="NCI CGAP Lym12"
  /note="Organ: lymph node; Vector: pCMV-SPORT6; Site.1:
  SalI; Site.2: NotI; Cloned unidirectionally. Primer:
  Oligo dt. Average insert size 1.25 kb. Life Technologies
  catalog #: 11547-015"

ORIGIN
  Query Match 67.0%; Score 13.4; DB 1; Length 49;
  Best Local Similarity 93.3%; Pred. No. 3e+05;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGGTTTTGGGTTT 20
Db 44 GGGTTTTGGGTTT 30

RESULT 46
AI2761211
LOCUS
DEFINITION
  IM0555122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0555122 F, genomic survey sequence.
ACCESSION
  AI2761211
  AI2761211.1 GI:12869877
  GSS.
  Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 22)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center

```

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0555 row: 1 column: 22

Seq primer: CGTGTAAACGACGCGCCACT

Class: plasmid ends

High quality sequence stop: 22.

## FEATURES

1. .22 Location/Qualifiers

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M055122"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1) a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

## ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 22;  
Best Local Similarity 83.3%; Pred. No. 3.5e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTTT 18

|||||

Db 5 TTTTGGGTTTGGGTTT 22

## RESULT 47

AJ590891

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone

576D12, genomic survey sequence.

AJ590891 24 bp DNA linear GSS 15-JAN-2004

VERSION AJ590891.1 GI:37940515

KEYWORDS GSS; left border; T-DNA flanking sequence.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1

AUTHORS

Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, P.,

Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G.,

Lepiniec, L., Caboche, M., and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences

of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

12446565

REFERENCE 2 (bases 1 to 24)

## AUTHORS

Direct Submission

JOURNAL

## COMMENT

Balzerque, S.  
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
http://absgap.versailles.inra.fr/publiclines/. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.infobiogen.fr).

## FEATURES

source

1. .24

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/db\_xref="taxon:3702"

/clone="576D12"

/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Massilewskija"

1. .24

/note="T-DNA flanking sequence

left border"

## ORIGIN

Query Match 66.0%; Score 13.2; DB 10; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.5e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTTT 18

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Db 7 TTATGGGTTTGGGGGT 24

## RESULT 48

AZ509683

LOCUS

DEFINITION

clone UUGC1M0352C18 R, genomic survey sequence.

AZ509683 37 bp DNA linear GSS 05-OCT-2000

VERSION AZ509683.1 GI:10690999

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1

(bases 1 to 37)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A., and Wright, D., Weis, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0352 row: C column: 18

Seq primer: CACACAGAAACGATGACC

Class: plasmid ends

High quality sequence stop: 37.

Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0352C18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 66.0%; Score 13.2; DB 9; Length 37;
Best Local Similarity 83.3%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTGGGTTTTCGGGTTT 19
Db 19 TTTGGGACATGGGGTTT 36

RESULT 49
BX120037/c
LOCUS BX120037
DEFINITION Danio rerio genomic clone DKEY-61C20, genomic survey sequence.
ACCESSION BX120037
VERSION BX120037.1 GI:27950952
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 40)
Humphray,S.J., Huckle,E. and Durham,J.L.
Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 61C20. 61C20 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1..40
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-61C20"
/tissue_type="Testis"
/notes="vector pindigBAC-536"

FEATURES
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/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-61C20"
/tissue_type="Testis"
/notes="vector pindigBAC-536"

ORIGIN
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Best Local Similarity 78.9%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0352C18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 66.0%; Score 13.2; DB 9; Length 37;
Best Local Similarity 83.3%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTGGGTTTTCGGGTTT 19
Db 19 TTTGGGACATGGGGTTT 36

RESULT 49
BX120037/c
LOCUS BX120037
DEFINITION Danio rerio genomic clone DKEY-61C20, genomic survey sequence.
ACCESSION BX120037
VERSION BX120037.1 GI:27950952
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 40)
Humphray,S.J., Huckle,E. and Durham,J.L.
Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 61C20. 61C20 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1..40
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-61C20"
/tissue_type="Testis"
/notes="vector pindigBAC-536"

FEATURES
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/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-61C20"
/tissue_type="Testis"
/notes="vector pindigBAC-536"

ORIGIN
Query Match 66.0%; Score 13.2; DB 10; Length 40;
Best Local Similarity 78.9%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Col-0"
/db_xref="taxon:3702"
/clone="GK-284D09-015289"
/ecotype="Col-0"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 66.0%; Score 13.2; DB 10; Length 41;
Best Local Similarity 83.3%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTGGGTTTTCGGGTTT 20
Db 39 TTTGGGTTTTCGGTNTTT 21

RESULT 50
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LOCUS AL944738
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-284D09-015289, genomic survey sequence.
ACCESSION AL944738
VERSION AL944738.1 GI:24401360
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060
2
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321
3
Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weisshaar,B.
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 41)
Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F3F19. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
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/db_xref="taxon:3702"
/clone="GK-284D09-015289"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

FEATURES
source
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 66.0%; Score 13.2; DB 10; Length 41;
Best Local Similarity 83.3%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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| | | | | | | | | |  
Db 41 TAGGGGTTTAGGGTATT 24

Search completed: February 15, 2006, 21:09:47  
Job time : 1353.25 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:56:18 ; Search time 44.9587 Seconds  
(without alignments)  
790.754 Million cell updates/sec

**Title:** US-09-669-187A-73

Perfect score:

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Sequence: 1 ttttgggggttttgggggtttt 20
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Scoring table: IDENTITY NUC

scoring table: IDENT1\_NOC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0

|                |            |
|----------------|------------|
| Minimum DB seq | length: 0  |
| Maximum DB seq | length: 50 |

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum match 100%  
Listing first 300 summaries

Database : Tested Patents NA: \*

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2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
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4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
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7: /cgn2_6/ptodata/1/ina/pp COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfileseq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Query |       |        | DB | ID                 | Description       |
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| 1          | 20    | 100.0 | 39     | 3  | US-08-403-880A-121 | Sequence 121, App |
| 2          | 20    | 100.0 | 44     | 2  | US-08-851-843A-42  | Sequence 42, App1 |
| 3          | 20    | 100.0 | 44     | 3  | US-08-851-843A-42  | Sequence 42, App1 |
| 4          | 20    | 100.0 | 44     | 3  | US-08-851-843A-42  | Sequence 42, App1 |
| 5          | 20    | 100.0 | 44     | 3  | US-08-851-843A-42  | Sequence 42, App1 |
| 6          | 20    | 100.0 | 44     | 3  | US-08-851-843A-42  | Sequence 42, App1 |
| 7          | 20    | 100.0 | 44     | 3  | US-08-851-843A-42  | Sequence 42, App1 |
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| 11         | 20    | 100.0 | 46     | 3  | US-08-851-843A-41  | Sequence 41, App1 |
| 12         | 20    | 100.0 | 46     | 3  | US-08-851-843A-41  | Sequence 41, App1 |
| 13         | 20    | 100.0 | 46     | 3  | US-08-851-843A-41  | Sequence 41, App1 |
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| 20         | 20    | 100.0 | 48     | 3  | US-08-851-843A-37  | Sequence 37, App1 |
| 21         | 20    | 100.0 | 48     | 3  | US-08-851-843A-37  | Sequence 37, App1 |
| 22         | 20    | 100.0 | 48     | 3  | US-08-851-843A-37  | Sequence 37, App1 |
| 23         | 20    | 100.0 | 48     | 3  | US-08-851-843A-37  | Sequence 37, App1 |
| 24         | 20    | 100.0 | 48     | 3  | US-08-851-843A-37  | Sequence 37, App1 |





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246 12 60.0 30 3 US-08-535-168-12 Sequence 12, Appl  
247 12 60.0 30 3 US-09-017-974-12 Sequence 12, Appl  
248 12 60.0 30 3 US-08-682-255A-12 Sequence 12, Appl  
249 12 60.0 30 3 US-09-429-130-12 Sequence 12, Appl  
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251 12 60.0 30 6 PCT-US95-06639-55 Sequence 55, Appl  
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254 12 60.0 32 3 US-10-053-883-56 Sequence 56, Appl  
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256 12 60.0 34 2 US-07-753-738B-3 Sequence 3, Appl  
257 12 60.0 36 3 US-10-053-883-67 Sequence 67, Appl  
258 12 60.0 36 6 PCT-US93-07743-4 Sequence 4, Appl  
259 12 60.0 36 6 PCT-US93-07743-9 Sequence 9, Appl  
260 12 60.0 38 6 PCT-US93-08329-9 Sequence 9, Appl  
261 12 60.0 38 6 PCT-US93-08329-10 Sequence 10, Appl  
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271 12 60.0 47 3 US-10-071-179-50 Sequence 50, Appl  
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273 12 60.0 50 3 US-10-131-827-5760 Sequence 5760, Ap  
274 11.8 59.0 20 2 US-08-117-952-297 Sequence 297, Appl  
275 11.8 59.0 20 3 US-08-755-587-89 Sequence 89, Appl  
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277 11.8 59.0 20 3 US-09-313-932-183 Sequence 183, App  
278 11.8 59.0 24 2 US-08-844-521-46 Sequence 46, Appl  
279 11.8 59.0 24 2 US-08-891-463-24 Sequence 24, Appl  
280 11.8 59.0 24 3 US-08-766-528-46 Sequence 46, Appl  
281 11.8 59.0 24 3 US-08-766-528-47 Sequence 47, Appl  
282 11.8 59.0 24 3 US-08-817-575-7 Sequence 7, Appl  
283 11.8 59.0 24 3 US-09-769-352-7 Sequence 7, Appl  
284 11.8 59.0 24 3 US-09-151-376-58 Sequence 58, Appl  
285 11.8 59.0 24 3 US-09-661-858-46 Sequence 46, Appl  
286 11.8 59.0 24 3 US-09-661-858-47 Sequence 47, Appl  
287 11.8 59.0 25 3 US-09-396-196G-27658 Sequence 27658, A  
288 11.8 59.0 26 2 US-08-033-320-2 Sequence 2, Appl  
289 11.8 59.0 26 2 US-08-336-069-2 Sequence 2, Appl  
290 11.8 59.0 27 2 US-08-483-743-13 Sequence 13, Appl  
291 11.8 59.0 27 2 US-08-483-743-14 Sequence 14, Appl  
292 11.8 59.0 27 2 US-08-474-624-13 Sequence 13, Appl  
293 11.8 59.0 27 3 US-09-109-957-1 Sequence 1, Appl  
294 11.8 59.0 27 3 US-09-109-957-2 Sequence 2, Appl  
295 11.8 59.0 28 3 US-09-296-840A-8 Sequence 8, Appl  
296 11.8 59.0 30 6 PCT-US93-01901-34 Sequence 34, Appl  
297 11.8 59.0 35 3 US-09-302-620B-11 Sequence 11, Appl  
298 11.8 59.0 35 3 US-09-912-161-21 Sequence 21, Appl  
299 11.8 59.0 35 3 US-09-911-781-25 Sequence 25, Appl  
300 11.8 59.0 35 3 US-10-400-902-25 Sequence 25, Appl

## ALIGNMENTS

RESULT 1  
US-08-403-888A-121  
; Sequence 121, Application US/08403888A  
; Patent No. 5952490  
; GENERAL INFORMATION:  
; APPLICANT: Hanecak et al.  
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core  
; TITLE OF INVENTION: Sequence  
; NUMBER OF SEQUENCES: 146  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP

; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,888A  
; FILING DATE: 12-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/954,185  
; FILING DATE: 29-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul K. Legaard  
; REGISTRATION NUMBER: 38,534  
; REFERENCE/DOCKET NUMBER: ISIS-1229  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 121:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: N is A or C or G or T/U  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 2  
; OTHER INFORMATION: N is A or C or G or T/U  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 3  
; OTHER INFORMATION: N is A or C or G or T/U  
; US-08-403-888A-121  
Query Match 100.0%; Score 20; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 6.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTTTGGGGTTTTGGGGTTTT 20  
Db 8 TTTTGGGGTTTTGGGGTTTT 27  
RESULT 2  
US-08-851-843A-42  
; Sequence 42, Application US/08851843A  
; Patent No. 6093809  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6093809el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America



APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6261836el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US/08/854,050  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

US-08-854-050-42

Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20  
Db 25 TTTTGGGGTTTGGGGTTT 44

RESULT 5  
US-09-430-323-42  
Sequence 42, Application US/09430323  
Patent No. 6309867  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.

Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 6309867el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

US-09-430-323-42

Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20  
Db 25 TTTTGGGGTTTGGGGTTT 44

RESULT 6  
US-09-402-181B-568  
Sequence 568, Application US/09402181B  
Patent No. 6610839  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181B  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausehus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 568:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..44  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 25 TTTTGGGTTTGGGGTTTT 44

## RESULT 7

US-09-721-456-568  
Sequence 568, Application US/09721456  
Patent No. 6617110  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.

Morin, Gregg B.  
Harley, Calvin B. H.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-No. 6617110-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 568:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..44  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 568:  
US-09-721-456-568

Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 25 TTTTGGGTTTGGGGTTTT 44

RESULT 8  
US-09-766-253-42  
; Sequence 42, Application US/09766253  
; Patent No. 6808880  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. 6808880el Telomerase  
; NUMBER OF SEQUENCES: 171  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/766.253  
; FILING DATE: 19-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/846.017  
; FILING DATE: 1997-04-25  
; APPLICATION NUMBER: US 08/724.643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002920US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-09-766-253-42  
Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
DB 25 TTTTGGGGTTTGGGGTTTT 44  
RESULT 9  
US-10-054-295-42  
; Sequence 42, Application US/10054295  
; Patent No. 6921664  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.

; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. 6921664el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/054.295  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/854.050  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/846.017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844.419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724.643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-10-054-295-42  
Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
DB 25 TTTTGGGGTTTGGGGTTTT 44  
RESULT 10  
US-09-438-486A-42  
; Sequence 42, Application US/09438486A  
; Patent No. 6927285  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: LINGNER, JOACHIM  
; APPLICANT: NAKAMURA, TORU  
; APPLICANT: CHAPMAN, KAREN B.  
; APPLICANT: MORIN, GREGG B.  
; APPLICANT: HARLEY, CALVIN  
; APPLICANT: ANDREWS, WILLIAM H.  
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND  
; TITLE OF INVENTION: TELOMERASE VARIANTS  
; FILE REFERENCE: 018/062  
; CURRENT APPLICATION NUMBER: US/09/438,486A  
; CURRENT FILING DATE: 1999-11-12

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/ PRIOR APPLICATION NUMBER: 08/851,843
/ PRIOR FILING DATE: 1997-05-06
/ PRIOR APPLICATION NUMBER: 08/846,017
/ PRIOR FILING DATE: 1997-04-25
/ PRIOR APPLICATION NUMBER: 08/844,419
/ PRIOR FILING DATE: 1997-04-18
/ PRIOR APPLICATION NUMBER: 08/724,643
/ PRIOR FILING DATE: 1996-10-01
/ NUMBER OF SEQ ID NOS: 223
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 42
/ LENGTH: 44
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
/
US-09-438-486A-42

Query Match          100.0%; Score 20; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   |||||||
Db 25 TTTTGGGTTTGGGGTTTT 44

RESULT 11
US-08-851-843A-41
/ Sequence 41, Application US/08851843A
/ Patent No. 6093809
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: No. 6093809el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/851,843A
/ FILING DATE: 06-MAY-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/
```

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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/
US-08-851-843A-41

Query Match          100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   |||||||
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 12
US-08-974-549A-567
/ Sequence 567, Application US/08974549A
/ Patent No. 6166178
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin B.
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/974,549A
/ FILING DATE: 19-NOV-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 567:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..46
; OTHER INFORMATION: /note= "hairpin primer"
;
US-08-974-549A-567

Query Match 100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTGGGGTTTT 20
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 13
US-08-854-050-41
; Sequence 41, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..46
; OTHER INFORMATION: /desc = "DNA"
;
US-08-854-050-41

Query Match 100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTGGGGTTTT 20
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 14
US-09-430-323-41
; Sequence 41, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
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/ FILING DATE: 25-APR-1997  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002930US  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 41:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 46 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-09-430-323-41  
  
Query Match 100.0%; Score 20; DB 3; Length 46;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 27 TTTTGGGGTTTGGGGTTTT 46  
  
RESULT 15  
US-09-402-181B-567  
/ Sequence 567, Application US/09402181B  
/ Patent No. 6610839  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin B.  
/ Andrews, William H.  
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
/ NUMBER OF SEQUENCES: 633  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, Eighth Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 94111-3834  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/402,181B  
/ FILING DATE: 29-Sep-1997  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997  
/ APPLICATION NUMBER: US 08/851,843  
/ FILING DATE: 06-MAY-1997  
/ APPLICATION NUMBER: US 08/854,050  
/ FILING DATE: 09-MAY-1997

/ APPLICATION NUMBER: US 08/911,312  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: US 08/912,951  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: US 08/915,503  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: WO PCT/US97/17885  
/ FILING DATE: 01-OCT-1997  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Ausenhus, Scott L.  
/ REGISTRATION NUMBER: 42,271  
/ REFERENCE/DOCKET NUMBER: 015389-002620US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 567:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 46 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA  
/ FEATURE:  
/ NAME/KEY: -  
/ LOCATION: 1..46  
/ OTHER INFORMATION: /note= "hairpin primer"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 567:  
US-09-402-181B-567  
  
Query Match 100.0%; Score 20; DB 3; Length 46;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 27 TTTTGGGGTTTGGGGTTTT 46  
  
RESULT 16  
US-09-721-456-567  
/ Sequence 567, Application US/09721456  
/ Patent No. 6617110  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin B.  
/ Andrews, William H.  
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
/ NUMBER OF SEQUENCES: 727  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, Eighth Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 94111-3834  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/721,456  
/ FILING DATE: 22-No. 6617110-2000  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/974,549A  
/ FILING DATE: 19-NOV-1997  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996



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/
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 567:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..46
/ OTHER INFORMATION: /note= "hairpin primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 567:
US-09-721-456-567

Query Match 100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 17
US-09-766-253-41
; Sequence 41, Application US/09766253
; Patent No. 680880
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 680880a1 Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
;

/
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09766,253
/ FILING DATE: 19-Jan-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/846,017
/ FILING DATE: 1997-04-25
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002920US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-766-253-41

Query Match 100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 18
US-10-054-295-41
; Sequence 41, Application US/10054295
; Patent No. 6921664
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6921664e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
;
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; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 46 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: other nucleic acid
;   DESCRIPTION: /desc = "DNA"
;   SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-054-295-41

Query Match          100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 27 TTTTGGGGTTTGGGGTTTT 46

RESULT 19
US-09-438-486A-41
; Sequence 41, Application US/09438486A
; Patent No. 6927285
; GENERAL INFORMATION:
;   APPLICANT: CECH, THOMAS R.
;   APPLICANT: LINGNER, JOACHIM
;   APPLICANT: NAKAMURA, TORU
;   APPLICANT: CHAPMAN, KAREN B.
;   APPLICANT: MORIN, GREGG B.
;   APPLICANT: HARLEY, CALVIN
;   APPLICANT: ANDREWS, WILLIAM H.
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
; FILE REFERENCE: 018/062
; CURRENT APPLICATION NUMBER: US/09/438,486A
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 08/851,843
; PRIOR FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: 08/846,017
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/844,419
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 08/724,643
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 41
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-438-486A-41

Query Match          100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 20
US-08-851-843A-37
; Sequence 37, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
;   APPLICANT: Cech, Thomas R.
;   APPLICANT: Lingner, Joachim
;   APPLICANT: Nakamura, Toru
;   APPLICANT: Chapman, Karen B.
;   APPLICANT: Morin, Gregg B.
;   APPLICANT: Harley, Calvin
;   APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, 8th Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 94111
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/851,843A
;   FILING DATE: 06-MAY-1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/846,017
;     FILING DATE: 25-APR-1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/844,419
;     FILING DATE: 18-APR-1997
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/724,643
;     FILING DATE: 01-OCT-1996
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Apple, Randolph T.
;     REGISTRATION NUMBER: 36,429
;     REFERENCE/DOCKET NUMBER: 015389-002930US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (415) 576-0200
;       TELEFAX: (415) 576-0300
;     INFORMATION FOR SEQ ID NO: 37:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 48 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;         MOLECULE TYPE: other nucleic acid
;         DESCRIPTION: /desc = "DNA"
US-08-851-843A-37

Query Match          100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 21
US-08-851-843A-40
; Sequence 40, Application US/08851843A
; Patent No. 6093809
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GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin H.  
TITLE OF INVENTION: No. 6093809e1 Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

US-08-851-843A-40

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGTTTGGGGTTTT 48

## RESULT 22

US-08-974-549A-564  
Sequence 564, Application US/08974549A  
Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin H.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 564:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..48  
OTHER INFORMATION: /note= "hairpin primer"

US-08-974-549A-564

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
 Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 23  
 US-08-854-050-37  
 ; Sequence 37, Application US/08854050  
 ; Patent No. 6261836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cech, Thomas R.  
 ; APPLICANT: Lingner, Joachim  
 ; APPLICANT: Nakamura, Toru  
 ; APPLICANT: Chapman, Karen B.  
 ; APPLICANT: Morin, Gregg B.  
 ; APPLICANT: Harley, Calvin  
 ; APPLICANT: Andrews, William H.  
 ; TITLE OF INVENTION: No. 6261836el Telomerase  
 ; NUMBER OF SEQUENCES: 225  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States of America  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/854,050  
 ; FILING DATE: 09-MAY-1997  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/851,843  
 ; FILING DATE: 06-MAY-1997  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/846,017  
 ; FILING DATE: 25-APR-1997  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/844,419  
 ; FILING DATE: 18-APR-1997  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/724,643  
 ; FILING DATE: 01-OCT-1996  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Apple, Randolph T.  
 ; REGISTRATION NUMBER: 36,429  
 ; REFERENCE/DOCKET NUMBER: 015389-002930US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 37:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 48 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; DESCRIPTION: /desc = "DNA"  
 US-08-854-050-37

Query Match 100.0%; Score 20; DB 3; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
 Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 24  
 US-08-854-050-40  
 ; Sequence 40, Application US/08854050  
 ; Patent No. 6261836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cech, Thomas R.  
 ; APPLICANT: Lingner, Joachim  
 ; APPLICANT: Nakamura, Toru  
 ; APPLICANT: Chapman, Karen B.  
 ; APPLICANT: Morin, Gregg B.  
 ; APPLICANT: Harley, Calvin  
 ; APPLICANT: Andrews, William H.  
 ; TITLE OF INVENTION: No. 6261836el Telomerase  
 ; NUMBER OF SEQUENCES: 225  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States of America  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/854,050  
 ; FILING DATE: 09-MAY-1997  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/851,843  
 ; FILING DATE: 06-MAY-1997  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/846,017  
 ; FILING DATE: 25-APR-1997  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/844,419  
 ; FILING DATE: 18-APR-1997  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/724,643  
 ; FILING DATE: 01-OCT-1996  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Apple, Randolph T.  
 ; REGISTRATION NUMBER: 36,429  
 ; REFERENCE/DOCKET NUMBER: 015389-002930US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 40:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 48 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; DESCRIPTION: /desc = "DNA"  
 US-08-854-050-40

Query Match 100.0%; Score 20; DB 3; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 7;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 25  
US-09-430-323-37  
; Sequence 37, Application US/09430323  
; Patent No. 6309867  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. 6309867el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/430,323  
; FILING DATE: 29-Oct-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 48 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-430-323-37

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 26  
US-09-430-323-40  
; Sequence 40, Application US/09430323  
; Patent No. 6309867  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. 6309867el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/430,323  
; FILING DATE: 29-Oct-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 48 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-09-430-323-40

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 27  
US-09-402-181B-564  
; Sequence 564, Application US/09402181B  
; Patent No. 6610839  
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181B  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Aussenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 564:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..48  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 564:  
US-09-402-181B-564

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 28  
US-09-721-456-564  
Sequence 564, Application US/09721456  
Patent No. 6617110  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-No. 6617110-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 564:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..48  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 564:

US-09-721-456-564

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 29

US-09-766-253-37  
; Sequence 37, Application US/09766253  
; Patent No. 6808880

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.

; TITLE OF INVENTION: No. 6808880el Telomerase

; NUMBER OF SEQUENCES: 171

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION NUMBER: US/09/766,253

; FILING DATE: 19-Jan-2001

; CLASSIFICATION: <Unknown>

; APPLICATION DATA:

; APPLICATION NUMBER: 08/846,017

; FILING DATE: 1997-04-25

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002920US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 48 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA"

; SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-766-253-37

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 30

US-09-766-253-40

; Sequence 40, Application US/09766253

; Patent No. 6808880

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.

; TITLE OF INVENTION: No. 6808880el Telomerase

; NUMBER OF SEQUENCES: 171

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION NUMBER: US/09/766,253

; FILING DATE: 19-Jan-2001

; CLASSIFICATION: <Unknown>

; APPLICATION DATA:

; APPLICATION NUMBER: 08/846,017

; FILING DATE: 1997-04-25

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002920US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 48 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA"

; SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-766-253-40

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 31

US-10-054-295-37

; Sequence 37, Application US/10054295

; Patent No. 6921664

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin

```
; Andrews, William H.
; TITLE OF INVENTION: No. 6921664e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-054-295-37

Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTTGGGGTTTT 48

RESULT 32
US-10-054-295-40
; Sequence 40, Application US/10054295
; Patent No. 6921664
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6921664e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
```

```
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-054-295-40

Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTTGGGGTTTT 48

RESULT 33
US-09-438-486A-37
; Sequence 37, Application US/09438486A
; Patent No. 6927285
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
; TITLE OF INVENTION: TELOMERASE VARIANTS
; FILE REFERENCE: 018/062
; CURRENT APPLICATION NUMBER: US/09/438,486A
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 08/851,843
; PRIOR FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: 08/846,017
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/844,419
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 08/724,643
; PRIOR FILING DATE: 1996-10-01
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; NUMBER OF SEQ ID NOS: 223
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-438-486A-37

Query Match          100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
   |||||||
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 34
US-09-438-486A-40
; Sequence 40, Application US/09438486A
; Patent No. 6927285
; GENERAL INFORMATION:
; APPLICANT: CECHE, THOMAS R.
; APPLICANT: LINGNER, JOACHIM
; APPLICANT: NAKAMURA, TORU
; APPLICANT: CHAPMAN, KAREN B.
; APPLICANT: MORIN, GREGG B.
; APPLICANT: HARLEY, CALVIN
; APPLICANT: ANDREWS, WILLIAM H.
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
; TITLE OF INVENTION: TELOMERASE VARIANTS
; FILE REFERENCE: 018/062
; CURRENT APPLICATION NUMBER: US/09/438,486A
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 08/851,843
; PRIOR FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: 08/846,017
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/844,419
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 08/724,643
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 223
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 40
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-438-486A-40

Query Match          100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
   |||||||
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 35
US-08-851-843A-39
; Sequence 39, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
```

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; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-851-843A-39

Query Match          100.0%; Score 20; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
   |||||||
Db 31 TTTTGGGGTTTGGGGTTTT 50

RESULT 36
US-08-974-549A-566
; Sequence 566, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
```

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;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/974,549A
;; FILING DATE: 19-NOV-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 566:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 50 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..50
;; OTHER INFORMATION: /note= "hairpin primer"
US-08-974-549A-566
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Query Match 100.0%; Score 20; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TTTTGGGGTTTGGGGTTTT 20
    ||||||||||||||||
Db 31 TTTTGGGGTTTGGGGTTTT 50
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```
RESULT 37
US-08-854-050-39
; Sequence 39, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-854-050-39
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Query Match 100.0%; Score 20; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 TTTTGGGGTTTGGGGTTTT 20
    ||||||||||||||||
Db 31 TTTTGGGGTTTGGGGTTTT 50
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## RESULT 38

US-09-430-323-39

; Sequence 39, Application US/09430323

; Patent No. 6309867

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. 6309867el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/430,323

; FILING DATE: 29-Oct-1999

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 50 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA"

; SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-430-323-39

Query Match 100.0%; Score 20; DB 3; Length 50;

Best Local Similarity 100.0%; Pred. No. 7.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20

Db 31 TTTTGGGGTTTGGGGTTTT 50

## RESULT 39

US-09-402-181B-566

; Sequence 566, Application US/09402181B

; Patent No. 6610839

; GENERAL INFORMATION:

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RESULT 40  
US-09-721-456-566  
; Sequence 566, Application US/09721456  
; Patent No. 6617110  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; ; Lingner, Joachim  
; ; Nakamura, Toru  
; ; Chapman, Karen B.  
; ; Morin, Gregg B.  
; ; Harley, Calvin B.  
; ; Andrews, William H.  
; ;  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/721,456  
; FILING DATE: 22-Nov. 6617110-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 566:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..50  
; OTHER INFORMATION: /note= "hairpin primer"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 566:

US-09-721-456-566

Query Match 100.0%; Score 20; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20  
|||||  
Db 31 TTTTGGGGTTTGGGGTTT 50  
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RESULT 41

US-09-766-253-39  
; Sequence 39, Application US/09766253  
; Patent No. 6808880  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; ; Lingner, Joachim  
; ; Nakamura, Toru  
; ; Chapman, Karen B.  
; ; Morin, Gregg B.  
; ; Harley, Calvin  
; ; Andrews, William H.  
; ;  
; TITLE OF INVENTION: No. 6808880el Telomerase  
; NUMBER OF SEQUENCES: 171  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/766,253  
; FILING DATE: 19-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/846,017  
; FILING DATE: 1997-04-25  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002920US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-766-253-39

Query Match 100.0%; Score 20; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20  
|||||  
Db 31 TTTTGGGGTTTGGGGTTT 50  
|||||

RESULT 42  
US-10-054-295-39  
Sequence 39, Application US/10054295  
Patent No. 6921664  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
LINGNER, JOACHIM  
NAKAMURA, TORU  
CHAPMAN, KAREN B.  
MORIN, GREGG B.  
HARLEY, CALVIN  
ANDREWS, WILLIAM H.  
TITLE OF INVENTION: No. 6921664e1 Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/054,295  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-10-054-295-39  
Query Match 100.0%; Score 20; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 31 TTTTGGGGTTTGGGGTTTT 50  
RESULT 43  
US-09-438-486A-39  
Sequence 39, Application US/09438486A  
Patent No. 6927285  
GENERAL INFORMATION:  
APPLICANT: CECH, THOMAS R.  
LINGNER, JOACHIM

APPLICANT: NAKAMURA, TORU  
APPLICANT: CHAPMAN, KAREN B.  
APPLICANT: MORIN, GREGG B.  
APPLICANT: HARLEY, CALVIN  
APPLICANT: ANDREWS, WILLIAM H.  
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND  
TELOMERASE VARIANTS  
FILE REFERENCE: 018/062  
CURRENT APPLICATION NUMBER: US/09/438,486A  
CURRENT FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 08/851,843  
PRIOR FILING DATE: 1997-05-06  
PRIOR APPLICATION NUMBER: 08/846,017  
PRIOR FILING DATE: 1997-04-25  
PRIOR APPLICATION NUMBER: 08/844,419  
PRIOR FILING DATE: 1997-04-18  
PRIOR APPLICATION NUMBER: 08/724,643  
PRIOR FILING DATE: 1996-10-01  
NUMBER OF SEQ ID NOS: 223  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 39  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide  
US-09-438-486A-39  
Query Match 100.0%; Score 20; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 31 TTTTGGGGTTTGGGGTTTT 50  
RESULT 44  
US-08-851-843A-39/c  
Sequence 39, Application US/08851843A  
Patent No. 6093809  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809e1 Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419

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/ FILING DATE: 18-APR-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
US-08-851-843A-39

Query Match 90.0%; Score 18; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 18
Db 18 TTTTGGGTTTGGGGTTT 1

RESULT 45
US-08-974-549A-566/c
/ Sequence 566, Application US/08974549A
/ Patent No. 6166178
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin B.
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/ APPLICATION NUMBER: US/08/974,549A
/ FILING DATE: 19-NOV-1997
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/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/851,843
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/ FILING DATE: 06-MAY-1997
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/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 566:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..50
/ OTHER INFORMATION: /note= "hairpin primer"
US-08-974-549A-566

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 18
Db 18 TTTTGGGTTTGGGGTTT 1

RESULT 46
US-08-854-050-39/c
/ Sequence 39, Application US/08854050
/ Patent No. 6261836
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: No. 6261836el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/ FILING DATE: 06-MAY-1997
/ CLASSIFICATION: 536
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ CLASSIFICATION: 536
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ CLASSIFICATION: 536
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION: 536
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
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/ US-08-854-050-39
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/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ Db 18 TTTTGGGTTTGGGGTT 1
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/ RESULT 47
/ US-09-430-323-39/c
/ Sequence 39, Application US/09430323
/ Patent No. 6309867
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/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/
/ TITLE OF INVENTION: No. 6309867el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
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/ Best Local Similarity 100.0%; Pred. No. 50;
/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ RESULT 48
/ US-09-402-181B-566/c
/ Sequence 566, Application US/09402181B
/ Patent No. 6610839
/
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/
/ COMPUTER READABLE FORM:
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/ COMPUTER: IBM PC compatible
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/ PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/724,643
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; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 566:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..50
; OTHER INFORMATION: /note= "hairpin primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 566:
US-09-402-181B-566

Query Match 90.0%; Score 18; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 18 TTTTGGGTTTGGGTT 1

RESULT 49
US-09-721-456-566/c
; Sequence 566, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 566:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..50
; OTHER INFORMATION: /note= "hairpin primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 566:
US-09-721-456-566

Query Match 90.0%; Score 18; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTT 18
Db 18 TTTTGGGTTTGGGTT 1

RESULT 50
US-09-766-253-39/c
; Sequence 39, Application US/09766253
; Patent No. 6808880
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6808880el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:

```



ADDRESSES: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,253  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/846,017  
FILING DATE: 1997-04-25  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002920US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-766-253-39

Query Match 90.0%; Score 18; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 18 TTTTGGGGTTTGGGGTT 1

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC

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Searched: 9793542 seqs, 4134689005 residues

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Minimum DB seq length: 0

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Maximum Match 100%

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## SUMMARIES

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| 4          | 20    | 100.0 | 20     | 5  | US-10-017-995-73  | Sequence 73, Appl  |
| 5          | 20    | 100.0 | 20     | 6  | US-10-314-578-73  | Sequence 73, Appl  |
| 6          | 20    | 100.0 | 20     | 8  | US-10-831-778-73  | Sequence 73, Appl  |
| 7          | 20    | 100.0 | 28     | 6  | US-10-118-854-28  | Sequence 28, Appl  |
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| 9          | 20    | 100.0 | 28     | 9  | US-10-683-480-28  | Sequence 28, Appl  |
| 10         | 20    | 100.0 | 28     | 9  | US-10-690-984-11  | Sequence 11, Appl  |
| 11         | 20    | 100.0 | 28     | 9  | US-10-961-479-29  | Sequence 29, Appl  |
| 12         | 20    | 100.0 | 44     | 3  | US-09-843-676-42  | Sequence 42, Appl  |
| 13         | 20    | 100.0 | 44     | 3  | US-09-766-253-42  | Sequence 42, Appl  |
| 14         | 20    | 100.0 | 44     | 3  | US-09-438-486-42  | Sequence 42, Appl  |
| 15         | 20    | 100.0 | 44     | 5  | US-10-053-758-42  | Sequence 42, Appl  |
| 16         | 20    | 100.0 | 44     | 5  | US-10-054-295-42  | Sequence 42, Appl  |
| 17         | 20    | 100.0 | 44     | 5  | US-10-054-611-42  | Sequence 42, Appl  |
| 18         | 20    | 100.0 | 44     | 6  | US-10-325-810-568 | Sequence 568, Appl |
| 19         | 20    | 100.0 | 44     | 8  | US-10-877-124-568 | Sequence 568, Appl |
| 20         | 20    | 100.0 | 44     | 8  | US-10-877-022-568 | Sequence 568, Appl |
| 21         | 20    | 100.0 | 44     | 8  | US-10-877-146-568 | Sequence 568, Appl |
| 22         | 20    | 100.0 | 46     | 3  | US-09-843-676-41  | Sequence 41, Appl  |
| 23         | 20    | 100.0 | 46     | 3  | US-09-766-253-41  | Sequence 41, Appl  |

|       |      |      |    |    |                      |                   |       |      |      |    |    |                      |                   |
|-------|------|------|----|----|----------------------|-------------------|-------|------|------|----|----|----------------------|-------------------|
| C 97  | 16.8 | 84.0 | 48 | 5  | US-10-053-758-37     | Sequence 37, Appl | C 170 | 14.2 | 71.0 | 26 | 5  | US-10-054-611-30     | Sequence 30, Appl |
| C 98  | 16.8 | 84.0 | 48 | 5  | US-10-053-758-40     | Sequence 40, Appl | C 171 | 14.2 | 71.0 | 26 | 5  | US-10-054-611-60     | Sequence 60, Appl |
| C 99  | 16.8 | 84.0 | 48 | 5  | US-10-054-295-37     | Sequence 37, Appl | C 172 | 14.2 | 71.0 | 26 | 6  | US-10-325-810-557    | Sequence 557, App |
| C 100 | 16.8 | 84.0 | 48 | 5  | US-10-054-295-40     | Sequence 40, Appl | C 173 | 14.2 | 71.0 | 26 | 8  | US-10-877-124-557    | Sequence 557, App |
| C 101 | 16.8 | 84.0 | 48 | 5  | US-10-054-611-37     | Sequence 37, Appl | C 174 | 14.2 | 71.0 | 26 | 8  | US-10-877-023-557    | Sequence 557, App |
| C 102 | 16.8 | 84.0 | 48 | 5  | US-10-054-611-40     | Sequence 40, Appl | C 175 | 14.2 | 71.0 | 26 | 8  | US-10-877-146-557    | Sequence 557, App |
| C 103 | 16.8 | 84.0 | 48 | 6  | US-10-325-810-564    | Sequence 564, App | C 176 | 14.2 | 71.0 | 32 | 6  | US-10-369-214-99     | Sequence 99, Appl |
| C 104 | 16.8 | 84.0 | 48 | 8  | US-10-877-124-564    | Sequence 564, App | C 177 | 14.2 | 71.0 | 46 | 10 | US-11-049-446-117    | Sequence 117, App |
| C 105 | 16.8 | 84.0 | 48 | 8  | US-10-877-022-564    | Sequence 564, App | C 178 | 14.2 | 71.0 | 50 | 6  | US-10-131-827-4217   | Sequence 4217, Ap |
| C 106 | 16.8 | 84.0 | 48 | 8  | US-10-877-146-564    | Sequence 564, App | C 179 | 14.2 | 71.0 | 50 | 6  | US-10-131-827-7605   | Sequence 7605, Ap |
| C 107 | 16.8 | 84.0 | 50 | 6  | US-10-131-827-5734   | Sequence 5734, Ap | C 180 | 14   | 70.0 | 15 | 3  | US-09-843-676-43     | Sequence 43, Appl |
| C 108 | 16   | 80.0 | 16 | 3  | US-09-843-676-61     | Sequence 61, Appl | C 181 | 14   | 70.0 | 15 | 3  | US-09-843-676-45     | Sequence 45, Appl |
| C 109 | 16   | 80.0 | 16 | 3  | US-09-766-253-61     | Sequence 61, Appl | C 182 | 14   | 70.0 | 15 | 3  | US-09-766-253-43     | Sequence 43, Appl |
| C 110 | 16   | 80.0 | 16 | 3  | US-09-438-486-61     | Sequence 61, Appl | C 183 | 14   | 70.0 | 15 | 3  | US-09-766-253-45     | Sequence 45, Appl |
| C 111 | 16   | 80.0 | 16 | 5  | US-10-053-758-61     | Sequence 61, Appl | C 184 | 14   | 70.0 | 15 | 3  | US-09-438-486-43     | Sequence 43, Appl |
| C 112 | 16   | 80.0 | 16 | 5  | US-10-054-295-61     | Sequence 61, Appl | C 185 | 14   | 70.0 | 15 | 3  | US-09-438-486-45     | Sequence 45, Appl |
| C 113 | 16   | 80.0 | 16 | 6  | US-10-054-611-61     | Sequence 61, Appl | C 186 | 14   | 70.0 | 15 | 5  | US-10-053-758-43     | Sequence 43, Appl |
| C 114 | 16   | 80.0 | 16 | 6  | US-10-325-810-114    | Sequence 114, App | C 187 | 14   | 70.0 | 15 | 5  | US-10-053-758-45     | Sequence 45, Appl |
| C 115 | 16   | 80.0 | 16 | 8  | US-10-877-124-114    | Sequence 114, App | C 188 | 14   | 70.0 | 15 | 5  | US-10-054-295-43     | Sequence 43, Appl |
| C 116 | 16   | 80.0 | 16 | 8  | US-10-877-022-114    | Sequence 114, App | C 189 | 14   | 70.0 | 15 | 5  | US-10-054-295-45     | Sequence 45, Appl |
| C 117 | 16   | 80.0 | 16 | 8  | US-10-877-146-114    | Sequence 114, App | C 190 | 14   | 70.0 | 15 | 5  | US-10-054-611-43     | Sequence 43, Appl |
| C 118 | 15.8 | 79.0 | 20 | 10 | US-11-166-990-39     | Sequence 39, Appl | C 191 | 14   | 70.0 | 15 | 5  | US-10-054-611-45     | Sequence 45, Appl |
| C 119 | 15.4 | 77.0 | 19 | 8  | US-10-845-667-1035   | Sequence 1035, Ap | C 192 | 14   | 70.0 | 15 | 6  | US-10-325-810-113    | Sequence 113, App |
| C 120 | 15.4 | 77.0 | 19 | 9  | US-10-973-783-1416   | Sequence 1416, Ap | C 193 | 14   | 70.0 | 15 | 8  | US-10-877-124-113    | Sequence 113, App |
| C 121 | 15.4 | 77.0 | 25 | 9  | US-10-956-157-129722 | Sequence 129722,  | C 194 | 14   | 70.0 | 15 | 8  | US-10-877-023-113    | Sequence 113, App |
| C 122 | 15.4 | 77.0 | 26 | 10 | US-11-049-446-60     | Sequence 60, Appl | C 195 | 14   | 70.0 | 15 | 8  | US-10-877-146-113    | Sequence 113, App |
| C 123 | 15.2 | 76.0 | 26 | 6  | US-10-085-906-51     | Sequence 51, Appl | C 196 | 14   | 70.0 | 20 | 7  | US-10-240-454-66     | Sequence 66, Appl |
| C 124 | 15.2 | 76.0 | 50 | 6  | US-10-131-827-1029   | Sequence 1029, Ap | C 197 | 14   | 70.0 | 50 | 6  | US-10-131-827-5325   | Sequence 5325, Ap |
| C 125 | 14.8 | 74.0 | 22 | 9  | US-10-708-204-67     | Sequence 67, Appl | C 198 | 13.8 | 69.0 | 17 | 3  | US-09-848-754A-1981  | Sequence 1981, Ap |
| C 126 | 14.8 | 74.0 | 22 | 9  | US-10-708-204-1790   | Sequence 1790, Ap | C 199 | 13.8 | 69.0 | 24 | 7  | US-10-456-930-32     | Sequence 32, Appl |
| C 127 | 14.8 | 74.0 | 24 | 3  | US-09-888-326-735    | Sequence 735, App | C 200 | 13.8 | 69.0 | 24 | 8  | US-10-266-103-11     | Sequence 11, Appl |
| C 128 | 14.8 | 74.0 | 24 | 3  | US-09-776-479-692    | Sequence 692, App | C 201 | 13.8 | 69.0 | 24 | 8  | US-10-266-103-48     | Sequence 48, Appl |
| C 129 | 14.8 | 74.0 | 24 | 3  | US-09-776-479-694    | Sequence 694, App | C 202 | 13.8 | 69.0 | 25 | 7  | US-10-719-956-257773 | Sequence 257773,  |
| C 130 | 14.8 | 74.0 | 24 | 3  | US-09-776-479-883    | Sequence 883, App | C 203 | 13.8 | 69.0 | 25 | 8  | US-10-719-900-750629 | Sequence 750629,  |
| C 131 | 14.8 | 74.0 | 24 | 3  | US-09-776-479-692    | Sequence 692, App | C 204 | 13.8 | 69.0 | 25 | 2  | US-08-781-986A-2244  | Sequence 2244, Ap |
| C 132 | 14.8 | 74.0 | 24 | 3  | US-09-776-479-694    | Sequence 694, App | C 205 | 13.8 | 69.0 | 50 | 7  | US-10-329-624-2244   | Sequence 2244, Ap |
| C 133 | 14.8 | 74.0 | 24 | 3  | US-09-776-479-883    | Sequence 883, App | C 206 | 13.6 | 68.0 | 22 | 9  | US-10-708-204-371    | Sequence 371, App |
| C 134 | 14.8 | 74.0 | 24 | 5  | US-10-112-653-665    | Sequence 665, App | C 207 | 13.6 | 68.0 | 22 | 9  | US-10-708-204-2154   | Sequence 2154, Ap |
| C 135 | 14.8 | 74.0 | 24 | 5  | US-10-112-653-667    | Sequence 667, App | C 208 | 13.6 | 68.0 | 25 | 7  | US-10-719-956-474680 | Sequence 474680,  |
| C 136 | 14.8 | 74.0 | 24 | 5  | US-10-112-653-854    | Sequence 854, App | C 209 | 13.6 | 68.0 | 25 | 7  | US-10-719-956-692527 | Sequence 692527,  |
| C 137 | 14.8 | 74.0 | 24 | 5  | US-10-017-995-692    | Sequence 692, App | C 210 | 13.6 | 68.0 | 25 | 10 | US-11-036-317-102555 | Sequence 102555,  |
| C 138 | 14.8 | 74.0 | 24 | 5  | US-10-017-995-694    | Sequence 694, App | C 211 | 13.6 | 68.0 | 25 | 10 | US-11-036-317-433201 | Sequence 433201,  |
| C 139 | 14.8 | 74.0 | 24 | 6  | US-10-163-862-4      | Sequence 4, Appl  | C 212 | 13.6 | 68.0 | 27 | 3  | US-09-931-583-35     | Sequence 35, Appl |
| C 140 | 14.8 | 74.0 | 24 | 6  | US-10-140-013-32     | Sequence 32, Appl | C 213 | 13.6 | 68.0 | 27 | 8  | US-10-649-584-35     | Sequence 35, Appl |
| C 141 | 14.8 | 74.0 | 24 | 6  | US-10-314-578-692    | Sequence 692, App | C 214 | 13.6 | 68.0 | 29 | 3  | US-09-888-326-131    | Sequence 131, App |
| C 142 | 14.8 | 74.0 | 24 | 6  | US-10-314-578-694    | Sequence 694, App | C 215 | 13.6 | 68.0 | 29 | 3  | US-09-776-479-305    | Sequence 305, App |
| C 143 | 14.8 | 74.0 | 24 | 6  | US-10-314-578-883    | Sequence 883, App | C 216 | 13.6 | 68.0 | 29 | 3  | US-09-776-479-305    | Sequence 305, App |
| C 144 | 14.8 | 74.0 | 24 | 6  | US-10-309-775A-6     | Sequence 6, Appl  | C 217 | 13.6 | 68.0 | 29 | 5  | US-10-017-995-305    | Sequence 295, App |
| C 145 | 14.8 | 74.0 | 24 | 8  | US-10-831-778-692    | Sequence 692, App | C 218 | 13.6 | 68.0 | 29 | 5  | US-10-017-995-305    | Sequence 305, App |
| C 146 | 14.8 | 74.0 | 24 | 8  | US-10-831-778-694    | Sequence 694, App | C 219 | 13.6 | 68.0 | 29 | 8  | US-10-314-578-305    | Sequence 305, App |
| C 147 | 14.8 | 74.0 | 24 | 8  | US-10-831-778-883    | Sequence 883, App | C 220 | 13.6 | 68.0 | 29 | 8  | US-10-831-778-305    | Sequence 305, App |
| C 148 | 14.8 | 74.0 | 24 | 8  | US-10-163-862-3      | Sequence 3, Appl  | C 221 | 13.6 | 68.0 | 32 | 3  | US-09-888-326-734    | Sequence 734, App |
| C 149 | 14.8 | 74.0 | 46 | 6  | US-10-845-667-285    | Sequence 285, App | C 222 | 13.6 | 68.0 | 32 | 3  | US-09-776-479-429    | Sequence 429, App |
| C 150 | 14.4 | 72.0 | 17 | 8  | US-10-973-783-662    | Sequence 662, App | C 223 | 13.6 | 68.0 | 32 | 3  | US-09-776-479-429    | Sequence 429, App |
| C 151 | 14.4 | 72.0 | 17 | 9  | US-10-845-667-1250   | Sequence 1250, Ap | C 224 | 13.6 | 68.0 | 32 | 5  | US-10-112-653-411    | Sequence 411, App |
| C 152 | 14.4 | 72.0 | 23 | 8  | US-10-845-667-1480   | Sequence 1480, Ap | C 225 | 13.6 | 68.0 | 32 | 5  | US-10-017-995-429    | Sequence 429, App |
| C 153 | 14.4 | 72.0 | 23 | 8  | US-10-845-667-1480   | Sequence 1480, Ap | C 226 | 13.6 | 68.0 | 32 | 5  | US-10-207-655-238    | Sequence 228, App |
| C 154 | 14.4 | 72.0 | 50 | 6  | US-10-131-827-5465   | Sequence 5465, Ap | C 227 | 13.6 | 68.0 | 32 | 6  | US-10-076-674-1      | Sequence 1, Appl  |
| C 155 | 14.2 | 71.0 | 25 | 7  | US-10-719-956-215749 | Sequence 215749,  | C 228 | 13.6 | 68.0 | 32 | 6  | US-10-314-578-429    | Sequence 429, App |
| C 156 | 14.2 | 71.0 | 25 | 7  | US-10-719-956-215750 | Sequence 215750,  | C 229 | 13.6 | 68.0 | 32 | 6  | US-10-355-161A-1     | Sequence 1, Appl  |
| C 157 | 14.2 | 71.0 | 25 | 8  | US-10-719-900-519045 | Sequence 519045,  | C 230 | 13.6 | 68.0 | 32 | 6  | US-10-831-778-429    | Sequence 429, App |
| C 158 | 14.2 | 71.0 | 25 | 8  | US-10-719-900-910968 | Sequence 910968,  | C 231 | 13.6 | 68.0 | 32 | 9  | US-10-627-556-543    | Sequence 543, App |
| C 159 | 14.2 | 71.0 | 25 | 10 | US-11-036-317-433201 | Sequence 433201,  | C 232 | 13.6 | 68.0 | 42 | 5  | US-10-140-164-70     | Sequence 70, Appl |
| C 160 | 14.2 | 71.0 | 26 | 3  | US-09-843-676-30     | Sequence 30, Appl | C 233 | 13.6 | 68.0 | 42 | 8  | US-10-073-333A-38    | Sequence 38, Appl |
| C 161 | 14.2 | 71.0 | 26 | 3  | US-09-843-676-60     | Sequence 60, Appl | C 234 | 13.6 | 68.0 | 42 | 8  | US-10-841-471-38     | Sequence 38, Appl |
| C 162 | 14.2 | 71.0 | 26 | 3  | US-09-766-253-30     | Sequence 30, Appl | C 235 | 13.6 | 68.0 | 47 | 6  | US-10-349-143-842    | Sequence 842, App |
| C 163 | 14.2 | 71.0 | 26 | 3  | US-09-766-253-60     | Sequence 60, Appl | C 236 | 13.6 | 68.0 | 47 | 6  | US-10-349-143-2476   | Sequence 2476, Ap |
| C 164 | 14.2 | 71.0 | 26 | 3  | US-09-438-486-30     | Sequence 30, Appl | C 237 | 13.4 | 67.0 | 25 | 10 | US-11-036-317-34432  | Sequence 34432, A |
| C 165 | 14.2 | 71.0 | 26 | 3  | US-09-438-486-60     | Sequence 60, Appl | C 238 | 13.4 | 67.0 | 30 | 6  | US-10-369-214-100    | Sequence 100, App |
| C 166 | 14.2 | 71.0 | 26 | 5  | US-10-053-758-30     | Sequence 30, Appl | C 239 | 13.2 | 66.0 | 21 | 3  | US-09-253-150-50     | Sequence 50, Appl |
| C 167 | 14.2 | 71.0 | 26 | 5  | US-10-053-758-60     | Sequence 60, Appl | C 240 | 13.2 | 66.0 | 21 | 8  | US-10-646-381-50     | Sequence 50, Appl |
| C 168 | 14.2 | 71.0 | 26 | 5  | US-10-054-298-30     | Sequence 30, Appl | C 241 | 13.2 | 66.0 | 25 | 6  | US-10-316-194-123    | Sequence 123, App |
| C 169 | 14.2 | 71.0 | 26 | 5  | US-10-054-298-60     | Sequence 60, Appl | C 242 | 13.2 | 66.0 | 25 | 7  | US-10-719-956-1069   | Sequence 1069, Ap |

|       |      |      |    |    |                       |                   |
|-------|------|------|----|----|-----------------------|-------------------|
| c 243 | 13.2 | 66.0 | 25 | 7  | US-10-719-956-1070    | Sequence 1070, Ap |
| c 244 | 13.2 | 66.0 | 25 | 7  | US-10-719-956-653453  | Sequence 653453,  |
| c 245 | 13.2 | 66.0 | 25 | 8  | US-10-719-900-161728  | Sequence 161728,  |
| c 246 | 13.2 | 66.0 | 25 | 8  | US-10-719-900-912559  | Sequence 912559,  |
| c 247 | 13.2 | 66.0 | 25 | 8  | US-10-732-180-141     | Sequence 141, App |
| c 248 | 13.2 | 66.0 | 25 | 9  | US-10-843-527-93343   | Sequence 93343, A |
| c 249 | 13.2 | 66.0 | 25 | 9  | US-10-843-527-95877   | Sequence 95876, A |
| c 250 | 13.2 | 66.0 | 25 | 9  | US-10-843-527-95877   | Sequence 95877, A |
| c 251 | 13.2 | 66.0 | 25 | 9  | US-10-843-527-103736  | Sequence 103736,  |
| c 252 | 13.2 | 66.0 | 25 | 9  | US-10-843-527-134441  | Sequence 134441,  |
| c 253 | 13.2 | 66.0 | 25 | 9  | US-10-843-527-142300  | Sequence 142300,  |
| c 254 | 13.2 | 66.0 | 25 | 9  | US-10-843-527-142301  | Sequence 142301,  |
| c 255 | 13.2 | 66.0 | 25 | 9  | US-10-843-527-144834  | Sequence 144834,  |
| c 256 | 13.2 | 66.0 | 25 | 10 | US-11-036-317-925595  | Sequence 925595,  |
| c 257 | 13.2 | 66.0 | 25 | 10 | US-11-060-756-130181  | Sequence 130181,  |
| c 258 | 13.2 | 66.0 | 25 | 10 | US-11-060-756-164159  | Sequence 164159,  |
| c 259 | 13.2 | 66.0 | 25 | 10 | US-11-060-756-235930  | Sequence 235930,  |
| c 260 | 13.2 | 66.0 | 29 | 10 | US-11-049-446-84      | Sequence 84, Appl |
| c 261 | 13.2 | 66.0 | 36 | 8  | US-10-311-645A-103    | Sequence 103, App |
| c 262 | 13   | 65.0 | 13 | 8  | US-10-257-017B-80391  | Sequence 80391, A |
| c 263 | 13   | 65.0 | 13 | 8  | US-10-257-017B-80392  | Sequence 80392, A |
| c 264 | 13   | 65.0 | 13 | 8  | US-10-257-017B-90443  | Sequence 90443, A |
| c 265 | 13   | 65.0 | 13 | 8  | US-10-257-017B-90444  | Sequence 90444, A |
| c 266 | 13   | 65.0 | 13 | 8  | US-10-257-017B-188477 | Sequence 188477,  |
| c 267 | 13   | 65.0 | 13 | 8  | US-10-257-017B-188478 | Sequence 188478,  |
| c 268 | 13   | 65.0 | 25 | 10 | US-11-036-317-750062  | Sequence 750062,  |
| c 269 | 12.8 | 64.0 | 17 | 3  | US-09-848-754A-1382   | Sequence 1382, Ap |
| c 270 | 12.8 | 64.0 | 18 | 6  | US-10-282-174-165     | Sequence 165, App |
| c 271 | 12.8 | 64.0 | 18 | 6  | US-10-349-143-9236    | Sequence 9236, Ap |
| c 272 | 12.8 | 64.0 | 18 | 8  | US-10-473-126-558     | Sequence 558, App |
| c 273 | 12.8 | 64.0 | 18 | 8  | US-10-473-126-692     | Sequence 692, App |
| c 274 | 12.8 | 64.0 | 18 | 8  | US-10-473-126-1035    | Sequence 1035, Ap |
| c 275 | 12.8 | 64.0 | 18 | 8  | US-10-473-126-1036    | Sequence 1036, Ap |
| c 276 | 12.8 | 64.0 | 18 | 8  | US-10-473-126-1132    | Sequence 1132, Ap |
| c 277 | 12.8 | 64.0 | 18 | 8  | US-10-600-009-165     | Sequence 165, App |
| c 278 | 12.8 | 64.0 | 19 | 9  | US-10-881-118-158     | Sequence 158, App |
| c 279 | 12.8 | 64.0 | 19 | 9  | US-10-881-118-321     | Sequence 321, App |
| c 280 | 12.8 | 64.0 | 20 | 7  | US-10-467-126-86      | Sequence 86, Appl |
| c 281 | 12.8 | 64.0 | 21 | 6  | US-10-349-143-8417    | Sequence 8417, Ap |
| c 282 | 12.8 | 64.0 | 22 | 8  | US-10-845-667-500     | Sequence 500, App |
| c 283 | 12.8 | 64.0 | 22 | 8  | US-10-845-667-730     | Sequence 730, App |
| c 284 | 12.8 | 64.0 | 22 | 9  | US-10-973-783-879     | Sequence 879, App |
| c 285 | 12.8 | 64.0 | 22 | 9  | US-10-973-783-1109    | Sequence 1109, Ap |
| c 286 | 12.8 | 64.0 | 23 | 6  | US-10-084-555-107     | Sequence 107, App |
| c 287 | 12.8 | 64.0 | 23 | 9  | US-10-889-898-107     | Sequence 107, App |
| c 288 | 12.8 | 64.0 | 24 | 3  | US-09-888-326-727     | Sequence 727, App |
| c 289 | 12.8 | 64.0 | 24 | 3  | US-09-888-326-847     | Sequence 847, App |
| c 290 | 12.8 | 64.0 | 24 | 3  | US-09-888-326-848     | Sequence 848, App |
| c 291 | 12.8 | 64.0 | 24 | 3  | US-09-776-479-304     | Sequence 304, App |
| c 292 | 12.8 | 64.0 | 24 | 3  | US-09-776-479-358     | Sequence 358, App |
| c 293 | 12.8 | 64.0 | 24 | 3  | US-09-776-479-435     | Sequence 435, App |
| c 294 | 12.8 | 64.0 | 24 | 3  | US-09-776-479-304     | Sequence 304, App |
| c 295 | 12.8 | 64.0 | 24 | 3  | US-09-776-479-358     | Sequence 358, App |
| c 296 | 12.8 | 64.0 | 24 | 3  | US-09-776-479-435     | Sequence 435, App |
| c 297 | 12.8 | 64.0 | 24 | 5  | US-10-112-653-417     | Sequence 417, App |
| c 298 | 12.8 | 64.0 | 24 | 5  | US-10-017-995-304     | Sequence 304, App |
| c 299 | 12.8 | 64.0 | 24 | 5  | US-10-017-995-358     | Sequence 358, App |
| c 300 | 12.8 | 64.0 | 24 | 5  | US-10-017-995-435     | Sequence 435, App |

ALIGNMENTS

RESULT 1

US-09-776-479-73  
; Sequence 73, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; Treatment of Asthma and Allergy

; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 73  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-73

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||  
Db 1 TTTTGGGGTTTGGGGTTTT 20

RESULT 2

US-09-776-479-73  
; Sequence 73, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 73  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-73

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||  
Db 1 TTTTGGGGTTTGGGGTTTT 20

RESULT 3

US-10-112-653-67  
; Sequence 67, Application US/10112653  
; Publication No. US20030050268A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR  
; TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES  
; FILE REFERENCE: C01039/70060(AWS)  
; CURRENT APPLICATION NUMBER: US/10/112,653  
; CURRENT FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-67

Query Match          100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   |||||
Db 1 TTTTGGGTTTGGGGTTTT 20

RESULT 4
US-10-017-995-73
; Sequence 73, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-73

Query Match          100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   |||||
Db 1 TTTTGGGTTTGGGGTTTT 20

RESULT 5
US-10-314-578-73
; Sequence 73, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
US-10-314-578-73

Query Match          100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   |||||
Db 1 TTTTGGGTTTGGGGTTTT 20

RESULT 6
US-10-831-778-73
; Sequence 73, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-73

Query Match          100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   |||||
Db 1 TTTTGGGTTTGGGGTTTT 20

RESULT 7
US-10-118-854-28
; Sequence 28, Application US/10118854
; Publication No. US20030194754A1
; GENERAL INFORMATION:
; APPLICANT: Bates, Paula J
; APPLICANT: Miller, Donald M
; APPLICANT: Trent, John O
; APPLICANT: Xu, Xiaohua
; TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF MALIGNANT
; FILE REFERENCE: 9799910-
; CURRENT APPLICATION NUMBER: US/10/118,854
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-118-854-28

Query Match          100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 5 TTTTGGGGTTTGGGGTTTT 24

## RESULT 8

US-10-607-455-28  
; Sequence 28, Application US/10607455  
; Publication No. US20040132049A1  
; GENERAL INFORMATION:  
; APPLICANT: Bates, Paula J  
; APPLICANT: Mi, Yingchang  
; TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF MALIGNANT  
; DISEASES  
; FILE REFERENCE: 09799910-0034  
; CURRENT APPLICATION NUMBER: US/10/607,455  
; CURRENT FILING DATE: 2003-06-26  
; PRIOR APPLICATION NUMBER: 60/392,143  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 28  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-10-607-455-28

Query Match 100.0%; Score 20; DB 7; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 5 TTTTGGGGTTTGGGGTTTT 24

## RESULT 9

US-10-683-480-28  
; Sequence 28, Application US/10683480  
; Publication No. US20050053607A1  
; GENERAL INFORMATION:  
; APPLICANT: BATES, PAULA J.  
; APPLICANT: MILLER, DONALD M.  
; APPLICANT: TRENT, JOHN O.  
; APPLICANT: XU, XIAOHUA  
; TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF  
; MALIGNANT DISEASES  
; FILE REFERENCE: LOU01-012-CIP-US  
; CURRENT APPLICATION NUMBER: US/10/683,480  
; CURRENT FILING DATE: 2003-10-09  
; PRIOR APPLICATION NUMBER: 10/118,854  
; PRIOR FILING DATE: 2002-04-08  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 28  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: polynucleotide sequence  
US-10-683-480-28

Query Match 100.0%; Score 20; DB 9; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||

Db 5 TTTTGGGGTTTGGGGTTTT 24

## RESULT 10

US-10-690-984-11  
; Sequence 11, Application US/10690984  
; Publication No. US20050090671A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Ta-Chau  
; APPLICANT: Chang, Cheng-Chung  
; APPLICANT: Wu, Jin-Yi  
; TITLE OF INVENTION: QUADRUPEX STABILIZER  
; FILE REFERENCE: 08919-112001  
; CURRENT APPLICATION NUMBER: US/10/690,984  
; CURRENT FILING DATE: 2003-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated oligonucleotide  
US-10-690-984-11

Query Match 100.0%; Score 20; DB 9; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 5 TTTTGGGGTTTGGGGTTTT 24

## RESULT 11

US-10-961-479-29  
; Sequence 29, Application US/10961479  
; Publication No. US20050187176A1  
; GENERAL INFORMATION:  
; APPLICANT: BATES, PAULA J.  
; APPLICANT: GIRVAN, ALLICIA C.  
; APPLICANT: BARVE, SHIRISH S.  
; TITLE OF INVENTION: METHOD FOR INHIBITING NF-KAPPA B SIGNALING AND USE TO  
; TREAT OR PREVENT HUMAN DISEASES  
; FILE REFERENCE: LOU01-010-US  
; CURRENT APPLICATION NUMBER: US/10/961,479  
; CURRENT FILING DATE: 2004-10-08  
; PRIOR APPLICATION NUMBER: 60/510,466  
; PRIOR FILING DATE: 2003-10-10  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 29  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: polynucleotide sequence  
US-10-961-479-29

Query Match 100.0%; Score 20; DB 9; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 5 TTTTGGGGTTTGGGGTTTT 24

## RESULT 12

US-09-843-676-42  
; Sequence 42, Application US/09843676  
; Patent No. US20020164786A1

```
/
/
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin
/ Andrews, William H.
/
/ TITLE OF INVENTION: No. US20020164786A1el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/843,676
/ FILING DATE: 26-Apr-2001
/ CLASSIFICATION: 536
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 44 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 42:
/
/ US-09-843-676-42
/
/ Query Match 100.0%; Score 20; DB 3; Length 44;
/ Best Local Similarity 100.0%; Pred. No. 1.2e+02;
/ Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 TTTTGGGGTTTGGGGTTTT 20
/ Db 25 TTTTGGGGTTTGGGGTTTT 44
/
/ RESULT 13
/ US-09-766-253-42
/ Sequence 42, Application US/09766253
/ Publication No. US2002018741A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin
/
/ TITLE OF INVENTION: No. US2002018741A1el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/
/ COMPUTER READABLE FORM:
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/
/
/ Andrews, William H.
/
/ TITLE OF INVENTION: No. US2002018741A1el Telomerase
/ NUMBER OF SEQUENCES: 171
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/766,253
/ FILING DATE: 19-Jan-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/846,017
/ FILING DATE: 1997-04-25
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002920US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 44 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 42:
/
/ US-09-766-253-42
/
/ Query Match 100.0%; Score 20; DB 3; Length 44;
/ Best Local Similarity 100.0%; Pred. No. 1.2e+02;
/ Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 TTTTGGGGTTTGGGGTTTT 20
/ Db 25 TTTTGGGGTTTGGGGTTTT 44
/
/ RESULT 14
/ US-09-438-486-42
/ Sequence 42, Application US/09438486
/ Publication No. US20030009019A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/
/ TITLE OF INVENTION: No. US20030009019A1el Telomerase
/ NUMBER OF SEQUENCES: 223
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111-3834
/
/ COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
;
US-09-438-486-42

Query Match 100.0%; Score 20; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20
Db 25 TTTTGGGTTTGGGGTTT 44

RESULT 15
US-10-053-758-42
; Sequence 42, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
;
US-10-053-758-42

Query Match 100.0%; Score 20; DB 5; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20
Db 25 TTTTGGGTTTGGGGTTT 44

RESULT 16
US-10-054-295-42
; Sequence 42, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
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/
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/854,050
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION/DOCKET NUMBER: 015389-002930US
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 44 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-054-295-42

Query Match 100.0%; Score 20; DB 5; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20
Db 25 TTTTGGGGTTTGGGGTTTT 44

RESULT 17
US-10-054-611-42
/ Sequence 42, Application US/10054611
/ Publication No. US20030059787A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin
/ Andrews, William H.
/ TITLE OF INVENTION: No. US20030059787A1el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/054,611
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/854,050
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
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/
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION/DOCKET NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 44 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-054-611-42

Query Match 100.0%; Score 20; DB 5; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20
Db 25 TTTTGGGGTTTGGGGTTTT 44

RESULT 18
US-10-325-810-568
/ Sequence 568, Application US/10325810
/ Publication No. US20030204069A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/325,810
/ FILING DATE: 20-Dec-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181
/ FILING DATE: 29-Sep-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
```

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/
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Aussenhus, Scott L.
/ REGISTRATION NUMBER: 42,271
/ REFERENCE/DOCKET NUMBER: 015389-002620US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 568:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 44 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..44
/ OTHER INFORMATION: /note= "hairpin primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 568:
US-10-325-810-568

Query Match 100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 25 TTTTGGGTTTGGGGTTTT 44

RESULT 19
US-10-877-124-568
/ Sequence 568, Application US/10877124
/ Publication No. US20040242529A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/877,124
/ FILING DATE: 24-Jun-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/432,503
/ FILING DATE: 02-Nov-1999
/ APPLICATION NUMBER: 08/974,549
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/
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 568:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 44 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..44
/ OTHER INFORMATION: /note= "hairpin primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 568:
US-10-877-124-568

Query Match 100.0%; Score 20; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 25 TTTTGGGTTTGGGGTTTT 44

RESULT 20
US-10-877-022-568
/ Sequence 568, Application US/10877022
/ Publication No. US20040247613A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,022  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 568:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..44  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 568:  
US-10-877-022-568  
Query Match 100.0%; Score 20; DB 8; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 25 TTTTGGGTTTGGGGTTTT 44  
RESULT 21  
US-10-877-146-568  
Sequence 568, Application US/10877146  
Publication No. US20050013825A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,146  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 568:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..44  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 568:  
US-10-877-146-568  
Query Match 100.0%; Score 20; DB 8; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 25 TTTTGGGTTTGGGGTTTT 44  
RESULT 22  
US-09-843-676-41  
Sequence 41, Application US/09843676  
Patent No. US20020164786A1

/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin  
/ Andrews, William H.  
/ TITLE OF INVENTION: No. US20020164786A1el Telomerase  
/ NUMBER OF SEQUENCES: 225  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/843,676  
/ FILING DATE: 26-Apr-2001  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/854,050  
/ FILING DATE: 09-MAY-1997  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002930US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 41:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 46 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-09-843-676-41  
  
Query Match 100.0%; Score 20; DB 3; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 27 TTTTGGGGTTTGGGGTTTT 46  
  
RESULT 23  
US-09-766-253-41  
/ Sequence 41, Application US/09766253  
/ Publication No. US2002018741A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin

/ Andrews, William H.  
/ TITLE OF INVENTION: No. US2002018741A1el Telomerase  
/ NUMBER OF SEQUENCES: 171  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/766,253  
/ FILING DATE: 19-Jan-2001  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/846,017  
/ FILING DATE: 1997-04-25  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002920US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 41:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 46 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-09-766-253-41  
  
Query Match 100.0%; Score 20; DB 3; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 27 TTTTGGGGTTTGGGGTTTT 46  
  
RESULT 24  
US-09-438-486-41  
/ Sequence 41, Application US/09438486  
/ Publication No. US20030009019A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ APPLICANT: Lingner, Joachim  
/ APPLICANT: Nakamura, Toru  
/ APPLICANT: Chapman, Karen B.  
/ APPLICANT: Morin, Gregg B.  
/ APPLICANT: Andrews, William H.  
/ TITLE OF INVENTION: No. US20030009019A1el Telomerase  
/ NUMBER OF SEQUENCES: 223  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111-3834  
/ COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
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US-09-438-486-41
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Query Match      100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTTGGGGTTTGGGGTTTT 20
Db      27 TTTTGGGGTTTGGGGTTTT 46
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RESULT 25
US-10-053-758-41
; Sequence 41, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: No. US20030032075A1e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
;
US-10-053-758-41

Query Match      100.0%; Score 20; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTTGGGGTTTGGGGTTTT 20
Db      27 TTTTGGGGTTTGGGGTTTT 46

RESULT 26
US-10-054-295-41
; Sequence 41, Application US/10054295
; Publication No. US2003004953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: No. US2003004953A1e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
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/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/854,050
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0300
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-054-295-41

Query Match 100.0%; Score 20; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 27
US-10-054-611-41
/ Sequence 41, Application US/10054611
/ Publication No. US20030059787A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin
/ Andrews, William H.
/ TITLE OF INVENTION: No. US20030059787A1el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/054,611
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/854,050
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
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/
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-054-611-41

Query Match 100.0%; Score 20; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 28
US-10-325-810-567
/ Sequence 567, Application US/10325810
/ Publication No. US20030204069A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/325,810
/ FILING DATE: 20-Dec-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181
/ FILING DATE: 29-Sep-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
```

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/
/
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ausenhus, Scott L.
/ REGISTRATION NUMBER: 42,271
/ REFERENCE/DOCKET NUMBER: 015389-002620US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 567:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..46
/ OTHER INFORMATION: /note= "hairpin primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 567:
US-10-325-810-567

Query Match 100.0%; Score 20; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTTTT 20
Db 27 TTTTGGGTTTGGGTTTT 46

RESULT 29
US-10-877-124-567
; Sequence 567, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
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/
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Red
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 567:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..46
/ OTHER INFORMATION: /note= "hairpin primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 567:
US-10-877-124-567

Query Match 100.0%; Score 20; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTTTT 20
Db 27 TTTTGGGTTTGGGTTTT 46

RESULT 30
US-10-877-022-567
; Sequence 567, Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,022  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 567:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..46  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 567:  
US-10-877-022-567  
Query Match 100.0%; Score 20; DB 8; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 27 TTTTGGGGTTTGGGGTTTT 46  
RESULT 31  
US-10-877-146-567  
Sequence 567, Application US/10877146  
Publication No. US20050013825A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,146  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 567:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..46  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 567:  
US-10-877-146-567  
Query Match 100.0%; Score 20; DB 8; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 27 TTTTGGGGTTTGGGGTTTT 46  
RESULT 32  
US-09-843-676-37  
Sequence 37, Application US/09843676  
Patent No. US20020164786A1

```
/
/
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin
/ Andrews, William H.
/ TITLE OF INVENTION: No. US20020164786A1el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION NUMBER: US/09/843,676
/ FILING DATE: 26-Apr-2001
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0300
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-843-676-37
Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20
Db 29 TTTTGGGTTTGGGGTTT 48

RESULT 33
US-09-843-676-40
/ Sequence 40, Application US/09843676
/ Patent No. US20020164786A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin
/ Andrews, William H.
/ TITLE OF INVENTION: No. US20020164786A1el Telomerase
/ NUMBER OF SEQUENCES: 171
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/
```

```
/
/
/ Andrews, William H.
/ TITLE OF INVENTION: No. US20020164786A1el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION NUMBER: US/09/843,676
/ FILING DATE: 26-Apr-2001
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0300
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-843-676-40
Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20
Db 29 TTTTGGGTTTGGGGTTT 48

RESULT 34
US-09-766-253-37
/ Sequence 37, Application US/09766253
/ Publication No. US20020187471A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin
/ Andrews, William H.
/ TITLE OF INVENTION: No. US20020187471A1el Telomerase
/ NUMBER OF SEQUENCES: 171
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/
```

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; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; BEST LOCAL SIMILARITY 100.0%; Pred. No. 1.2e+02;
; Mismatches 0; Indels 0; Gaps 0;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-766-253-37

Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 35
US-09-766-253-40
; Sequence 40, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-766-253-40

Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 36
US-09-438-486-37
; Sequence 37, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419

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/ FILING DATE: 18-APR-1997  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ CLASSIFICATION: 536  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002931US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 37:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 48 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
/ US-09-438-486-37

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 37  
US-09-438-486-40  
/ Sequence 40, Application US/09438486  
/ Publication No. US20030009019A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ APPLICANT: Lingner, Joachim  
/ APPLICANT: Nakamura, Toru  
/ APPLICANT: Chapman, Karen B.  
/ APPLICANT: Morin, Gregg B.  
/ APPLICANT: Harley, Calvin  
/ APPLICANT: Andrews, William H.  
/ TITLE OF INVENTION: No. US20030009019A1e1 Telomerase  
/ NUMBER OF SEQUENCES: 223  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111-3834  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/438,486  
/ FILING DATE: 12-NOV-1999  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/851,843  
/ FILING DATE: 06-MAY-1997  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997

/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ CLASSIFICATION: 536  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002931US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 40:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 48 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
/ US-09-438-486-40

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 38  
US-10-053-758-37  
/ Sequence 37, Application US/10053758  
/ Publication No. US20030032075A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ APPLICANT: Lingner, Joachim  
/ APPLICANT: Nakamura, Toru  
/ APPLICANT: Chapman, Karen B.  
/ APPLICANT: Morin, Gregg B.  
/ APPLICANT: Harley, Calvin  
/ APPLICANT: Andrews, William H.  
/ TITLE OF INVENTION: No. US20030032075A1e1 Telomerase  
/ NUMBER OF SEQUENCES: 225  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/10/053,758  
/ FILING DATE: 18-Jan-2002  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/854,050  
/ FILING DATE: 09-MAY-1997  
/ APPLICATION NUMBER: US 08/851,843  
/ FILING DATE: 06-MAY-1997  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300

## INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-10-053-758-37

Query Match 100.0%; Score 20; DB 5; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGGTTTGGGGTTTT 48

## RESULT 39

US-10-053-758-40

Sequence 40, Application US/10053758  
Publication No. US20030032075A1  
GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.

TITLE OF INVENTION: No. US20030032075A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/053,758  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-10-053-758-40

Query Match 100.0%; Score 20; DB 5; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGGTTTGGGGTTTT 48

## RESULT 40

US-10-054-295-37

Sequence 37, Application US/10054295  
Publication No. US20030044953A1  
GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.

TITLE OF INVENTION: No. US20030044953A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/054,295  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

```

; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-054-295-37
Query Match      100.0%; Score 20; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 41
US-10-054-295-40
; Sequence 40, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-054-295-40
Query Match      100.0%; Score 20; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 42
US-10-054-611-37
; Sequence 37, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-054-611-37
Query Match      100.0%; Score 20; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48
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## RESULT 43

US-10-054-611-40  
; Sequence 40, Application US/10054611  
; Publication No. US20030059787A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim

; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.

TITLE OF INVENTION: No. US20030059787A1e1 Telomerase  
NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/10/054,611

FILING DATE: 18-Jan-2002

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELEPHONE: (415) 576-0300

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-10-054-611-40

Query Match 100.0%; Score 20; DB 5; Length 48;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTTGGGGTTTT 20

|||||

Db 29 TTTTGGGGTTTTGGGGTTTT 48

|||||

RESULT 44

US-10-325-810-564

; Sequence 564, Application US/10325810

; Publication No. US20030204069A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

;

; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181

FILING DATE: 29-Sep-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Aussenhus, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 564:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: -

LOCATION: 1..48

OTHER INFORMATION: /note= "hairpin primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 564:

US-10-325-810-564

Query Match 100.0%; Score 20; DB 6; Length 48;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTTGGGGTTTT 20

|||||

Db 29 TTTTGGGGTTTTGGGGTTTT 48

|||||

RESULT 45  
US-10-877-124-564  
; Sequence 564, Application US/10877124  
; Publication No. US20040242529A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/877,124  
; FILING DATE: 24-Jun-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 564:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 48 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..48  
; OTHER INFORMATION: /note= "hairpin primer"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 564:

## US-10-877-124-564

Query Match 100.0%; Score 20; DB 8; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGGTTTGGGGTTTT 48  
|||||

## RESULT 46

US-10-877-022-564  
; Sequence 564, Application US/10877022  
; Publication No. US20040247613A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/877,022  
; FILING DATE: 24-Jun-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 564:  
; SEQUENCE CHARACTERISTICS:



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/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..48
/ OTHER INFORMATION: /note= "hairpin primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 564:
US-10-877-022-564

Query Match 100.0%; Score 20; DB 8; Length 48;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 29 TTTTGGGTTTGGGGTTTT 48

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; Sequence 564, Application US/10877146
; Publication No. US20050013825A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,146
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885

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/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
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/ NAME/KEY: -
/ LOCATION: 1..48
/ OTHER INFORMATION: /note= "hairpin primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 564:
US-10-877-146-564

Query Match 100.0%; Score 20; DB 8; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
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Db 29 TTTTGGGTTTGGGGTTTT 48

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; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
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; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
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; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-843-676-39

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; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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Db 31 TTTTGGGTTTGGGGTTTT 50

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; Sequence 39, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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  Db 31 TTTTGGGGTTTGGGGTTT 50

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 11812030

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Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 4          | 16.8  | 84.0        | 25     | 7  | US-10-310-914A-596068  |
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| 8          | 16.4  | 82.0        | 22     | 7  | US-10-310-914A-138179  |
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| 10         | 16.4  | 82.0        | 23     | 7  | US-10-310-914A-138196  |
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| 15         | 16.4  | 82.0        | 27     | 7  | US-10-310-914A-227197  |
| 16         | 15.8  | 79.0        | 20     | 11 | US-11-170-693-39       |
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| C 97  | 14.4 | 72.0 | 22 | 7  | US-10-310-914A-238252  | Sequence 238252,  | C 170 | 14.2 | 71.0 | 26 | 7  | US-10-310-914A-208739  | Sequence 208739,  |
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| C 99  | 14.4 | 72.0 | 22 | 7  | US-10-310-914A-626237  | Sequence 626237,  | C 172 | 14.2 | 71.0 | 26 | 7  | US-10-310-914A-467814  | Sequence 467814,  |
| C 100 | 14.4 | 72.0 | 22 | 7  | US-10-310-914A-1143345 | Sequence 1143345, | C 173 | 14.2 | 71.0 | 26 | 7  | US-10-310-914A-526421  | Sequence 526421,  |
| C 101 | 14.4 | 72.0 | 23 | 7  | US-10-310-914A-238202  | Sequence 238202,  | C 174 | 14.2 | 71.0 | 26 | 7  | US-10-310-914A-621501  | Sequence 621501,  |
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| C 103 | 14.4 | 72.0 | 25 | 7  | US-10-310-914A-238163  | Sequence 238163,  | C 176 | 14.2 | 71.0 | 27 | 7  | US-10-310-914A-803774  | Sequence 803774,  |
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| C 125 | 14.2 | 71.0 | 22 | 7  | US-10-310-914A-445665  | Sequence 445665,  | C 198 | 14   | 70.0 | 24 | 7  | US-10-310-914A-227190  | Sequence 227190,  |
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| C 128 | 14.2 | 71.0 | 22 | 7  | US-10-310-914A-621472  | Sequence 621472,  | C 201 | 13.8 | 69.0 | 18 | 7  | US-10-310-914A-111256  | Sequence 111256,  |
| C 129 | 14.2 | 71.0 | 22 | 7  | US-10-310-914A-803700  | Sequence 803700,  | C 202 | 13.8 | 69.0 | 18 | 7  | US-10-310-914A-1342360 | Sequence 1342360, |
| C 130 | 14.2 | 71.0 | 22 | 7  | US-10-310-914A-845459  | Sequence 845459,  | C 203 | 13.8 | 69.0 | 19 | 7  | US-10-310-914A-255657  | Sequence 255657,  |
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| C 132 | 14.2 | 71.0 | 23 | 7  | US-10-310-914A-208749  | Sequence 208749,  | C 205 | 13.8 | 69.0 | 20 | 7  | US-10-310-914A-239913  | Sequence 239913,  |
| C 133 | 14.2 | 71.0 | 23 | 7  | US-10-310-914A-322142  | Sequence 322142,  | C 206 | 13.8 | 69.0 | 20 | 7  | US-10-310-914A-467827  | Sequence 467827,  |
| C 134 | 14.2 | 71.0 | 23 | 7  | US-10-310-914A-322176  | Sequence 322176,  | C 207 | 13.8 | 69.0 | 21 | 7  | US-10-310-914A-111268  | Sequence 111268,  |
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| C 136 | 14.2 | 71.0 | 23 | 7  | US-10-310-914A-465292  | Sequence 465292,  | C 209 | 13.8 | 69.0 | 21 | 7  | US-10-310-914A-239892  | Sequence 239892,  |
| C 137 | 14.2 | 71.0 | 23 | 7  | US-10-310-914A-467819  | Sequence 467819,  | C 210 | 13.8 | 69.0 | 21 | 7  | US-10-310-914A-239912  | Sequence 239912,  |
| C 138 | 14.2 | 71.0 | 23 | 7  | US-10-310-914A-467906  | Sequence 467906,  | C 211 | 13.8 | 69.0 | 21 | 7  | US-10-310-914A-251546  | Sequence 251546,  |
| C 139 | 14.2 | 71.0 | 23 | 7  | US-10-310-914A-526398  | Sequence 526398,  | C 212 | 13.8 | 69.0 | 21 | 7  | US-10-310-914A-427324  | Sequence 427324,  |
| C 140 | 14.2 | 71.0 | 23 | 7  | US-10-310-914A-845463  | Sequence 845463,  | C 213 | 13.8 | 69.0 | 21 | 7  | US-10-310-914A-565958  | Sequence 565958,  |
| C 141 | 14.2 | 71.0 | 23 | 7  | US-10-310-914A-1035982 | Sequence 1035982, | C 214 | 13.8 | 69.0 | 21 | 7  | US-10-310-914A-1043348 | Sequence 1043348, |
| C 142 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-111296  | Sequence 111296,  | C 215 | 13.8 | 69.0 | 21 | 7  | US-10-310-914A-1222944 | Sequence 1222944, |
| C 143 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-322181  | Sequence 322181,  | C 216 | 13.8 | 69.0 | 22 | 7  | US-10-310-914A-239917  | Sequence 239917,  |
| C 144 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-348737  | Sequence 348737,  | C 217 | 13.8 | 69.0 | 22 | 7  | US-10-310-914A-255658  | Sequence 255658,  |
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| C 146 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-465293  | Sequence 465293,  | C 219 | 13.8 | 69.0 | 22 | 7  | US-10-310-914A-887834  | Sequence 887834,  |
| C 147 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-465676  | Sequence 465676,  | C 220 | 13.8 | 69.0 | 23 | 7  | US-10-310-914A-507619  | Sequence 507619,  |
| C 148 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-490858  | Sequence 490858,  | C 221 | 13.8 | 69.0 | 23 | 7  | US-10-310-914A-1043651 | Sequence 1043651, |
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| C 151 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-621491  | Sequence 621491,  | C 224 | 13.8 | 69.0 | 24 | 7  | US-10-310-914A-251487  | Sequence 251487,  |
| C 152 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-621493  | Sequence 621493,  | C 225 | 13.8 | 69.0 | 24 | 7  | US-10-310-914A-507599  | Sequence 507599,  |
| C 153 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-845464  | Sequence 845464,  | C 226 | 13.8 | 69.0 | 24 | 7  | US-10-310-914A-507626  | Sequence 507626,  |
| C 154 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-1059987 | Sequence 1059987, | C 227 | 13.8 | 69.0 | 24 | 7  | US-10-310-914A-1043567 | Sequence 1043567, |
| C 155 | 14.2 | 71.0 | 24 | 7  | US-10-310-914A-1177640 | Sequence 1177640, | C 228 | 13.8 | 69.0 | 24 | 7  | US-10-310-914A-1043652 | Sequence 1043652, |
| C 156 | 14.2 | 71.0 | 25 | 7  | US-10-310-914A-111266  | Sequence 111266,  | C 229 | 13.8 | 69.0 | 25 | 7  | US-10-750-185-22623    | Sequence 22623, A |
| C 157 | 14.2 | 71.0 | 25 | 7  | US-10-310-914A-208725  | Sequence 208725,  | C 230 | 13.8 | 69.0 | 25 | 7  | US-10-750-623-22623    | Sequence 22623, A |
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| C 162 | 14.2 | 71.0 | 25 | 7  | US-10-310-914A-1107886 | Sequence 1107886, | C 235 | 13.6 | 68.0 | 20 | 7  | US-10-310-914A-95371   | Sequence 95371, A |
| C 163 | 14.2 | 71.0 | 25 | 7  | US-10-310-914A-1222945 | Sequence 1222945, | C 236 | 13.6 | 68.0 | 20 | 7  | US-10-310-914A-1182490 | Sequence 1182490, |
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ALIGNMENTS

RESULT 1  
US-11-127-654-67  
; Sequence 67, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

; TITLE OF INVENTION: INFLAMMATORY DISEASES  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 67  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-67  
  
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Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 TTTTGGGGTTTGGGGTTTT 20  
  
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US-10-310-914A-596008/c  
; Sequence 596008, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 596008  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-596008  
  
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Best Local Similarity 90.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
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US-10-310-914A-185978/c  
; Sequence 185978, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
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; LENGTH: 24  
; TYPE: RNA

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; ORGANISM: Human
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; Sequence 596068, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
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; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-596068

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Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 596011
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-596011

Query Match          84.0%; Score 16.8; DB 7; Length 27;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
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; Sequence 138168, Application US/10310914A
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
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; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-138168

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Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138169
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-138169

Query Match          82.0%; Score 16.4; DB 7; Length 22;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138179
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
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US-10-310-914A-138179

Query Match 82.0%; Score 16.4; DB 7; Length 22;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
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; Sequence 138228, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 138228

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-138228

Query Match

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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 20 TTGGGGTTTGGGGTTT 3

RESULT 10

US-10-310-914A-138180/c

; Sequence 138180, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 138180

; LENGTH: 23

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-138180

Query Match

Best Local Similarity 82.0%; Score 16.4; DB 7; Length 23;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20  
|||||

Db 22 TTGGGGTTTGGGGTTT 5

RESULT 11

US-10-310-914A-138196/c

; Sequence 138196, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 138196

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-138196

Query Match

Best Local Similarity 82.0%; Score 16.4; DB 7; Length 24;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20  
|||||

Db 21 TTGGGGTTTGGGGTTT 4

RESULT 12

US-10-310-914A-227183/c

; Sequence 227183, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 227183

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-227183

Query Match

Best Local Similarity 82.0%; Score 16.4; DB 7; Length 24;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGGGGTTTGGGGTTT 19  
|||||

Db 18 TTGGGGTTTGGGGTTT 1

RESULT 13

US-10-310-914A-138229/c

; Sequence 138229, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 138229

; LENGTH: 25

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-138229

```
Query Match      82.0%; Score 16.4; DB 7; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20
Db 20 TTGGGGTTTGGGGTTT 3

RESULT 14
US-10-310-914A-138236/c
; Sequence 138236, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138236
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-138236

Query Match      82.0%; Score 16.4; DB 7; Length 26;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20
Db 26 TTGGGGTTTGGGGTTT 9

RESULT 15
US-10-310-914A-227197/c
; Sequence 227197, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 227197
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-227197

Query Match      82.0%; Score 16.4; DB 7; Length 27;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGGGGTTTGGGGTTT 19
Db 19 TTGGGGTTTGGGGTTT 2

RESULT 16
US-11-170-693-39/c
; Sequence 39, Application US/11170693
; Publication No. US20060014186A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Hodge, Timothy A.
; TITLE OF INVENTION: METHODS FOR GENOTYPE SCREENING OF A STRAIN DISPOSED ON AN
; FILE OF INVENTION: ABSORBENT CARRIER
; FILE REFERENCE: 023131.41500
; CURRENT APPLICATION NUMBER: US/11/170,693
; CURRENT FILING DATE: 2005-06-29
; PRIOR APPLICATION NUMBER: 60/230,371
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 09/945,952
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 11/074,995
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 11/
; PRIOR FILING DATE: 2005-06-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: Forward Primer
US-11-170-693-39

Query Match      79.0%; Score 15.8; DB 11; Length 20;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 19
Db 19 TGTGGGGTTCTGGGGTTT 1

RESULT 17
US-10-310-914A-271479/c
; Sequence 271479, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 271479
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-271479

Query Match      79.0%; Score 15.8; DB 7; Length 21;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTGGGGTTTGGGGTTT 20
Db 19 TTGTGGTTTGGGGTTT 1

RESULT 18
US-10-310-914A-1342346/c
; Sequence 1342346, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
```

; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1342346  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1342346

Query Match 79.0%; Score 15.8; DB 7; Length 22;  
Best Local Similarity 89.5%; Pred. No. 3.e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGTGGGGTTTGGGGTTT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 22 TTGTGGGGTTTGGGGTTT 4

RESULT 19  
US-10-310-914A-626125/c  
; Sequence 626125, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 626125  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626125

Query Match 79.0%; Score 15.8; DB 7; Length 23;  
Best Local Similarity 89.5%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGTGGGGTTTGGGGTTT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 23 TTGTGGGGTTTGGGGTTT 5

RESULT 20  
US-10-310-914A-626126/c  
; Sequence 626126, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 626126  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626126

Query Match 79.0%; Score 15.8; DB 7; Length 23;  
Best Local Similarity 89.5%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGTGGGGTTTGGGGTTT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 23 TTGTGGGGTTTGGGGTTT 5

RESULT 21  
US-10-310-914A-1143293/c  
; Sequence 1143293, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1143293  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1143293

Query Match 79.0%; Score 15.8; DB 7; Length 23;  
Best Local Similarity 89.5%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGTGGGGTTTGGGGTTT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 23 TTGTGGGGTTTGGGGTTT 5

RESULT 22  
US-10-310-914A-844567  
; Sequence 844567, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 844567  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-844567

Query Match 79.0%; Score 15.8; DB 7; Length 24;  
Best Local Similarity 36.8%; Pred. No. 3.1e+02;  
Matches 7; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGTGGGGTTTGGGGTTT 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 UUUUGGAUUUCGGGGUUU 19

RESULT 23  
US-10-310-914A-271527/c  
; Sequence 271527, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01



; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 626220  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626220

Query Match 77.0%; Score 15.4; DB 7; Length 19;  
Best Local Similarity 94.1%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
Db 19 TGGGGTTTTGGGGTTTT 3

## RESULT 29

US-10-310-914A-626221/c  
; Sequence 626221, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 626221  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626221

Query Match 77.0%; Score 15.4; DB 7; Length 19;  
Best Local Similarity 94.1%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
Db 19 TGGGGTTTTGGGGTTTT 3

## RESULT 30

US-10-310-914A-1143338/c  
; Sequence 1143338, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 1143338  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1143338

Query Match 77.0%; Score 15.4; DB 7; Length 19;  
Best Local Similarity 94.1%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20

Db 19 TGGGGTTTTGGGGTTTT 3  
|||||  
RESULT 31  
US-10-310-914A-626141/c  
; Sequence 626141, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 626141  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626141

Query Match 77.0%; Score 15.4; DB 7; Length 20;  
Best Local Similarity 94.1%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
Db 20 TGGGGTTTTGGGGTTTT 4

## RESULT 32

US-10-310-914A-138178/c  
; Sequence 138178, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 138178  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-138178

Query Match 77.0%; Score 15.4; DB 7; Length 21;  
Best Local Similarity 94.1%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
Db 21 TGGGGTTTTGGGGTTTT 5

## RESULT 33

US-10-310-914A-138235/c  
; Sequence 138235, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 138235  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-138235

Query Match 77.0%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 4.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
DB 25 TGGGGTTTTGGGGTTTT 9  
|||||

RESULT 34  
US-10-310-914A-626295/c  
; Sequence 626295, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 626295  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626295

Query Match 77.0%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 4.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
DB 24 TGGGGTTTTGGGGTTTT 8  
|||||

RESULT 35  
US-10-310-914A-626296/c  
; Sequence 626296, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 626296  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626296

Query Match 77.0%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 4.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||

Db 24 TGGGGTTTTGGGGTTTT 8  
|||||

RESULT 36  
US-10-310-914A-1143370/c  
; Sequence 1143370, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1143370  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1143370

Query Match 77.0%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 4.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
DB 24 TGGGGTTTTGGGGTTTT 8  
|||||

RESULT 37  
US-11-043-752-216/c  
; Sequence 216, Application US/11043752  
; Publication No. US20060014165A1  
; GENERAL INFORMATION:  
; APPLICANT: Hakonarson, Hakon  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Halapi, Eva  
; TITLE OF INVENTION: METHODS OF DIAGNOSIS AND TREATMENT FOR

; FILE REFERENCE: 2345.2044-003  
; CURRENT APPLICATION NUMBER: US/11/043,752  
; CURRENT FILING DATE: 2005-01-26  
; PRIOR APPLICATION NUMBER: PCT/US04/022446  
; PRIOR FILING DATE: 2004-07-14  
; PRIOR APPLICATION NUMBER: 60/487,072  
; PRIOR FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 60/559,611  
; PRIOR FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 4326  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 216  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-043-752-216

Query Match 76.0%; Score 15.2; DB 11; Length 20;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTTGGGGTTTT 20  
|||||  
DB 20 TTGTGGTGTTTGGGGATTT 1  
|||||

RESULT 38  
US-10-310-914A-84509/c  
; Sequence 84509, Application US/10310914A  
; Publication No. US20060003322A1

## ; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 84509  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-84509

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 21 TTTTGGGGTTTGGTTTTT 2

## RESULT 39

US-10-310-914A-455408/c  
; Sequence 455408, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 455408  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-455408

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 21 TTTTGGGGTTTATGTTTT 2

## RESULT 40

US-10-310-914A-622070/c  
; Sequence 622070, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 622070  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-622070

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 20 TTTTGGTTTGGGGTTTTT 1

## RESULT 41

US-10-310-914A-675377/c  
; Sequence 675377, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 675377  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-675377

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 20 TGTTCGGGTTTGGGGTTTT 1

## RESULT 42

US-10-310-914A-1222901/c  
; Sequence 1222901, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1222901  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1222901

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 21 TTTTGGGGTTTGTGTTTT 2

## RESULT 43

US-10-310-914A-238142/c  
; Sequence 238142, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

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; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 238142
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-238142

Query Match          76.0%; Score 15.2; DB 7; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 22 TTTTGGGGTTTGGGGCAIT 3

RESULT 44
US-10-310-914A-465689/c
; Sequence 465689, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465689
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-465689

Query Match          76.0%; Score 15.2; DB 7; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 22 TTTTGGGGTTTGGGGCAIT 3

RESULT 44
US-10-310-914A-465689/c
; Sequence 465689, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465689
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-465689

Query Match          76.0%; Score 15.2; DB 7; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 21 TTTTGGGGTTTGGGGTTGT 2

RESULT 45
US-10-310-914A-1222898/c
; Sequence 1222898, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1222898
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1222898
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Query Match          76.0%; Score 15.2; DB 7; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 22 TTTTGGGGTTTGTGTTTT 3

RESULT 46
US-10-310-914A-282917/c
; Sequence 282917, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 282917
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-282917

Query Match          76.0%; Score 15.2; DB 7; Length 23;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 23 TTTTGGGTGTTTGTGTTTT 4

RESULT 47
US-10-310-914A-465697/c
; Sequence 465697, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465697
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-465697

Query Match          76.0%; Score 15.2; DB 7; Length 23;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 20 TTTTGGGGTTTGGGGTTGT 1

RESULT 48
US-10-310-914A-501657/c
; Sequence 501657, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
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; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 501657  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-501657

Query Match 76.0%; Score 15.2; DB 7; Length 23;  
Best Local Similarity 85.0%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTGGGGTTTT 20  
||| || ||||| |||||  
Db 21 TTTAGGTGTTTGGGGTTTT 2

## RESULT 49

US-10-310-914A-651609/c  
; Sequence 651609, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 651609  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-651609

Query Match 76.0%; Score 15.2; DB 7; Length 23;  
Best Local Similarity 85.0%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTGGGGTTTT 20  
||| ||||| |||||  
Db 21 TTTTGGGTTTGGGGTTTT 2

## RESULT 50

US-10-310-914A-675445/c  
; Sequence 675445, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 675445  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-675445

Query Match 76.0%; Score 15.2; DB 7; Length 23;

Best Local Similarity 85.0%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTGGGGTTTT 20  
||| ||||| |||||  
Db 22 TGTTCGGGTTTGGGGTTTT 3

Search completed: February 16, 2006, 02:52:56  
Job time : 188.446 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:51:58 ; Search time 455.843 Seconds  
(without alignments)  
2369.293 Million cell updates/sec

Title: US-09-669-187A-80

Perfect score: 19

Sequence: 1 ggggtgacgttcagggggg 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.sts.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description       |
|------------|-------|---------------|--------|----|-------------------|
| 1          | 19    | 100.0         | 19     | 6  | AX103888 Sequence |
| 2          | 19    | 100.0         | 19     | 6  | AX355419 Sequence |
| 3          | 19    | 100.0         | 19     | 6  | AX546941 Sequence |
| 4          | 17.4  | 91.6          | 19     | 6  | AX103890 Sequence |
| 5          | 17.4  | 91.6          | 19     | 6  | AX355420 Sequence |
| 6          | 17.4  | 91.6          | 19     | 6  | AX546943 Sequence |
| 7          | 14.2  | 74.7          | 20     | 6  | AR096686 Sequence |
| 8          | 14.2  | 74.7          | 20     | 6  | AR135030 Sequence |
| 9          | 14.2  | 74.7          | 20     | 6  | AR182891 Sequence |
| 10         | 14.2  | 74.7          | 20     | 6  | AR607454 Sequence |
| 11         | 14.2  | 74.7          | 20     | 6  | AX104032 Sequence |
| 12         | 14.2  | 74.7          | 20     | 6  | AX342378 Sequence |
| 13         | 14.2  | 74.7          | 20     | 6  | AX342405 Sequence |
| 14         | 14.2  | 74.7          | 20     | 6  | AX342438 Sequence |
| 15         | 14.2  | 74.7          | 20     | 6  | AX355421 Sequence |
| 16         | 14.2  | 74.7          | 20     | 6  | AX547085 Sequence |
| 17         | 14    | 73.7          | 39     | 6  | AR337615 Sequence |
| 18         | 13.4  | 70.5          | 22     | 6  | AR137717 Sequence |

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| 30 | 6 | CQ874726 | CQ874726 Sequence  |
| 30 | 6 | AX514115 | AX514115 Sequence  |
| 41 | 6 | AX520264 | AX520264 Sequence  |
| 41 | 6 | AX104329 | AX104329 Sequence  |
| 20 | 6 | AX104332 | AX104332 Sequence  |
| 20 | 6 | AX355395 | AX355395 Sequence  |
| 20 | 6 | AX355396 | AX355396 Sequence  |
| 20 | 6 | AX355396 | AX355396 Sequence  |
| 20 | 6 | AX547382 | AX547382 Sequence  |
| 20 | 6 | AX547385 | AX547385 Sequence  |
| 20 | 6 | CS121639 | CS121639 Sequence  |
| 32 | 6 | AX805700 | AX805700 Sequence  |
| 32 | 6 | CS087335 | CS087335 Sequence  |
| 47 | 6 | CS087338 | CS087338 Sequence  |
| 47 | 6 | CS087376 | CS087376 Sequence  |
| 47 | 6 | CS087377 | CS087377 Sequence  |
| 47 | 6 | AX455113 | AX455113 Sequence  |
| 20 | 6 | CQ827797 | CQ827797 Sequence  |
| 19 | 6 | AR135661 | AR135661 Sequence  |
| 20 | 6 | CQ775024 | CQ775024 Sequence  |
| 20 | 6 | AX814043 | AX814043 Sequence  |
| 20 | 6 | CQ760615 | CQ760615 Sequence  |
| 21 | 6 | CQ760697 | CQ760697 Sequence  |
| 21 | 6 | AX249619 | AX249619 Sequence  |
| 31 | 6 | AR029533 | AR029533 Sequence  |
| 32 | 6 | AR098486 | AR098486 Sequence  |
| 32 | 6 | 141446   | 141446 Sequence 43 |
| 32 | 6 | AR494995 | AR494995 Sequence  |
| 32 | 6 | AX441412 | AX441412 Sequence  |
| 32 | 6 | AX453908 | AX453908 Sequence  |
| 41 | 6 | AX514624 | AX514624 Sequence  |
| 41 | 6 | FVBFOKIB | M18006 Flavobacter |
| 50 | 1 | FVBFOKIB | M18007 Flavobacter |
| 50 | 6 | AX190133 | AX190133 Sequence  |
| 50 | 6 | AX104784 | AX104784 Sequence  |
| 19 | 6 | AX104854 | AX104854 Sequence  |
| 19 | 6 | AX105129 | AX105129 Sequence  |
| 19 | 6 | AX547837 | AX547837 Sequence  |
| 19 | 6 | AX547907 | AX547907 Sequence  |
| 19 | 6 | AR140453 | AR140453 Sequence  |
| 20 | 6 | AR154761 | AR154761 Sequence  |
| 20 | 6 | BD069974 | BD069974 Use of nu |
| 20 | 6 | BD190419 | BD190419 Microemul |
| 20 | 6 | BD251267 | BD251267 Enhanceme |
| 20 | 6 | AR182880 | AR182880 Sequence  |
| 20 | 6 | AR182887 | AR182887 Sequence  |
| 20 | 6 | AR222213 | AR222213 Sequence  |
| 20 | 6 | AR432435 | AR432435 Sequence  |
| 20 | 6 | AR607443 | AR607443 Sequence  |
| 20 | 6 | AR607450 | AR607450 Sequence  |
| 20 | 6 | AX063578 | AX063578 Sequence  |
| 20 | 6 | AX088932 | AX088932 Sequence  |
| 20 | 6 | AX104327 | AX104327 Sequence  |
| 20 | 6 | AX104575 | AX104575 Sequence  |
| 20 | 6 | AX104717 | AX104717 Sequence  |
| 20 | 6 | AX104776 | AX104776 Sequence  |
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| 20 | 6 | AX105103 | AX105103 Sequence  |
| 20 | 6 | AX105107 | AX105107 Sequence  |
| 20 | 6 | AX105236 | AX105236 Sequence  |
| 20 | 6 | AX105237 | AX105237 Sequence  |
| 20 | 6 | AX135634 | AX135634 Sequence  |
| 20 | 6 | AX194489 | AX194489 Sequence  |
| 20 | 6 | AX355408 | AX355408 Sequence  |
| 20 | 6 | AX355409 | AX355409 Sequence  |
| 20 | 6 | AX355415 | AX355415 Sequence  |
| 20 | 6 | AX465439 | AX465439 Sequence  |
| 20 | 6 | AX468483 | AX468483 Sequence  |
| 20 | 6 | AX547380 | AX547380 Sequence  |
| 20 | 6 | AX547628 | AX547628 Sequence  |
| 20 | 6 | AX547770 | AX547770 Sequence  |
| 20 | 6 | AX547829 | AX547829 Sequence  |
| 20 | 6 | AX547830 | AX547830 Sequence  |
| 20 | 6 | BD009060 | BD009060 Immunosti |

|       |      |      |    |   |          |             |       |      |      |    |    |          |           |
|-------|------|------|----|---|----------|-------------|-------|------|------|----|----|----------|-----------|
| 92    | 12.6 | 66.3 | 21 | 6 | AX104812 | Sequence    | 165   | 12.2 | 64.2 | 48 | 6  | AR494672 | Sequence  |
| 93    | 12.6 | 66.3 | 21 | 6 | AX105257 | Sequence    | C 166 | 12.2 | 64.2 | 50 | 6  | CQ008444 | Sequence  |
| 94    | 12.6 | 66.3 | 21 | 6 | AX547855 | Sequence    | C 167 | 12.2 | 64.2 | 50 | 6  | AX093084 | Sequence  |
| 95    | 12.6 | 66.3 | 24 | 6 | AX104386 | Sequence    | C 168 | 11.8 | 62.1 | 18 | 6  | AR181702 | Sequence  |
| 96    | 12.6 | 66.3 | 24 | 6 | AX547379 | Sequence    | C 169 | 11.8 | 62.1 | 18 | 6  | ARG29692 | Sequence  |
|       | 12.6 | 66.3 | 25 | 6 | AX463125 | Sequence    | C 170 | 11.8 | 62.1 | 20 | 6  | AR137469 | Sequence  |
| 98    | 12.6 | 66.3 | 26 | 6 | BD078174 | Modulator   | C 171 | 11.8 | 62.1 | 20 | 6  | CS012607 | Sequence  |
|       | 12.6 | 66.3 | 26 | 6 | BD078225 | Modulator   | C 172 | 11.8 | 62.1 | 20 | 6  | AX664900 | Sequence  |
| 100   | 12.6 | 66.3 | 30 | 6 | E04679   | Sequence    | C 173 | 11.8 | 62.1 | 20 | 6  | AX670947 | Sequence  |
|       | 12.6 | 66.3 | 30 | 6 | E04682   | Sequence    | C 174 | 11.8 | 62.1 | 21 | 6  | CS081480 | Sequence  |
| 101   | 12.6 | 66.3 | 30 | 6 | AX105266 | Sequence    | C 175 | 11.8 | 62.1 | 21 | 6  | AX117610 | Sequence  |
| 103   | 12.6 | 66.3 | 30 | 6 | AX351709 | Sequence    | C 176 | 11.8 | 62.1 | 22 | 6  | CQ774347 | Sequence  |
| 104   | 12.6 | 66.3 | 30 | 6 | AX351712 | Sequence    | C 177 | 11.8 | 62.1 | 22 | 6  | CQ779543 | Sequence  |
| 105   | 12.6 | 66.3 | 30 | 6 | AX351714 | Sequence    | C 178 | 11.8 | 62.1 | 24 | 6  | A56967   | Sequence  |
|       | 12.6 | 66.3 | 34 | 6 | AR410782 | Sequence    | C 179 | 11.8 | 62.1 | 25 | 6  | A92794   | Sequence  |
| C 107 | 12.6 | 66.3 | 44 | 6 | AR439146 | Sequence    | C 180 | 11.8 | 62.1 | 25 | 6  | BD238067 | Sequence  |
| C 108 | 12.6 | 66.3 | 44 | 6 | AR473166 | Sequence    | C 181 | 11.8 | 62.1 | 25 | 6  | AX023972 | Sequence  |
| C 109 | 12.6 | 66.3 | 44 | 6 | AR527152 | Sequence    | C 182 | 11.8 | 62.1 | 25 | 6  | AX609210 | Sequence  |
| C 110 | 12.6 | 66.3 | 44 | 6 | AR566185 | Sequence    | C 183 | 11.8 | 62.1 | 30 | 6  | AR090268 | Sequence  |
| C 111 | 12.6 | 66.3 | 44 | 6 | AR592203 | Sequence    | C 184 | 11.8 | 62.1 | 30 | 6  | AR197303 | Sequence  |
| C 112 | 12.6 | 66.3 | 44 | 6 | AR604477 | Sequence    | C 185 | 11.8 | 62.1 | 30 | 6  | AR259457 | Sequence  |
| C 113 | 12.6 | 66.3 | 44 | 6 | AR605063 | Sequence    | C 186 | 11.8 | 62.1 | 31 | 6  | BD233524 | Formation |
| C 114 | 12.6 | 66.3 | 44 | 6 | AR613728 | Sequence    | C 187 | 11.8 | 62.1 | 31 | 6  | AR448494 | Sequence  |
| C 115 | 12.6 | 66.3 | 44 | 6 | AR635899 | Sequence    | C 188 | 11.8 | 62.1 | 31 | 6  | AX078480 | Sequence  |
| C 116 | 12.6 | 66.3 | 44 | 6 | AR650628 | Sequence    | C 189 | 11.8 | 62.1 | 32 | 6  | CS050648 | Sequence  |
| C 117 | 12.6 | 66.3 | 44 | 6 | AR657569 | Sequence    | C 190 | 11.8 | 62.1 | 36 | 6  | AR272252 | Sequence  |
| C 118 | 12.6 | 66.3 | 44 | 6 | AR697634 | Sequence    | C 191 | 11.8 | 62.1 | 47 | 6  | AR290405 | Sequence  |
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| 128   | 12.4 | 65.3 | 20 | 6 | AX354978 | Sequence    | C 201 | 11.6 | 61.1 | 19 | 6  | CQ888169 | Sequence  |
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## ALIGNMENTS

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LOCUS AX103888 19 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 80 from Patent WO0122972.  
ACCESSION AX103888

VERSION AX103888.1 GI:13920085  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.  
TITLE Immunostimulatory nucleic acids  
JOURNAL Patent: WO 0122972-A 80 05-APR-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
GmbH (DE)  
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
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AX355419  
LOCUS AX355419 19 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 447 from Patent WO0197843.  
ACCESSION AX355419  
VERSION AX355419.1 GI:18620087  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Weiner,G. and Hartmann,G.  
TITLE Methods for enhancing antibody-induced cell lysis and treating  
cancer  
JOURNAL Patent: WO 0197843-A 447 27-DEC-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
FEATURES Location/Qualifiers  
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LOCUS AX546941 19 bp DNA linear PAT 01-MAR-2003  
DEFINITION Sequence 80 from Patent WO02053141.  
ACCESSION AX546941  
VERSION AX546941.1 GI:25812085  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1

AUTHORS Bratzler,R.L.  
 TITLE Inhibition of angiogenesis by nucleic acids  
 JOURNAL Patent: WO 02053141-A 80 11-JUL-2002;  
 Coley Pharmaceutical Group, Inc. (US)

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 DEFINITION Sequence 82 from Patent WO0122972.  
 ACCESSION AX103890  
 VERSION AX103890.1 GI:13920087  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.  
 TITLE Immunostimulatory nucleic acids  
 JOURNAL Patent: WO 0122972-A 82 05-APR-2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
 GmbH (DE)  
 FEATURES Location/Qualifiers  
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 Best Local Similarity 94.7%; Pred. No. 8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 LOCUS AX355420 19 bp DNA linear PAT 06-FEB-2002  
 DEFINITION Sequence 448 from Patent WO0197843.  
 ACCESSION AX355420  
 VERSION AX355420.1 GI:18620088  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Weiner,G. and Hartmann,G.  
 TITLE Methods for enhancing antibody-induced cell lysis and treating  
 cancer  
 JOURNAL Patent: WO 0197843-A 448 27-DEC-2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
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ORIGIN

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 LOCUS AX546943 19 bp DNA linear PAT 01-MAR-2003  
 DEFINITION Sequence 82 from Patent WO02053141.  
 ACCESSION AX546943  
 VERSION AX546943.1 GI:25812087  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Bratzler,R.L.  
 TITLE Inhibition of angiogenesis by nucleic acids  
 JOURNAL Patent: WO 02053141-A 82 11-JUL-2002;  
 Coley Pharmaceutical Group, Inc. (US)  
 FEATURES Location/Qualifiers  
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RESULT 7  
 AR096686  
 LOCUS AR096686 20 bp DNA linear PAT 08-SEP-2000  
 DEFINITION Sequence 1 from patent US 6008200.  
 ACCESSION AR096686  
 VERSION AR096686.1 GI:10025701  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Krieg,A.M.  
 TITLE Immunomodulatory oligonucleotides  
 JOURNAL Patent: US 6008200-A 1 28-DEC-1999;  
 FEATURES Location/Qualifiers  
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Db 2 GGCTCAACGTTTCAGGGGG 20

RESULT 8

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DEFINITION Sequence 1 from patent US 6194388.

ACCESSION AR135030

VERSION AR135030.1 GI:14123935

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Krieg, A.M., Klinman, D. and Steinberg, A.D.

TITLE Immunomodulatory oligonucleotides

JOURNAL Patent: US 6194388-A 1:27-FEB-2001;

FEATURES Location/Qualifiers

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ORIGIN

Query Match 74.7%; Score 14.2; DB 6; Length 20;

Best Local Similarity 84.2%; Pred. No. 3.2e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 2 GGCTCAACGTTTCAGGGGG 20

RESULT 9

LOCUS AR182891 20 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 63 from patent US 6339068.

ACCESSION AR182891

VERSION AR182891.1 GI:20226098

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Krieg, A.M., Davis, H.L., Wu, T. and Schorr, J.

TITLE Vectors and methods for immunization or therapeutic protocols

JOURNAL Patent: US 6339068-A 63:15-JAN-2002;

FEATURES Location/Qualifiers

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Query Match 74.7%; Score 14.2; DB 6; Length 20;

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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCGTGACGTTTCAGGGGG 19

Db 2 GGCTCAACGTTTCAGGGGG 20

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LOCUS AR607454 20 bp DNA linear PAT 15-DEC-2004

DEFINITION Sequence 63 from patent US 6821957.

ACCESSION AR607454

VERSION AR607454.1 GI:56659871

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Krieg, A.M., Davis, H.L., Wu, T. and Joachim, S.

Db 2 GGCTCAACGTTTCAGGGGG 20

RESULT 11

LOCUS AX104032 20 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 224 from Patent WO0122972.

ACCESSION AX104032

VERSION AX104032.1 GI:13920229

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.

TITLE Immunostimulatory nucleic acids

JOURNAL Patent: WO 0122972-A 224:05-APR-2001;

FEATURES Location/Qualifiers

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ORIGIN

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Best Local Similarity 84.2%; Pred. No. 3.2e+04;

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LOCUS AX342378 20 bp DNA linear PAT 12-JAN-2002

DEFINITION Sequence 1 from Patent EP1167377.

ACCESSION AX342378

VERSION AX342378.1 GI:18151821

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Krieg, A.M.

TITLE Immunomodulatory oligonucleotides

JOURNAL Patent: EP 1167377-A 1:02-JAN-2002;

FEATURES Location/Qualifiers

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ORIGIN

Query Match 74.7%; Score 14.2; DB 6; Length 20;

Best Local Similarity 84.2%; Pred. No. 3.2e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCGTGACGTTTCAGGGGG 19

Db 2 GGCTCAACGTTTCAGGGGG 20

TITLE Vectors and methods for immunization or therapeutic protocols

JOURNAL Patent: US 6821957-A 63:23-NOV-2004;

University of Iowa Research Foundation; Iowa City, IA

Location/Qualifiers

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DEFINITION Sequence 1 from Patent EP1167377.

ACCESSION AX342378

VERSION AX342378.1 GI:18151821

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Krieg, A.M.

TITLE Immunomodulatory oligonucleotides

JOURNAL Patent: EP 1167377-A 1:02-JAN-2002;

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ACCESSION AX342405
VERSION AX342405.1 GI:18151848
KEYWORDS .
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ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M.
TITLE Immunomodulatory oligonucleotides
JOURNAL Patent: EP 1167379-A 1 02-JAN-2002;
          UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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LOCUS AX342438
DEFINITION Sequence 1 from Patent EP1167378.
ACCESSION AX342438
VERSION AX342438.1 GI:18151881
KEYWORDS .
SOURCE .
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M.
TITLE Immunomodulatory oligonucleotides
JOURNAL Patent: EP 1167378-A 1 02-JAN-2002;
          UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
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ORIGIN
Query Match 74.7%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 15
LOCUS AX355421
DEFINITION Sequence 449 from Patent WO0197843.
ACCESSION AX355421
VERSION AX355421.1 GI:18620089
KEYWORDS .
SOURCE .
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
          cancer
JOURNAL Patent: WO 0197843-A 449 27-DEC-2001;
          UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide
chimeric phosphorothioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"

ORIGIN
Query Match 74.7%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTTCACGTTTTCAGGGGG 20

RESULT 16
LOCUS AX547085
DEFINITION Sequence 224 from Patent WO02053141.
ACCESSION AX547085
VERSION AX547085.1 GI:25812229
KEYWORDS .
SOURCE .
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 224 11-JUL-2002;
          Coley Pharmaceutical Group, Inc. (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

ORIGIN
Query Match 74.7%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTTCACGTTTTCAGGGGG 20

RESULT 17
LOCUS AR337615/c
DEFINITION Sequence 18 from patent US 6566500.
ACCESSION AR337615
VERSION AR337615.1 GI:33724021
KEYWORDS .
SOURCE .
ORGANISM Unknown.
          Unknown.
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[illegible]

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QY 1 GGGGTGACGTTTCAGGGG 17
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Db 26 GGGTGGGTTTCAGGGG 10

RESULT 22
AX104329 AX104329 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 521 from Patent WO0122972..
ACCESSION AX104329
VERSION AX104329.1 GI:13920526
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 521 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 69.5%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGG 18
|||: |||||
Db 3 GGCATGACGTTTCGGGGG 20

RESULT 23
AX104332 AX104332 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 524 from Patent WO0122972..
ACCESSION AX104332
VERSION AX104332.1 GI:13920529
KEYWORDS
SOURCE synthetic construct
other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 524 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 69.5%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGG 18
|||: |||||
Db 3 GGCATGACGTTTCGGGGG 20

RESULT 24
AX355395 AX355395 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 423 from Patent WO0197843..
ACCESSION AX355395
VERSION AX355395.1 GI:18620062
KEYWORDS
SOURCE synthetic construct
other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 423 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="Synthetic oligonucleotide
phosphorodithioate backbone"
ORIGIN
Query Match 69.5%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGG 18
|||: |||||
Db 3 GGCATGACGTTTCGGGGG 20

RESULT 25
AX355396 AX355396 20 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 424 from Patent WO0197843..
DEFINITION
ACCESSION AX355396
VERSION AX355396.1 GI:18620064
KEYWORDS
SOURCE synthetic construct
other sequences; artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 424 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="Synthetic oligonucleotide
chimeric phosphorothioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"
ORIGIN
Query Match 69.5%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGG 18
|||: |||||
Db 3 GGCATGACGTTTCGGGGG 20

RESULT 26
AX547382 AX547382 20 bp DNA linear PAT 01-MAR-2003
LOCUS Sequence 521 from Patent WO02053141..
DEFINITION
ACCESSION AX547382
VERSION AX547382.1 GI:25812526
KEYWORDS
SOURCE synthetic construct
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ORGANISM      synthetic construct
other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Bratzler,R.L.
TITLE          Inhibition of angiogenesis by nucleic acids
JOURNAL        Patent: WO 02053141-A 521 11-JUL-2002;
                Coley Pharmaceutical Group, Inc. (US)
FEATURES
source         1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Description of artificial sequence:
                Oligonucleotide"
ORIGIN
Query Match   69.5%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 18
        |||||
Db      3 GGCAATGACGTTTCAGGGGG 20

RESULT 27
AX547385
LOCUS          AX547385          20 bp      DNA      linear      PAT 01-MAR-2003
DEFINITION     Sequence 524 from Patent WO02053141.
ACCESSION      AX547385
VERSION        AX547385.1 GI:25812529
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Bratzler,R.L.
TITLE          Inhibition of angiogenesis by nucleic acids
JOURNAL        Patent: WO 02053141-A 524 11-JUL-2002;
                Coley Pharmaceutical Group, Inc. (US)
FEATURES
source         1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic Sequence"
ORIGIN
Query Match   69.5%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 18
        |||||
Db      3 GGCAATGACGTTTCAGGGGG 20

RESULT 28
CS121639
LOCUS          CS121639          32 bp      DNA      linear      PAT 16-JUL-2005
DEFINITION     Sequence 97 from Patent WO2005058967.
ACCESSION      CS121639
VERSION        CS121639.1 GI:70910466
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Goetsch,L.
TITLE          Novel anti-insulin/igf-i hybrid receptor or anti-insulin/igf-i
                hybrid receptor and igf-ir antibodies and uses thereof
JOURNAL        Patent: WO 2005058967-A 97 30-JUN-2005;
                Pierre Fabre Medicament (FR)
FEATURES
source         Location/Qualifiers
                1..47
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Primers"
ORIGIN
Query Match   69.5%; Score 13.2; DB 6; Length 47;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 18
        |||||
Db      7 GGCGTGACGGCAGGGGAG 24

RESULT 30
CS087335
LOCUS          CS087335          47 bp      DNA      linear      PAT 25-MAY-2005
DEFINITION     Sequence 463 from Patent WO2005042743.
ACCESSION      CS087335
VERSION        CS087335.1 GI:66712784
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Dall-Acqua,W., Damschroder,M. and Wu,H.
TITLE          Humanization of antibodies
JOURNAL        Patent: WO 2005042743-A 463 12-MAY-2005;
                MedImmune, Inc. (US)
FEATURES
source         Location/Qualifiers
                1..47
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Primers"
ORIGIN
Query Match   69.5%; Score 13.2; DB 6; Length 47;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 18
        |||||
Db      7 GGCGTGACGGCAGGGGAG 24

RESULT 32
CS087335
LOCUS          CS087335          32 bp      DNA      linear      PAT 25-NOV-2003
DEFINITION     Sequence 97 from Patent WO03059951.
ACCESSION      AX805700
VERSION        AX805700.1 GI:38522611
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Goetsch,L., Corvaia,N. and Leger,O.
TITLE          Novel anti-IGF-IR antibodies and uses thereof
JOURNAL        Patent: WO 03059951-A 97 24-JUL-2003;
                PIERRE FABRE MEDICAMENT (FR)
FEATURES
source         Location/Qualifiers
                1..32
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"
ORIGIN
Query Match   69.5%; Score 13.2; DB 6; Length 32;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 18
        |||||
Db      7 GGCGTGACGGCAGGGGAG 24
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Best Local Similarity 83.3%; Pred. No. 9.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 18
Db 26 GGGGTGACGGCAGGGAG 43

RESULT 31
CS087338
LOCUS CS087338 47 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 466 from Patent WO2005042743.
ACCESSION CS087338
VERSION CS087338.1 GI:66712787
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Dall-Acqua,W., Damschroder,M. and Wu,H.
TITLE Humanization of antibodies
JOURNAL Patent: WO 2005042743-A 466 12-MAY-2005;
MedImmune, Inc. (US)
FEATURES
source
1..47
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primers"

ORIGIN
Query Match 69.5%; Score 13.2; DB 6; Length 47;
Best Local Similarity 83.3%; Pred. No. 9.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 18
Db 26 GGGGTGACGGCAGGGAG 43

RESULT 32
CS087376
LOCUS CS087376 47 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 504 from Patent WO2005042743.
ACCESSION CS087376
VERSION CS087376.1 GI:66712825
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Dall-Acqua,W., Damschroder,M. and Wu,H.
TITLE Humanization of antibodies
JOURNAL Patent: WO 2005042743-A 504 12-MAY-2005;
MedImmune, Inc. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primers"

ORIGIN
Query Match 69.5%; Score 13.2; DB 6; Length 47;
Best Local Similarity 83.3%; Pred. No. 9.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 18
Db 26 GGGGTGACGGCAGGGAG 43

RESULT 33
CS087377
LOCUS CS087377 47 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 505 from Patent WO2005042743.
ACCESSION CS087377
VERSION CS087377.1 GI:66712826
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Dall-Acqua,W., Damschroder,M. and Wu,H.
TITLE Humanization of antibodies
JOURNAL Patent: WO 2005042743-A 505 12-MAY-2005;
MedImmune, Inc. (US)
FEATURES
source
1..47
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primers"

ORIGIN
Query Match 69.5%; Score 13.2; DB 6; Length 47;
Best Local Similarity 83.3%; Pred. No. 9.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 18
Db 26 GGGGTGACGGCAGGGAG 43

RESULT 34
AX455113/c
LOCUS AX455113/c 20 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 180 from Patent WO0208453.
ACCESSION AX455113
VERSION AX455113.1 GI:21714298
KEYWORDS .
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1
AUTHORS Farr,S.B., Pickett,G.G., Neft,R.E. and Dunn,R.T.
TITLE Canine toxicity genes
JOURNAL Patent: WO 0208453-A 180 31-JAN-2002;
Phase-1 Molecular Toxicology (US)
FEATURES
source
1..20
/organism="Canis familiaris"
/mol_type="unassigned DNA"
/db_xref="taxon:9615"

ORIGIN
Query Match 68.4%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGG 15
Db 18 GGTGACGTTTCAGG 6

RESULT 35
CQ827797
LOCUS CQ827797 19 bp DNA linear PAT 29-JUN-2004
DEFINITION Sequence 20 from Patent WO2004051269.
ACCESSION CQ827797
VERSION CQ827797.1 GI:49456213
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS Dawn,C.
TITLE Replication protein
JOURNAL Patent: WO 2004051269-A 20 17-JUN-2004;
Yorkshire Cancer Research (GB)
FEATURES
SOURCE Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGG 18
Db 3 GGTGACCTTCAGGGAG 18

RESULT 36
AR135661/c
LOCUS AR135661 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 29 from patent US 6136544.
ACCESSION AR135661
VERSION AR135661.1 GI:14476333
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kamboj,R. and Nutt,S.
TITLE Glutamate receptor (or EAA receptor) polynucleotides and their uses
JOURNAL Patent: US 6136544-A 29 24-OCT-2000;
FEATURES
SOURCE Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGTGACGTTTCAGGGG 17
Db 16 GGTGATGTTTCAGGGG 1

RESULT 37
CQ775024
LOCUS CQ775024 20 bp DNA linear PAT 06-MAR-2004
DEFINITION Sequence 47 from Patent WO2004012503.
ACCESSION CQ775024
VERSION CQ775024.1 GI:45238149
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS de Bari,C., Luyten,F. and Dell'Accio,F.
TITLE Compositions comprising muscle progenitor cells and uses thereof
JOURNAL Patent: WO 2004012503-A 47 12-FEB-2004;
Tigenix N.V. (BE)
FEATURES
SOURCE Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"

other sequences; artificial sequences.
1
REFERENCE
AUTHORS Nex,B.R., Vogel,U., Rockenbauer,E. and Bukowy,Z.K.
TITLE Disease risk estimating method using sequence polymorphisms in a
JOURNAL Patent: WO 2004003229-A 57 08-JAN-2004;
Aarhus University (DK); Arbejdsmilj Institutttet (National
Institute of Occupational Health) (DK)
FEATURES
SOURCE Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGG 16
Db 5 GGTGACGTTTCGGG 20

RESULT 39
CQ760615/c
LOCUS CQ760615 21 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 57 from Patent WO2004003229.
ACCESSION CQ760615
VERSION CQ760615.1 GI:44904118
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nex,B.R., Vogel,U., Rockenbauer,E. and Bukowy,Z.K.
TITLE Disease risk estimating method using sequence polymorphisms in a
JOURNAL Patent: WO 2004003229-A 57 08-JAN-2004;
Aarhus University (DK); Arbejdsmilj Institutttet (National
Institute of Occupational Health) (DK)
FEATURES
SOURCE Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGG 16
Db 5 GGTGACGTTTCGGG 20

RESULT 38
AX814043
LOCUS AX814043 20 bp DNA linear PAT 02-DEC-2003
DEFINITION Sequence 26 from Patent EP1334981.
ACCESSION AX814043
VERSION AX814043.1 GI:38636358
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hsu,E.W., Kenney,W.C. and Tressel,T.
TITLE Method for purifying keratinocyte growth factors
JOURNAL Patent: EP 1334981-A 26 13-AUG-2003;
Amgen Inc. (US)
FEATURES
SOURCE Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGG 16
Db 5 GGTGACGTTTCGGG 20

RESULT 39
CQ760615/c
LOCUS CQ760615 21 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 57 from Patent WO2004003229.
ACCESSION CQ760615
VERSION CQ760615.1 GI:44904118
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nex,B.R., Vogel,U., Rockenbauer,E. and Bukowy,Z.K.
TITLE Disease risk estimating method using sequence polymorphisms in a
JOURNAL Patent: WO 2004003229-A 57 08-JAN-2004;
Aarhus University (DK); Arbejdsmilj Institutttet (National
Institute of Occupational Health) (DK)
FEATURES
SOURCE Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Probe"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGG 16
Db 5 GGTGACGTTTCGGG 20
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QY 3 GGTGACGTTTCAGGGGG 18  
|||||  
Db 21 GGTGACGCTCTGGGGG 6

RESULT 40  
CQ760697/c  
LOCUS CQ760697 21 bp DNA linear PAT 03-MAR-2004  
DEFINITION Sequence 139 from Patent WO2004003229.  
ACCESSION CQ760697  
VERSION CQ760697.1 GI:44904200  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Nex,B.R., Vogel,U., Rockenbauer,E. and Bukowy,Z.K.  
TITLE Disease risk estimating method using sequence polymorphisms in a specific region of chromosome 19  
JOURNAL Patent: WO 2004003229-A 139 08-JAN-2004;  
Aarhus University (DK) ; Arbejdsmilj Institutttet (National Institute of Occupational Health) (DK)  
FEATURES Location/Qualifiers  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32830"  
/note="Probe"

ORIGIN  
Query Match 67.4%; Score 12.8; DB 6; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18  
|||||  
Db 21 GGTGACGCTCTGGGGG 6

RESULT 41  
AX249619/c  
LOCUS AX249619 31 bp DNA linear PAT 28-SEP-2001  
DEFINITION Sequence 1698 from Patent WO0166800.  
ACCESSION AX249619  
VERSION AX249619.1 GI:15864242  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.  
TITLE Human single nucleotide polymorphisms  
JOURNAL Patent: WO 0166800-A 1698 13-SEP-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
FEATURES Location/Qualifiers  
source 1..31  
/organism="Homo sapiens"  
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Query Match 67.4%; Score 12.8; DB 6; Length 31;  
Best Local Similarity 77.8%; Pred. No. 1.6e+05;  
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGTGACGTTTCAGGGGG 19  
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Db 29 GGGAGACAGTCAGKGGGG 12

RESULT 42

AR029533/c  
LOCUS AR029533 32 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 43 from patent US 5859336.  
ACCESSION AR029533  
VERSION AR029533.1 GI:5941506  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Kozluel,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L., Bowman,C.G., Dawson,J.L., Dunder,E.M., Pace,G.M. and Suttie,J.L.  
TITLE Synthetic DNA sequence having enhanced activity in maize  
JOURNAL Patent: US 5859336-A 43 12-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..32  
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/mol\_type="unassigned DNA"

ORIGIN  
Query Match 67.4%; Score 12.8; DB 6; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 18 GGTGCGGTACAGGGGG 3

RESULT 43  
AR098486/c  
LOCUS AR098486 32 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 43 from patent US 6075185.  
ACCESSION AR098486  
VERSION AR098486.1 GI:12807743  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Kozluel,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V., Wright,M.S., Launis,K.L., Rothstein,S.J., Bowman,C.G., Dawson,J.L., Dunder,E.M., Pace,G.M. and Suttie,J.L.  
TITLE Synthetic DNA sequence having enhanced insecticidal activity in maize  
JOURNAL Patent: US 6075185-A 43 13-JUN-2000;  
FEATURES Location/Qualifiers  
source 1..32  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 67.4%; Score 12.8; DB 6; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18  
|||||  
Db 18 GGTGCGGTACAGGGGG 3

RESULT 44  
I41446/c  
LOCUS I41446 32 bp DNA linear PAT 13-MAY-1997  
DEFINITION Sequence 43 from patent US 5625136.  
ACCESSION I41446  
VERSION I41446.1 GI:2082036  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 32)

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ORIGIN

Query Match          67.4%; Score 12.8; DB 6; Length 32;
Best Local Similarity 87.5%; Pred. NO. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGG 18
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DB 18 GGTGCCGTACAGGGG 3

RESULT 47
AX453908/c
LOCUS AX453908 32 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 43 from Patent EP1213356.
ACCESSION AX453908
VERSION AX453908.1 GI:21713566
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Koziel,M.G., Desai,N.M., Lewis,K.S., Kramer,V.C., Warren,G.W.,
Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L.
and Rothstein,S.J.
TITLE Synthetic dna sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: EP 1213356-A 43 12-JUN-2002;
SYNGENTA Participations AG (CH)
FEATURES
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/notes="primer P5(a)"

ORIGIN

Query Match          67.4%; Score 12.8; DB 6; Length 32;
Best Local Similarity 87.5%; Pred. NO. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGG 18
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DB 18 GGTGCCGTACAGGGG 3

RESULT 48
AX514624/c
LOCUS AX514624 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 822 from Patent WO02052044.
ACCESSION AX514624
VERSION AX514624.1 GI:23561182
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 822 04-JUL-2002;
RIKEN (JP)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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ORIGIN

Query Match 67.4%; Score 12.8; DB 6; Length 41;  
Best Local Similarity 77.8%; Pred. No. 1.6e+05;  
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTCAGGGGG 18  
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Db 29 GGGTGACAGCTGGGGG 12

RESULT 49

FVBFOKIB/c

LOCUS FVBFOKIB 50 bp DNA linear BCT 26-APR-1993  
DEFINITION Flavobacterium okeanokoites FokI cleavage site F2/F7.

ACCESSION M18006 M10381

VERSION M18006.1 GI:148700

KEYWORDS

SOURCE Planomicrobium okeanokoites

ORGANISM

Planomicrobium okeanokoites  
Bacteria; Firmicutes; Bacilliales; Planococcaceae; Planomicrobium.

REFERENCE 1 (bases 1 to 50)

AUTHORS Sugisaki, H. and Kanazawa, S.

TITLE New restriction endonucleases from Flavobacterium okeanokoites

(FokI) and Micrococcus luteus (MluI)

JOURNAL Gene 16 (1-3), 73-78 (1981)

PUBMED 6282705

COMMENT Original source text: F.okeanokoites DNA, clone pAO43.

FEATURES

source

1..50

/organism="planomicrobium okeanokoites"

/mol\_type="genomic DNA"

/db\_xref="taxon:244"

26 bp upstream of FokI site.

ORIGIN

Query Match 67.4%; Score 12.8; DB 1; Length 50;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTGACGTTCAGGGGG 19  
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RESULT 50

FVBFOKIC

LOCUS FVBFOKIC 50 bp DNA linear BCT 26-APR-1993  
DEFINITION Flavobacterium okeanokoites FokI cleavage site F7/F1.

ACCESSION M18007 M10381

VERSION M18007.1 GI:148701

KEYWORDS

SOURCE Planomicrobium okeanokoites

ORGANISM

Planomicrobium okeanokoites  
Bacteria; Firmicutes; Bacilliales; Planococcaceae; Planomicrobium.

REFERENCE 1 (bases 1 to 50)

AUTHORS Sugisaki, H. and Kanazawa, S.

TITLE New restriction endonucleases from Flavobacterium okeanokoites

(FokI) and Micrococcus luteus (MluI)

JOURNAL Gene 16 (1-3), 73-78 (1981)

PUBMED 6282705

COMMENT Original source text: F.okeanokoites DNA, clone pAO43.

FEATURES

source

1..50

/organism="planomicrobium okeanokoites"

/mol\_type="genomic DNA"

/db\_xref="taxon:244"

26 bp upstream of FokI site.

ORIGIN

Query Match 67.4%; Score 12.8; DB 1; Length 50;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 35 GTGATGTTCAGGGAGG 50  
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Search completed: February 15, 2006, 18:55:32  
Job time : 469.843 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:25:23 ; Search time 143.207 Seconds  
(without alignments)  
884.241 Million cell updates/sec

Title: US-09-669-187A-80

Perfect score: 19

Sequence: 1 999gtgacgttcagggggg 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

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1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
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| 1          | 19    | 100.0       | 19     | 4  | Aaf98955 Immunosti |
| 2          | 19    | 100.0       | 19     | 6  | Abs77596 Angiogene |
| 3          | 19    | 100.0       | 19     | 6  | Abl39043 Immunosti |
| 4          | 19    | 100.0       | 19     | 9  | Adc93388 Immunosti |
| 5          | 19    | 100.0       | 19     | 9  | Adb36457 Immunosti |
| 6          | 19    | 100.0       | 19     | 13 | Adu89396 Allergic  |
| 7          | 17.4  | 91.6        | 19     | 4  | Aaf98957 Immunosti |
| 8          | 17.4  | 91.6        | 19     | 6  | Abs77598 Angiogene |
| 9          | 17.4  | 91.6        | 19     | 6  | Abl39044 Immunosti |
| 10         | 17.4  | 91.6        | 19     | 9  | Adc93390 Immunosti |
| 11         | 17.4  | 91.6        | 19     | 9  | Adb36459 Immunosti |
| 12         | 17.4  | 91.6        | 19     | 13 | Adu89398 Allergic  |
| 13         | 14.4  | 75.8        | 40     | 3  | Aaz95948 Polynucle |
| 14         | 14.2  | 74.7        | 20     | 2  | Aav27677 Immunosti |
| 15         | 14.2  | 74.7        | 20     | 2  | Aav74249 CpG-N mot |
| 16         | 14.2  | 74.7        | 20     | 3  | Aaz48834 B-cell sc |
| 17         | 14.2  | 74.7        | 20     | 4  | Aad02961 Immunosti |
| 18         | 14.2  | 74.7        | 20     | 4  | Aaf99097 Immunosti |
| 19         | 14.2  | 74.7        | 20     | 6  | Abs77740 Angiogene |

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|-----------|-----------|----|------|------|----|----|-----------|
| Abl39045  | Immunosti | 20 | 14.2 | 74.7 | 20 | 6  | ABL39045  |
| Adc91359  | B-cell st | 21 | 14.2 | 74.7 | 20 | 9  | ACD91359  |
| Adc99530  | Immunosti | 22 | 14.2 | 74.7 | 20 | 9  | ACD99530  |
| ACA62324  | Lymphocyt | 23 | 14.2 | 74.7 | 20 | 9  | ACA62324  |
| ADb36599  | Immunosti | 24 | 14.2 | 74.7 | 20 | 9  | ADb36599  |
| Ado58881  | Mitogenic | 25 | 14.2 | 74.7 | 20 | 12 | ADO58881  |
| Adq36558  | B-cell st | 26 | 14.2 | 74.7 | 20 | 12 | ADQ36558  |
| Adq36584  | Umethyla  | 27 | 14.2 | 74.7 | 20 | 12 | ADQ36584  |
| Adr20014  | B-cell st | 28 | 14.2 | 74.7 | 20 | 13 | ADR20014  |
| Adr28877  | CpG-conta | 29 | 14.2 | 74.7 | 20 | 13 | ADR28877  |
| Adr44692  | Mitogenic | 30 | 14.2 | 74.7 | 20 | 13 | ADR44692  |
| Adr45002  | CpG oligo | 31 | 14.2 | 74.7 | 20 | 13 | ADR45002  |
| Adr88228  | CpG Immun | 32 | 14.2 | 74.7 | 20 | 13 | ADR88228  |
| Adsi17223 | ODN1, oli | 33 | 14.2 | 74.7 | 20 | 13 | ADSI17223 |
| Adu89540  | Allergic  | 34 | 14.2 | 74.7 | 20 | 13 | ADU89540  |
| Adw28066  | Mitogenic | 35 | 14.2 | 74.7 | 20 | 14 | ADW28066  |
| Adv97282  | Immunosti | 36 | 14.2 | 74.7 | 20 | 14 | ADV97282  |
| Adx87198  | B cell-st | 37 | 14.2 | 74.7 | 20 | 14 | ADX87198  |
| Adx94981  | CpG oligo | 38 | 14.2 | 74.7 | 20 | 14 | ADX94981  |
| Adc24305  | Primer, D | 39 | 14   | 73.7 | 39 | 10 | ADC24305  |
| Abc89992  | Rabbit ti | 40 | 13.8 | 72.6 | 30 | 4  | AAC89992  |
| Abz43529  | Human SUL | 41 | 13.8 | 72.6 | 41 | 6  | ABZ43529  |
| Abz49680  | Human SUL | 42 | 13.8 | 72.6 | 41 | 6  | ABZ49680  |
| Aad07150  | PCR prime | 43 | 13.4 | 70.5 | 22 | 4  | AAD07150  |
| Aaf74944  | Bacteriop | 44 | 13.4 | 70.5 | 22 | 4  | AAF74944  |
| Adr99754  | Nucleic a | 45 | 13.4 | 70.5 | 30 | 13 | ADR99754  |
| Adw46519  | Human sur | 46 | 13.2 | 69.5 | 19 | 14 | ADW46519  |
| Adw46518  | Human sur | 47 | 13.2 | 69.5 | 19 | 14 | ADW46518  |
| Aaf99395  | Immunosti | 48 | 13.2 | 69.5 | 20 | 4  | AAF99395  |
| Aaf99392  | Immunosti | 49 | 13.2 | 69.5 | 20 | 4  | AAF99392  |
| Abst78040 | Angiogene | 50 | 13.2 | 69.5 | 20 | 6  | ABST78040 |
| Abst78037 | Angiogene | 51 | 13.2 | 69.5 | 20 | 6  | ABST78037 |
| Abl39019  | Immunosti | 52 | 13.2 | 69.5 | 20 | 6  | ABL39019  |
| Abl39020  | Immunosti | 53 | 13.2 | 69.5 | 20 | 6  | ABL39020  |
| Adc99815  | Immunosti | 54 | 13.2 | 69.5 | 20 | 9  | ADC99815  |
| Adc99812  | Immunosti | 55 | 13.2 | 69.5 | 20 | 9  | ADC99812  |
| ACA62351  | Lymphocyt | 56 | 13.2 | 69.5 | 20 | 9  | ACA62351  |
| Adb36897  | Immunosti | 57 | 13.2 | 69.5 | 20 | 9  | ADB36897  |
| Adb36894  | Immunosti | 58 | 13.2 | 69.5 | 20 | 9  | ADB36894  |
| Adu89837  | Allergic  | 59 | 13.2 | 69.5 | 20 | 13 | ADU89837  |
| Adu89840  | Allergic  | 60 | 13.2 | 69.5 | 20 | 13 | ADU89840  |
| Adw46375  | Human sur | 61 | 13.2 | 69.5 | 20 | 14 | ADW46375  |
| Adw46374  | Human sur | 62 | 13.2 | 69.5 | 20 | 14 | ADW46374  |
| ACK07484  | Human mic | 63 | 13.2 | 69.5 | 25 | 9  | ACK07484  |
| Aai31210  | Human sin | 64 | 13.2 | 69.5 | 31 | 4  | AAI31210  |
| Adi76931  | Anti-IGF- | 65 | 13.2 | 69.5 | 32 | 10 | ADI76931  |
| Adz67101  | Humanized | 66 | 13.2 | 69.5 | 32 | 14 | ADZ67101  |
| Abz56947  | Alpha-1 i | 67 | 13.2 | 69.5 | 33 | 6  | ABZ56947  |
| ACC49874  | Human mut | 68 | 13.2 | 69.5 | 39 | 10 | ACC49874  |
| Abz56949  | Alpha-1 i | 69 | 13.2 | 69.5 | 41 | 6  | ABZ56949  |
| Ady35036  | Kappa VL  | 70 | 13.2 | 69.5 | 47 | 14 | ADY35036  |
| Ady35075  | Kappa VL  | 71 | 13.2 | 69.5 | 47 | 14 | ADY35075  |
| Ady35033  | Kappa VL  | 72 | 13.2 | 69.5 | 47 | 14 | ADY35033  |
| Ady35074  | Kappa VL  | 73 | 13.2 | 69.5 | 47 | 14 | ADY35074  |
| Abz03672  | Human leu | 74 | 13.2 | 69.5 | 50 | 6  | ABZ03672  |
| Ab199541  | Canine su | 75 | 13   | 68.4 | 20 | 6  | AB199541  |
| Abz83722  | Toxicolog | 76 | 13   | 68.4 | 30 | 10 | ABZ83722  |
| Adz51509  | HB PCR pr | 77 | 13   | 68.4 | 42 | 14 | ADZ51509  |
| Adn11956  | Primer of | 78 | 12.8 | 67.4 | 19 | 12 | ADN11956  |
| Adp83591  | Human Ciz | 79 | 12.8 | 67.4 | 19 | 12 | ADP83591  |
| Aaq91247  | EAA5 rece | 80 | 12.8 | 67.4 | 20 | 2  | AAQ91247  |
| Aaa95526  | Primer 1  | 81 | 12.8 | 67.4 | 20 | 3  | AAA95526  |
| Aac62057  | PCR prime | 82 | 12.8 | 67.4 | 20 | 4  | AAC62057  |
| Adh93300  | Human gen | 83 | 12.8 | 67.4 | 20 | 10 | ADH93300  |
| Abz48834  | Human tra | 84 | 12.8 | 67.4 | 20 | 10 | ABZ48834  |
| Abd21084  | Human tra | 85 | 12.8 | 67.4 | 20 | 11 | ABD21084  |
| Ado15471  | Human CB9 | 86 | 12.8 | 67.4 | 20 | 12 | ADO15471  |
| Adk41381  | Human chr | 87 | 12.8 | 67.4 | 21 | 12 | ADK41381  |
| Adk41299  | Human chr | 88 | 12.8 | 67.4 | 21 | 12 | ADK41299  |
| Ac102236  | Human mic | 89 | 12.8 | 67.4 | 25 | 9  | AC102236  |
| Aeb79114  | Mouse lac | 90 | 12.8 | 67.4 | 26 | 14 | AEB79114  |
| Aaq38984  | Synthetic | 91 | 12.8 | 67.4 | 32 | 2  | AAQ38984  |
| Aah90432  | Human clo | 92 | 12.8 | 67.4 | 50 | 4  | AAH90432  |

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|---|-----|------|------|----|----|----------|--------------------|-----|------|------|------|----|----------|--------------------|--------------------|
| c | 93  | 12.8 | 67.4 | 50 | 6  | AB204742 | Abz04742 Human leu | 166 | 12.6 | 66.3 | 20   | 13 | ADU90284 | Adu90284 Allergic  |                    |
|   | 94  | 12.6 | 66.3 | 19 | 4  | AAF98757 | Aaf98757 Human IFN | 167 | 12.6 | 66.3 | 20   | 14 | ADW29187 | Adw29187 Immunosti |                    |
|   | 95  | 12.6 | 66.3 | 19 | 4  | AAF99840 | Aaf99840 Immunosti | 168 | 12.6 | 66.3 | 20   | 14 | ADY53603 | Ady53603 Anti-canc |                    |
|   | 96  | 12.6 | 66.3 | 19 | 4  | AAF99771 | Aaf99771 Immunosti | 169 | 12.6 | 66.3 | 20   | 14 | ADY39617 | Ady39617 Phosphoro |                    |
|   | 97  | 12.6 | 66.3 | 19 | 6  | ABS78492 | Abs78492 Angiogene | 170 | 12.6 | 66.3 | 20   | 14 | ADZ88500 | Adz88500 CpG ODNI5 |                    |
|   | 98  | 12.6 | 66.3 | 19 | 6  | ABS78562 | Abs78562 Angiogene | 171 | 12.6 | 66.3 | 20   | 14 | AEA16606 | Aea16606 CpG immun |                    |
|   | 99  | 12.6 | 66.3 | 19 | 9  | ACH03295 | Acho3295 Immunosti | 172 | 12.6 | 66.3 | 20   | 14 | ABE07462 | Aeb07462 Novel vir |                    |
|   | 100 | 12.6 | 66.3 | 19 | 9  | ADB37342 | Adb37342 Immunosti | 173 | 12.6 | 66.3 | 20   | 14 | ABE07462 | Aeb07462 Novel vir |                    |
|   | 101 | 12.6 | 66.3 | 19 | 9  | ADB37273 | Adb37273 Immunosti | 174 | 12.6 | 66.3 | 21   | 4  | AAF98875 | Aaf98875 Immunosti |                    |
|   | 102 | 12.6 | 66.3 | 19 | 13 | ADU90362 | Adu90362 Allergic  | 175 | 12.6 | 66.3 | 21   | 4  | AAF99798 | Aaf99798 Immunosti |                    |
|   | 103 | 12.6 | 66.3 | 19 | 13 | ADU90292 | Adu90292 Allergic  | 176 | 12.6 | 66.3 | 21   | 6  | ABS78520 | Abs78520 Angiogene |                    |
|   | 104 | 12.6 | 66.3 | 20 | 2  | AAT16894 | Aat16894 Immunomod | 177 | 12.6 | 66.3 | 21   | 8  | ABZ80185 | Abz80185 Immunosti |                    |
|   | 105 | 12.6 | 66.3 | 20 | 2  | AAV47684 | Aav47684 Urmethyla | 178 | 12.6 | 66.3 | 21   | 9  | ACH03322 | Acho3322 Immunosti |                    |
|   | 106 | 12.6 | 66.3 | 20 | 2  | AAV27654 | Aav27654 Immunosti | 179 | 12.6 | 66.3 | 21   | 9  | ADB37300 | Adb37300 Immunosti |                    |
|   | 107 | 12.6 | 66.3 | 20 | 2  | AAV74238 | Aav74238 CpG-N mot | 180 | 12.6 | 66.3 | 21   | 13 | ADU90320 | Adu90320 Allergic  |                    |
|   | 108 | 12.6 | 66.3 | 20 | 2  | AAV74245 | Aav74245 CpG-N mot | 181 | 12.6 | 66.3 | 24   | 4  | AAF99389 | Aaf99389 Immunosti |                    |
|   | 109 | 12.6 | 66.3 | 20 | 3  | AAA90449 | Aaa90449 CpG adjuv | 182 | 12.6 | 66.3 | 24   | 6  | ABS78034 | Abs78034 Angiogene |                    |
|   | 110 | 12.6 | 66.3 | 20 | 4  | AAH20394 | Aah20394 CpG motif | 183 | 12.6 | 66.3 | 24   | 9  | ACD99809 | Acd99809 Immunosti |                    |
|   | 111 | 12.6 | 66.3 | 20 | 4  | AAH50658 | Aah50658 Immune re | 184 | 12.6 | 66.3 | 24   | 9  | ADB36891 | Adb36891 Immunosti |                    |
|   | 112 | 12.6 | 66.3 | 20 | 4  | AAH19262 | Aah19262 Oligonuel | 185 | 12.6 | 66.3 | 24   | 13 | ADU89834 | Adu89834 Allergic  |                    |
|   | 113 | 12.6 | 66.3 | 20 | 4  | AAF98854 | Aaf98854 Poly-G im | c   | 186  | 12.6 | 66.3 | 25 | 6        | ABL59183           | Abi59183 Oligonuel |
|   | 114 | 12.6 | 66.3 | 20 | 4  | AAF98731 | Aaf98731 Human IFN | 187 | 12.6 | 66.3 | 25   | 9  | ACI09013 | Act09013 Human mic |                    |
|   | 115 | 12.6 | 66.3 | 20 | 4  | AAF98855 | Aaf98855 Poly-G im | 188 | 12.6 | 66.3 | 25   | 14 | ADX83315 | Adx83315 Human TEG |                    |
|   | 116 | 12.6 | 66.3 | 20 | 4  | AAF98735 | Aaf98735 Human IFN | 189 | 12.6 | 66.3 | 26   | 2  | AAx40773 | Aax40773 Oligonuel |                    |
|   | 117 | 12.6 | 66.3 | 20 | 4  | AAc80669 | Aac80669 Immunogen | c   | 190  | 12.6 | 66.3 | 26 | 2        | AAx40824           | Aax40824 Genomic s |
|   | 118 | 12.6 | 66.3 | 20 | 4  | AAE95904 | Aae95904 Immunosti | 191 | 12.6 | 66.3 | 26   | 12 | ADO55232 | Ado55232 Immune mo |                    |
|   | 119 | 12.6 | 66.3 | 20 | 4  | AAE99567 | Aae99567 Immunosti | 192 | 12.6 | 66.3 | 26   | 12 | ADO55229 | Ado55229 Immune mo |                    |
|   | 120 | 12.6 | 66.3 | 20 | 4  | AAE99704 | Aae99704 Immunosti | c   | 193  | 12.6 | 66.3 | 30 | 2        | AAQ20873           | Aaq20873 Immunosti |
|   | 121 | 12.6 | 66.3 | 20 | 4  | AAE99764 | Aae99764 Immunosti | 194 | 12.6 | 66.3 | 30   | 2  | AAQ20870 | Aaq20870 Immunosti |                    |
|   | 122 | 12.6 | 66.3 | 20 | 4  | AAE99390 | Aae99390 Immunosti | c   | 195  | 12.6 | 66.3 | 30 | 3        | AAA05777           | Aaa05777 Streptavi |
|   | 123 | 12.6 | 66.3 | 20 | 4  | AAE99763 | Aae99763 Immunosti | 196 | 12.6 | 66.3 | 30   | 4  | AAF98884 | Aaf98884 IFN-1 ind |                    |
|   | 124 | 12.6 | 66.3 | 20 | 4  | AAE92361 | Aae92361 CG motif  | 197 | 12.6 | 66.3 | 30   | 6  | ABL35104 | Abi35104 Phosphoro |                    |
|   | 125 | 12.6 | 66.3 | 20 | 4  | AAE99639 | Aae99639 Immunorea | 198 | 12.6 | 66.3 | 30   | 6  | ABL35099 | Abi35099 Phosphoro |                    |
|   | 126 | 12.6 | 66.3 | 20 | 5  | AAE27750 | Aae27750 P. falcip | 199 | 12.6 | 66.3 | 30   | 6  | ABL35102 | Abi35102 Phosphoro |                    |
|   | 127 | 12.6 | 66.3 | 20 | 6  | ABS78484 | Abs78484 Angiogene | 200 | 12.6 | 66.3 | 30   | 13 | ADU70018 | Adu70018 Immunosti |                    |
|   | 128 | 12.6 | 66.3 | 20 | 6  | ABS78485 | Abs78485 Angiogene | c   | 201  | 12.6 | 66.3 | 31 | 14       | ADU70016           | Adu70016 Immunosti |
|   | 129 | 12.6 | 66.3 | 20 | 6  | ABS78283 | Abs78283 Angiogene | 202 | 12.6 | 66.3 | 31   | 14 | ADU92126 | Adu92126 Leuconost |                    |
|   | 130 | 12.6 | 66.3 | 20 | 6  | ABS78035 | Abs78035 Angiogene | 203 | 12.6 | 66.3 | 33   | 10 | ADB61582 | Adb61582 Hepatocyt |                    |
|   | 131 | 12.6 | 66.3 | 20 | 6  | ABS78425 | Abs78425 Angiogene | c   | 204  | 12.6 | 66.3 | 44 | 8        | ACA60185           | Aca60185 Human sec |
|   | 132 | 12.6 | 66.3 | 20 | 6  | ABL39032 | Abi39032 Immunosti | c   | 205  | 12.6 | 66.3 | 44 | 8        | ACD07585           | Acd07585 Novel hum |
|   | 133 | 12.6 | 66.3 | 20 | 6  | ABL39033 | Abi39033 Immunosti | c   | 206  | 12.6 | 66.3 | 44 | 8        | ABX71633           | Abx71633 Human sec |
|   | 134 | 12.6 | 66.3 | 20 | 6  | ABL39039 | Abi39039 Immunosti | c   | 207  | 12.6 | 66.3 | 44 | 8        | ACH06965           | Acho6965 Human sec |
|   | 135 | 12.6 | 66.3 | 20 | 6  | ABK46517 | Abk46517 Immunosti | c   | 208  | 12.6 | 66.3 | 44 | 8        | ABX96202           | Abx96202 Human sec |
|   | 136 | 12.6 | 66.3 | 20 | 6  | AAI44488 | Aai44488 CpG motif | c   | 209  | 12.6 | 66.3 | 44 | 8        | ACA05523           | Aca05523 Human sec |
|   | 137 | 12.6 | 66.3 | 20 | 6  | ABS70558 | Abs70558 Dendritic | c   | 210  | 12.6 | 66.3 | 44 | 8        | ACD20190           | Acd20190 Human sec |
|   | 138 | 12.6 | 66.3 | 20 | 8  | ACC48308 | Acc48308 CpG oligo | c   | 211  | 12.6 | 66.3 | 44 | 8        | ACA54993           | Aca54993 Novel sec |
|   | 139 | 12.6 | 66.3 | 20 | 8  | ABZ80163 | Abz80163 Immunosti | c   | 212  | 12.6 | 66.3 | 44 | 9        | ACD19828           | Acd19828 Human sec |
|   | 140 | 12.6 | 66.3 | 20 | 9  | ACC83113 | Acc83113 D class C | c   | 213  | 12.6 | 66.3 | 44 | 9        | ADB29430           | Adb29430 Human sec |
|   | 141 | 12.6 | 66.3 | 20 | 9  | ACH03243 | Acho3243 Immunosti | c   | 214  | 12.6 | 66.3 | 44 | 9        | ADA18286           | Ada18286 Human sec |
|   | 142 | 12.6 | 66.3 | 20 | 9  | ACH09810 | Acho9810 Immunosti | c   | 215  | 12.6 | 66.3 | 44 | 9        | ACD66975           | Acd66975 Human sec |
|   | 143 | 12.6 | 66.3 | 20 | 9  | ACH03405 | Acho3405 Immunosti | c   | 216  | 12.6 | 66.3 | 44 | 9        | ACD83136           | Acd83136 Human PRO |
|   | 144 | 12.6 | 66.3 | 20 | 9  | ACH03105 | Acho3105 Immunosti | c   | 217  | 12.6 | 66.3 | 44 | 9        | ADA16261           | Ada16261 Human sec |
|   | 145 | 12.6 | 66.3 | 20 | 9  | ACH03288 | Acho3288 Immunosti | c   | 218  | 12.6 | 66.3 | 44 | 9        | ADA42406           | Ada42406 Human sec |
|   | 146 | 12.6 | 66.3 | 20 | 9  | ADB37069 | Adb37069 Immunosti | c   | 219  | 12.6 | 66.3 | 44 | 9        | ACD23314           | Acd23314 Human PRO |
|   | 147 | 12.6 | 66.3 | 20 | 9  | ADB37266 | Adb37266 Immunosti | c   | 220  | 12.6 | 66.3 | 44 | 9        | ADA16685           | Ada16685 Human sec |
|   | 148 | 12.6 | 66.3 | 20 | 9  | ADB36892 | Adb36892 Immunosti | c   | 221  | 12.6 | 66.3 | 44 | 9        | ADA13114           | Ada13114 Human sec |
|   | 149 | 12.6 | 66.3 | 20 | 9  | ADB37206 | Adb37206 Immunosti | c   | 222  | 12.6 | 66.3 | 44 | 9        | ADA41982           | Ada41982 Human sec |
|   | 150 | 12.6 | 66.3 | 20 | 9  | ADB37265 | Adb37265 Immunosti | c   | 223  | 12.6 | 66.3 | 44 | 9        | ADA17329           | Ada17329 Human sec |
|   | 151 | 12.6 | 66.3 | 20 | 10 | AAD60208 | Aad60208 Oligonuel | c   | 224  | 12.6 | 66.3 | 44 | 9        | ADA2832            | Ada2832 Human sec  |
|   | 152 | 12.6 | 66.3 | 20 | 10 | ADG68114 | Adg68114 Urmethyla | c   | 225  | 12.6 | 66.3 | 44 | 9        | ACD23676           | Acd23676 Human PRO |
|   | 153 | 12.6 | 66.3 | 20 | 12 | ADI01054 | Adi01054 Immunosti | c   | 226  | 12.6 | 66.3 | 44 | 10       | ADB77751           | Adb77751 Human sec |
|   | 154 | 12.6 | 66.3 | 20 | 12 | ACA63219 | Aca63219 Toll-like | c   | 227  | 12.6 | 66.3 | 44 | 10       | ADB74887           | Adb74887 Human sec |
|   | 155 | 12.6 | 66.3 | 20 | 12 | ADM99023 | Adm99023 Immunosti | c   | 228  | 12.6 | 66.3 | 44 | 10       | ADC28533           | Adc28533 Human sec |
|   | 156 | 12.6 | 66.3 | 20 | 12 | ADO04739 | Ado04739 CpG oligo | c   | 229  | 12.6 | 66.3 | 44 | 10       | ADC39733           | Adc39733 Human sec |
|   | 157 | 12.6 | 66.3 | 20 | 13 | ADR28904 | Adr28904 CpG-conta | c   | 230  | 12.6 | 66.3 | 44 | 10       | ADC40247           | Adc40247 Human sec |
|   | 158 | 12.6 | 66.3 | 20 | 13 | ADR69222 | Adr69222 CpG immun | c   | 231  | 12.6 | 66.3 | 44 | 10       | ADC19071           | Adc19071 Human sec |
|   | 159 | 12.6 | 66.3 | 20 | 13 | ADT61920 | Adt61920 Mitogenic | c   | 232  | 12.6 | 66.3 | 44 | 10       | ADC34371           | Adc34371 Human sec |
|   | 160 | 12.6 | 66.3 | 20 | 13 | ADU70246 | Adu70246 Immunosti | c   | 233  | 12.6 | 66.3 | 44 | 10       | ADC29426           | Adc29426 Human sec |
|   | 161 | 12.6 | 66.3 | 20 | 13 | ADU70022 | Adu70022 Immunosti | c   | 234  | 12.6 | 66.3 | 44 | 10       | ADC28957           | Adc28957 Human sec |
|   | 162 | 12.6 | 66.3 | 20 | 13 | ADU90225 | Adu90225 Allergic  | c   | 235  | 12.6 | 66.3 | 44 | 10       | ADC40842           | Adc40842 Human sec |
|   | 163 | 12.6 | 66.3 | 20 | 13 | ADU90285 | Adu90285 Allergic  | c   | 236  | 12.6 | 66.3 | 44 | 10       | ADC19499           | Adc19499 Human sec |
|   | 164 | 12.6 | 66.3 | 20 | 13 | ADU90083 | Adu90083 Allergic  | c   | 237  | 12.6 | 66.3 | 44 | 10       | ADC33947           | Adc33947 Human sec |
|   | 165 | 12.6 | 66.3 | 20 | 13 | ADU89835 | Adu89835 Allergic  | c   | 238  | 12.6 | 66.3 | 44 | 10       | ADC13017           | Adc13017 Human sec |

|       |      |      |    |    |           |           |
|-------|------|------|----|----|-----------|-----------|
| C 239 | 12.6 | 66.3 | 44 | 10 | ADCL12469 | Human sec |
| C 240 | 12.6 | 66.3 | 44 | 10 | ADD05024  | Human sec |
| C 241 | 12.6 | 66.3 | 44 | 10 | ADD04030  | Human sec |
| C 242 | 12.6 | 66.3 | 44 | 10 | ADD03606  | Human sec |
| C 243 | 12.6 | 66.3 | 44 | 10 | AD34858   | Human sec |
| C 244 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 245 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 246 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 247 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 248 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 249 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 250 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 251 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 252 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 253 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 254 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 255 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 256 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 257 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 258 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 259 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 260 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 261 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 262 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 263 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 264 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 265 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 266 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 267 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 268 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 269 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 270 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 271 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 272 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 273 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 274 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 275 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 276 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 277 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 278 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 279 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 280 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 281 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 282 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 283 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 284 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 285 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 286 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 287 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 288 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 289 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 290 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 291 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 292 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 293 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 294 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 295 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 296 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 297 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 298 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 299 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |
| C 300 | 12.6 | 66.3 | 44 | 10 | ADH59341  | Human sec |

ALIGNMENTS

RESULT 1  
 AAF98955 standard; DNA; 19 BP.  
 ID AAF98955  
 XX AAF98955;  
 AC AAF98955;  
 XX

DT 12-JUN-2001 (first entry)  
 XX Immunostimulatory nucleic acid #71.  
 DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 OS Synthetic.  
 XX WO200122972-A2.  
 PN 05-APR-2001.  
 XX 25-SEP-2000; 2000WO-US026383.  
 PF 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX Krieg AM, Schetter C, Vollmer J;  
 PI WPI; 2001-273485/28.  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX Disclosure; Page 40; 338pp; English.  
 CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 19; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGTGACCTTCAGGGGGG 19  
 Db 1 GGGGTGACCTTCAGGGGGG 19  
 RESULT 2  
 AAF98955 standard; DNA; 19 BP.  
 ID AAF98955  
 XX AAF98955;  
 AC AAF98955;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #80.  
 XX  
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW Plaque neovascularisation; telangiectasia; haemophilic joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 OS Synthetic.  
 XX  
 PN WO200253141-A2.  
 XX  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 14-DEC-2001; 2001WO-US048458.  
 XX  
 XX  
 PR 14-DEC-2000; 2000US-0255534P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 XX  
 PI Bratzler RL;  
 XX  
 DR WPI; 2002-566690/60.  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX  
 PS Claim 2; Page 21; 276pp; English.  
 XX  
 CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX  
 SQ Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGGGG 19  
 |||||  
 Db 1 GGGGTGACGTTTCAGGGGGG 19  
 |||||  
 RESULT 3  
 ABL39043  
 ID ABL39043 standard; DNA; 19 BP.  
 XX  
 AC ABL39043;  
 XX  
 DT 16-APR-2002 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid SEQ ID NO: 447.  
 XX  
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200197843-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 22-JUN-2001; 2001WO-US020154.  
 XX

PR 22-JUN-2000; 2000US-0213346P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 PI Weiner G, Hartmann G;  
 XX  
 DR WPI; 2002-154611/20.  
 XX  
 PT Treating or preventing cancer, such as basal cell carcinoma, comprises  
 PT administering immunostimulatory nucleic acids that induce expression of  
 PT cell surface antigens and antibodies to a subject having or at risk of  
 PT developing cancer.  
 XX  
 PS Disclosure; Page 208; 312pp; English.  
 XX  
 CC The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for  
 CC treating or preventing cancer such as basal cell carcinoma, bladder  
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
 CC present sequence is an immunostimulatory oligonucleotide described in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGGGG 19  
 |||||  
 Db 1 GGGGTGACGTTTCAGGGGGG 19  
 |||||  
 RESULT 4  
 ACD93388  
 ID ACD93388 standard; DNA; 19 BP.  
 XX  
 AC ACD93388;  
 XX  
 DT 25-SEP-2003 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #74.  
 XX  
 KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 OS Synthetic.  
 XX  
 PN US2003050268-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 29-MAR-2002; 2002US-00112653.  
 XX  
 PR 29-MAR-2001; 2001US-0279642P.  
 XX  
 PA (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX  
 PI Krieg AM, Berg DJ;  
 XX  
 DR WPI; 2003-521815/49.  
 XX

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PS disease by administering an immunostimulatory nucleic acid.  
XX  
PS Disclosure; Page 10; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
SQ Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
Db 1 GGGGTGACGTTTCAGGGGG 19

RESULT 5  
ADB36457  
ID ADB36457 standard; DNA; 19 BP.  
XX  
AC ADB36457;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #71.  
XX  
KW db; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX  
OS Synthetic.

XX  
PN US2003087848-A1.  
XX  
PD 08-MAY-2003.  
XX  
PE 02-FEB-2001; 2001US-00776479.  
XX  
PF 03-FEB-2000; 2000US-0179991P.

XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
PI WPI; 2003-657977/62.

XX  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX  
PS Disclosure; Page 6; 221pp; English.

XX The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX  
SQ Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 18;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGTGACGTTTCAGGGGG 19  
Db 1 GGGGTGACGTTTCAGGGGG 19

RESULT 6  
ADU89396  
ID ADU89396 standard; DNA; 19 BP.  
XX  
AC ADU89396;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Allergic response suppressor oligonucleotide #80.

XX ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;  
KW antibacterial; virucide; immunoglobulin E antagonist; allergy;  
KW immunostimulatory; asthma; rhinitis; urticaria; dermatitis;  
KW bacterial infection; viral infection.  
XX  
OS Synthetic.

XX  
PN US2004235774-A1.  
XX  
PD 25-NOV-2004.

XX 23-APR-2004; 2004US-00831778.  
XX  
PR 03-FEB-2000; 2000US-0179991P.  
PR 02-FEB-2001; 2001US-00776479.

XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2004-833006/82.

XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
PT dermatitis, in a subject, comprises administering a first and second dose  
PT of an immunostimulatory nucleic acid.

XX Disclosure; SEQ ID NO 80; 235pp; English.

XX The invention relates to a method of suppressing a symptom of an allergic  
CC response in a subject by administering a first and second dose of an  
CC immunostimulatory nucleic acid that comprises a nucleotide sequence  
CC comprising 5'-cg-3', and where the second dose is administered from 1 day  
CC to 8 weeks after the first dose. The methods and compositions of the  
CC present invention are useful for the treatment or prevention of asthma  
CC and allergy, including rhinitis, urticaria and atopic dermatitis, using  
CC an immunostimulatory nucleic acid alone or in combination with other  
CC medicaments. They can also be used in preventing bacterial and viral  
CC infections. This sequence represents an oligonucleotide used in the  
CC method of the invention.

XX Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
Db 1 GGGGTGACGTTTCAGGGGG 19

RESULT 7  
AAF98957  
ID AAF98957 standard; DNA; 19 BP.

```

XX AAF98957;
AC
XX 12-JUN-2001 (first entry)
DT
XX Immunostimulatory nucleic acid #73.
DE
XX
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
XX Synthetic.
OS
XX WO200122972-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 25-SEP-2000; 2000WO-US026383.
PF
XX
XX 25-SEP-1999; 99US-0156113P.
PR
XX
XX 27-SEP-1999; 99US-0156135P.
PR
XX
XX 23-AUG-2000; 2000US-0227436P.
PR
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA
XX (COLE-) COLEY PHARM GMBH.
PA
XX
XX Krieg AM, Schetter C, Vollmer J;
PI
XX
XX WPI; 2001-273485/28.
DR
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
PT
XX
XX Disclosure; Page 40; 338pp; English.
PS
XX
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
XX Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
SQ
Query Match 91.6%; Score 17.4; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db ||||| ||||| ||||| |||||
1 GGGGTGTCGTTTCAGGGGG 19

RESULT 8
AB877598
ID AB877598 standard; DNA; 19 BP.
XX
XX AB877598;
AC
XX
XX 13-DEC-2002 (first entry)
DT
XX
XX Angiogenesis inhibitory oligonucleotide #82.
DE
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW

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---

```

KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubrosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophilic joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
XX Synthetic.
OS
XX WO200253141-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 14-DEC-2001; 2001WO-US048458.
PF
XX
XX 14-DEC-2000; 2000US-0255534P.
PR
XX
XX (COLE-) COLEY PHARM GROUP INC.
PA
XX
XX Bratzler RL;
PI
XX
XX WPI; 2002-566690/60.
DR
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
PT
XX
XX Claim 2; Page 21; 276pp; English.
PS
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubrosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
XX Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
SQ
Query Match 91.6%; Score 17.4; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db ||||| ||||| ||||| |||||
1 GGGGTGTCGTTTCAGGGGG 19

RESULT 9
ABL39044
ID ABL39044 standard; DNA; 19 BP.
XX
XX ABL39044;
AC
XX
XX 16-APR-2002 (first entry)
DT
XX
XX Immunostimulatory nucleic acid SEQ ID NO: 448.
DE
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
XX Synthetic.
OS
XX WO200197843-A2.
PN
XX
XX 27-DEC-2001.
PD

```

XX 22-JUN-2001; 2001WO-US020154.  
PF  
XX  
PR 22-JUN-2000; 2000US-0213346P.  
XX  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Weiner G, Hartmann G;  
XX  
XX WPI; 2002-154611/20.  
XX  
XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.  
XX  
PS Disclosure; Page 209; 312pp; English.  
XX  
XX The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention  
XX  
XX Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;  
SQ

Query Match 91.6%; Score 17.4; DB 6; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGGG 19  
Db 1 GGGGTGTCGTTTCAGGGGGG 19

RESULT 10  
ACD99390  
ID ACD99390 standard; DNA; 19 BP.  
XX  
AC ACD99390;  
XX  
XX 25-SBP-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #76.  
XX  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX  
XX Synthetic.  
XX  
XX US2003050268-A1.  
PN  
XX 13-MAR-2003.  
XX  
XX 29-MAR-2002; 2002US-00112653.  
PF  
XX  
XX 29-MAR-2001; 2001US-0279642P.  
PR  
XX  
XX (KRIE/) KRIEG A M.  
PA (BERG/) BERG D J.  
PA  
XX Krieg AM, Berg DJ;  
PI

XX WPI; 2003-521815/49.  
XX  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX  
XX Disclosure; Page 10; 229pp; English.  
XX  
XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
XX Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;  
SQ

Query Match 91.6%; Score 17.4; DB 9; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGGG 19  
Db 1 GGGGTGTCGTTTCAGGGGGG 19

RESULT 11  
ADB36459  
ID ADB36459 standard; DNA; 19 BP.  
XX  
XX ADB36459;  
XX  
XX 04-DEC-2003 (first entry)  
XX  
XX Immunostimulatory nucleic acid #73.  
DE  
XX  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX  
XX Synthetic.  
XX  
XX US2003087848-A1.  
PN  
XX 08-MAY-2003.  
PD  
XX  
XX 02-FEB-2001; 2001US-00776479.  
PF  
XX  
XX 03-FEB-2000; 2000US-0179991P.  
PR  
XX  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
PI  
XX WPI; 2003-657977/62.  
XX  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
PT  
XX  
XX Disclosure; Page 6; 221pp; English.  
XX  
XX The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX  
XX Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;  
SQ

Query Match 91.6%; Score 17.4; DB 9; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
||||| |||||||  
Db 1 GGGGTGTCGTTTCAGGGGGG 19

RESULT 12  
ADU89398  
ID ADU89398 standard; DNA; 19 BP.  
XX  
AC ADU89398;  
XX  
XX 10-FEB-2005 (first entry)  
XX  
DE Allergic response suppressor oligonucleotide #82.  
XX ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;  
KW antibacterial; virucide; immunoglobulin E antagonist; allergy;  
KW immunostimulatory; asthma; rhinitis; urticaria; dermatitis;  
KW bacterial infection; viral infection.  
XX  
OS Synthetic.  
XX  
XX US2004235774-A1.  
PN  
XX  
XX 25-NOV-2004.  
PD  
XX 23-APR-2004; 2004US-00831778.  
PF  
XX 03-FEB-2000; 2000US-0179991P.  
PR 02-FEB-2001; 2001US-00776479.  
XX  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2004-833006/82.  
XX  
XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
PT dermatitis, in a subject, comprises administering a first and second dose  
PT of an immunostimulatory nucleic acid.  
XX  
XX Disclosure; SEQ ID NO 82; 235pp; English.

CC The invention relates to a method of suppressing a symptom of an allergic  
CC response in a subject by administering a first and second dose of an  
CC immunostimulatory nucleic acid that comprises a nucleotide sequence  
CC comprising 5'-cg-3', and where the second dose is administered from 1 day  
CC to 8 weeks after the first dose. The methods and compositions of the  
CC present invention are useful for the treatment or prevention of asthma  
CC and allergy, including rhinitis, urticaria and atopic dermatitis, using  
CC an immunostimulatory nucleic acid alone or in combination with other  
CC medicaments. They can also be used in preventing bacterial and viral  
CC infections. This sequence represents an oligonucleotide used in the  
CC method of the invention.

XX  
XX Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 91.6%; Score 17.4; DB 13; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
||||| |||||||  
Db 1 GGGGTGTCGTTTCAGGGGGG 19

RESULT 13  
AAZ95948  
ID AAZ95948 standard; DNA; 40 BP.  
XX  
AC AAZ95948;  
XX  
XX 10-APR-2000 (first entry)  
DT  
XX  
DE Polynucleotide sequence including binding site for BamHI.  
XX  
KW Ligand binding; restriction enzyme; nucleic acid determination;  
KW pharmaceutical; BamHI; ss.  
XX  
OS Synthetic.  
XX  
XX WO9963077-A2.  
PN  
XX 09-DEC-1999.  
PD  
XX 04-JUN-1999; 99WO-US012516.  
PF  
XX 04-JUN-1998; 98US-0087905P.  
PR 03-JUN-1999; 99US-00324672.  
PR  
XX (TMTE-) TM TECHNOLOGIES INC.  
PA  
XX Lane MJ, Benight AS, Faldasz BD;  
XX WPI; 2000-116369/10.  
DR  
XX Modulating polynucleotide ligand binding site affinity using  
PT determination of the flanking duplex sequences.  
PT  
XX Example 1; Page 40; 62pp; English.

CC The invention provides a method for determining the sequence of  
CC polynucleotide flanking regions that modulate ligand binding  
CC characteristics of an adjacent binding site. The method comprises: (i)  
CC providing a number of different duplex polynucleotides, each having the  
CC same polynucleotide ligand binding site and a randomly synthesised  
CC sequence flanking the binding site; (ii) exposing the duplex to a ligand  
CC selective for the binding site; (iii) isolating duplexes which bind or do  
CC not bind the ligand, and (iv) determining the nucleotide composition of  
CC the flanking duplex sequence by sequencing the duplex sequence adjacent  
CC to the binding site. The invention is used to modulate the ligand-binding  
CC characteristics of any nucleotide sequence. The invention is less costly  
CC and more efficient than prior art techniques that moderate ligand binding  
CC using small molecule pharmaceuticals. Sequences AAZ95962-296170 represent  
CC polynucleotide sequences including the binding site for the restriction  
CC enzyme BamHI and used in the course of the invention

XX  
XX Sequence 40 BP; 9 A; 9 C; 15 G; 7 T; 0 U; 0 Other;

Query Match 75.8%; Score 14.4; DB 3; Length 40;  
Best Local Similarity 93.8%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTGAGTTTCAGGGGGG 19  
||||| |||||||  
Db 9 GTGGGTTTCAGGGGGG 24

RESULT 14  
AAV27677  
ID AAV27677 standard; DNA; 20 BP.  
XX  
AC AAV27677;  
XX  
XX 01-OCT-1998 (first entry)  
DT  
XX Immunostimulatory oligodeoxyribonucleotide of the invention.  
DE  
XX Immunostimulatory; oligodeoxyribonucleotide; ODN;





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XX PD 28-DEC-1999.
XX PF 07-FEB-1995; 95US-00386063.
XX PR 15-JUL-1994; 94US-00276358.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI Krieg AM;
XX DR WPI; 2000-086224/07.
XX PT Immunostimulatory oligonucleotides which enhance B cell activation useful
XX PT for treating an immune system deficiency e.g. cancer.
XX PS Claim 10; Col 10; 19pp; English.
XX CC This sequence represents a B cell stimulatory oligonucleotide. The
XX CC invention relates to compositions comprising an oligonucleotide (I) with
XX CC unethylated guanine and cytosine nucleotides and an antigen in a
XX CC carrier. The oligonucleotides can be administered to a subject in a
XX CC composition with an antigen in a carrier to enhance an immune response by
XX CC enhancing B cell activation. The oligonucleotides are immunostimulatory
XX CC and can be used to treat, prevent or ameliorate an immune system
XX CC deficiency e.g. cancer or a viral, fungal, bacterial or parasitic
XX CC infection. They can also be administered as a vaccine adjuvant to
XX CC stimulate the response of a host to a vaccine. The compositions can be
XX CC used to treat humans or vertebrate animals including dogs, cats, sheep
XX CC pigs, cows, goats, chickens, mice and monkeys. Preceding chemotherapy
XX CC with the immunostimulatory oligonucleotides should be useful for
XX CC increasing the responsiveness of malignant cells to subsequent
XX CC chemotherapy. The 8-40 nucleotide size of the oligonucleotides
XX CC facilitates uptake into cells
XX SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 17
AAD02961
ID AAD02961 standard; DNA; 20 BP.
XX AC AAD02961;
XX DT 31-MAY-2001 (first entry)
XX DE Immunostimulatory oligodeoxyribonucleotide (ODN) 1585.
XX KW Oligodeoxyribonucleotide; ODN; cytosine-guanine dinucleotide; CpG;
XX KW immunostimulatory; therapy; immune system deficiency; tumour; cancer;
XX KW antibacterial; antiparasitic; fungicide; antiviral; cytostatic;
XX KW leukaemia; systemic lupus erythematosus; sepsis; autoimmune disease;
XX KW immunoinhibitory; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..2
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 16..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"

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XX PN US6194388-B1.
XX PD 27-FEB-2001.
XX PF 07-FEB-1995; 95US-00386063.
XX PR 15-JUL-1994; 94US-00276358.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI (COLE-) COLEY PHARM GROUP.
XX DR Krieg AM, Klinman D, Steinberg AD;
XX DR WPI; 2001-217934/22.
XX PT Immunostimulatory composition useful for stimulating immune response in a
XX PT subject, comprises antigen and immunostimulatory nucleic acid comprising
XX PT oligonucleotides having unethylated cytosine-guanine dinucleotides.
XX PS Claim 10; Col 10; 20pp; English.
XX CC The present invention relates to immunomodulatory
XX CC oligodeoxyribonucleotides (ODNs) containing methylated or unmethylated
XX CC cytosine-guanine (CpG) dinucleotides. Immunostimulatory ODN compositions
XX CC having unmethylated CpG dinucleotides are useful for activating
XX CC lymphocytes and for treating, preventing or ameliorating an immune system
XX CC deficiency e.g. tumour or cancer or viral, fungal, bacterial or parasitic
XX CC infection and leukaemia. Neural ODN that contains a methylated CpG
XX CC dinucleotide are useful for treating diseases such as systemic lupus
XX CC erythematosus, sepsis and autoimmune diseases. Immunoinhibitory ODN
XX CC containing CpG dinucleotides that are not in the stimulatory motif and
XX CC GCG trinucleotide sequences at or near both termini have antiviral
XX CC activity. The present sequence is an immunostimulatory
XX CC oligodeoxyribonucleotide (ODN) 1585
XX SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 74.7%; Score 14.2; DB 4; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 18
AAF99097
ID AAF99097 standard; DNA; 20 BP.
XX AC AAF99097;
XX DT 12-JUN-2001 (first entry)
XX DE Immunostimulatory nucleic acid #213.
XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX KW immunostimulatory; tumour; viral infection; bacterial infection;
XX KW fungal infection; parasitic infection; cancer; asthma;
XX KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX OS Synthetic.
XX PN WO200122972-A2.
XX PD 05-APR-2001.
XX PF 25-SEP-2000; 2000WO-US026383.
XX PR 25-SEP-1999; 99US-0156113P.
XX PR 27-SEP-1999; 99US-0156135P.
XX PR 23-AUG-2000; 2000US-0227436P.

```



CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
 CC present sequence is an immunostimulatory oligonucleotide described in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;  
 Query Match 74.7%; Score 14.2; DB 6; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGGG 19  
 Db ||| ||||| ||||| |||||  
 2 GGGTTCACGTTTGGGGG 20  
 RESULT 21  
 ACD91359  
 ID ACD91359 standard; DNA; 20 BP.  
 XX  
 AC ACD91359;  
 XX  
 DT 22-SEP-2003 (first entry)  
 XX  
 DE B-cell stimulatory, CpG containing oligonucleotide #1.  
 XX  
 KW CpG island; ss; HIV infection; gene therapy; vaccine; B-cell;  
 KW immunostimulatory; adjuvant.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003050263-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 16-AUG-2001; 2001US-00931583.  
 XX  
 PR 15-JUL-1994; 94US-00276358.  
 PR 07-FEB-1995; 95US-00386063.  
 PR 08-OCT-1999; 99US-00415142.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 PI Krieg AM, Klinman D, Steinberg AD;  
 XX  
 DR WPI; 2003-512356/48.  
 XX  
 PT Treating a subject infected with HIV by administering a CpG nucleic acid.  
 XX  
 PS Disclosure; Page 10; 22pp; English.  
 XX  
 CC The invention relates to treating a subject infected with HIV comprising  
 CC administering a CpG nucleic acid (e.g. an adjuvant type CpG  
 CC oligonucleotide, an immunostimulatory CpG oligonucleotide or a B cell  
 CC stimulatory CpG oligonucleotide). The CpG are used as gene therapy  
 CC vaccines to treat a subject infected with HIV. The present sequence is a  
 CC B-cell stimulatory CpG oligonucleotide  
 XX  
 SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
 Query Match 74.7%; Score 14.2; DB 9; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGGG 19  
 Db ||| ||||| ||||| |||||  
 2 GGGTTCACGTTTCAGGGGG 20

RESULT 22  
 ACD99530  
 ID ACD99530 standard; DNA; 20 BP.  
 XX  
 AC ACD99530;  
 XX  
 DT 25-SEP-2003 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #216.  
 XX  
 KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003050268-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 29-MAR-2002; 2002US-00112653.  
 XX  
 PR 29-MAR-2001; 2001US-0279642P.  
 XX  
 PA (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX  
 PI Krieg AM, Berg DJ;  
 XX  
 DR WPI; 2003-521815/49.  
 XX  
 PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX  
 PS Disclosure; Page 14; 229pp; English.  
 XX  
 CC The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 XX  
 SQ Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;  
 Query Match 74.7%; Score 14.2; DB 9; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGGG 19  
 Db ||| ||||| ||||| |||||  
 2 GGGTTCACGTTTTCAGGGG 20  
 RESULT 23  
 ACA62324  
 ID ACA62324 standard; DNA; 20 BP.  
 XX  
 AC ACA62324;  
 XX  
 DT 13-AUG-2003 (first entry)  
 XX  
 DE Lymphocyte (B cell) activating oligonucleotide #1.  
 XX  
 KW Immunostimulatory oligonucleotide; unmethylated CpG dinucleotide;  
 KW immunoinhibitory oligonucleotide; cellular transcription factor;  
 KW viral activity; lymphocyte activation; B cell; natural killer cell; NK;  
 KW immune system deficiency; viral infection; immune disease; SLE;

KW systemic lupus erythematosus; sepsis; cancer; immunomodulatory;  
KW immunostimulant; dermatological; antiinflammatory; cytostatic;  
KW antibacterial; virucide; ss.

OS Synthetic.

XX US2003026782-A1.

XX 06-FEB-2003.

XX 08-OCT-1999; 99US-00415142.

XX 07-FEB-1995; 95US-00386063.

XX (KRIE/) KRIEG A M.

XX Krieg AM;

XX WPI; 2003-466135/44.

XX Novel immunostimulatory oligonucleotide comprising 2-100 nucleotides and  
PT containing at least one unmethylated CpG dinucleotide, useful for  
PT activating a subject's B cells or natural killer cells.

XX Disclosure; Page 13; 19pp; English.

XX The present invention relates to immunostimulatory oligonucleotides  
CC containing at least one unmethylated CpG dinucleotide, and  
CC immunoinhibitory oligonucleotides which are capable of interfering with  
CC the activity of viral or cellular transcription factors. The  
CC immunostimulatory oligonucleotides are useful for activating a subject's  
CC lymphocytes (B cells or natural killer (NK) cells). They are useful for  
CC treating, preventing or ameliorating an immune system deficiency. The  
CC immunoinhibitory oligonucleotides are useful for treating or preventing a  
CC viral infection in a subject. They are also useful for treating or  
CC preventing or ameliorating an immune system deficiency in a subject. The  
CC immunoinhibitory oligonucleotides can be used in a pharmaceutical  
CC composition which may be used for vaccinating a subject. The  
CC oligonucleotides may be used for treating an immune disease such as  
CC systemic lupus erythematosus (SLE), sepsis, or cancer. The  
CC oligonucleotides are safe to use since they do not initiate an immune  
CC reaction when administered to a subject in vivo. ACA62324-ACA62352  
CC represent the immunomodulatory oligonucleotides of the invention. Note:  
CC The present sequence given as SEQ ID No:1 in the Sequence listing differs  
CC from that given on page 6 (ACA62351) and page 17 (ACA62352) of the  
CC specification

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 74.7%; Score 14.2; DB 9; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTACGTTTCAGGGGGG 19  
||| |||||  
Db 2 GGGTCAACGTTTCAGGGGGG 20

RESULT 24

ADB36599

ID ADB36599 standard; DNA; 20 BP.

XX ADB36599;

XX 04-DEC-2003 (first entry)

XX Immunostimulatory nucleic acid #213.

XX de; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.

XX Synthetic.

XX

PN US2003087848-A1.

XX 08-MAY-2003.

XX 02-FEB-2001; 2001US-00776479.

XX 03-FEB-2000; 2000US-0179991P.

XX (BRAT/) BRATZLER R L.

XX (PETE/) PETERSEN D M.

XX (FOUR/) FOURON Y.

PI Bratzler RL, Petersen DM, Fouron Y;

XX WPI; 2003-657977/62.

XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.

XX Disclosure; Page 9; 221pp; English.

XX The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.

XX Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 74.7%; Score 14.2; DB 9; Length 20;

Best Local Similarity 84.2%; Pred. No. 3.7e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTACGTTTCAGGGGGG 19

Db 2 GGGTTCACGTTTCAGGGGGG 20

RESULT 25

ADO58881

ID ADO58881 standard; DNA; 20 BP.

XX ADO58881;

XX 29-JUL-2004 (first entry)

XX Mitogenic oligonucleotide ODN1595 used in B-cell stimulation.

XX Lymphocyte; B cell; natural killer cell; immune response;  
KW systemic lupus erythematosus; sepsis; viral infection; immunosuppressive;  
KW immunostimulating; immunomodulating; antibacterial; antiinflammatory;  
KW dermatological; virucide; phosphorothioate backbone; ss.

XX Unidentified.

XX Key Location/Qualifiers

FT modified\_base 1..2

FT /tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified\_base 16..20

FT /tag= b

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX US2004087534-A1.

XX 06-MAY-2004.

XX 30-JUL-2003; 2003US-00631676.

XX 15-JUL-1994; 94US-00276358.

```

PR 07-FEB-1995; 95US-00386063.
PR 08-OCT-1999; 99US-00415142.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (COLE-) COLEY PHARM GROUP INC.
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
XX
XX KRIEG AM, Klinman D, Steinberg AD;
PI
XX
XX WPI; 2004-356245/33.
DR
XX
XX New immunomodulatory oligonucleotides containing at least one
PT unmethylated CpG dinucleotide, useful for treating diseases including
PT systemic lupus erythematosus and sepsis.
XX
XX Claim 5; SEQ ID NO 1; 19pp; English.
XX
XX The present invention provides oligonucleotides comprising unmethylated
CC CpG dinucleotides. The invention is useful to activate lymphocytes
CC specifically to activate B cells and natural killer cells, for treating
CC diseases associated with an immune system activation such as systemic
CC lupus erythematosus, sepsis and viral infections. The invention is useful
CC as an immunosuppressive, immunostimulating, immunomodulating,
CC antibacterial, antiinflammatory, dermatological and virucidal agent. The
CC present sequence is a mitogenic oligonucleotide used in the stimulation
CC of B-cells. This sequence is used in the invention.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
SQ
Query Match 74.7%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20
RESULT 26
ADQ36558
ID ADQ36558 standard; DNA; 20 BP.
XX
AC ADQ36558;
XX
XX 07-OCT-2004 (first entry)
XX
XX B-cell stimulatory CpG oligonucleotide ODN1585.
XX
XX B-cell stimulation; CpG island; ss; viral transcription factor;
KW cellular transcription factor; immunoinhibitor; immune system deficiency;
KW systemic lupus erythematosus; sepsis; tumour; cancer; viral infection;
KW fungal infection; bacterial infection; parasitic infection; vaccine;
KW antisense gene therapy.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..2
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkage"
FT misc_feature 9..10
FT /*tag= b
FT /note= "CpG island"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkage"
XX
XX US2004143112-A1.
XX
XX 22-JUL-2004.
XX
XX 21-OCT-2003; 2003US-00690495.
XX
XX 15-JUL-1994; 94US-00276358.
PR 07-FEB-1995; 95US-00386063.
PR 08-OCT-1999; 99US-00415142.
XX
XX (KRIE/) KRIEG A M.
PA (KLIN/) KLINMAN D.
PA (STEI/) STEINBERG A D.
XX
XX Krieg AM, Klinman D, Steinberg AD;
PI
XX
XX WPI; 2004-552597/53.
DR
XX
XX New oligonucleotides containing unmethylated CpG dinucleotide, useful for
PT treating, preventing or ameliorating an immune system deficiency, e.g.
PT tumor, cancer, or viral, fungal, bacterial or parasitic infection.
XX
XX Claim 5; SEQ ID NO 1; 14pp; English.
XX
XX The invention relates to a new oligonucleotide which: (a) comprises about
XX 2-100 nucleotides and containing at least one unmethylated CpG
CC dinucleotide; or (b) is capable of interfering with the activity of viral
CC or cellular transcription factors and containing a consensus
CC immunoinhibitor CpG motif represented by the formula (I): 5'GCGXnGCG3'
CC where X a nucleotide and n 0-50. Also included are an oligonucleotide
CC delivery complex (comprising the oligonucleotide, and a targeting means),
CC a pharmaceutical composition comprising the oligonucleotide and a
CC pharmaceutical carrier, activating a subject's B cells or natural killer
CC cells (by contacting the cells with the oligonucleotide) treating,
CC (preventing or ameliorating) an immune system deficiency in a subject,
CC vaccinating a subject by administering the composition in conjunction
CC with a vaccine, treating a disease associated with an immune system
CC activation in a subject (by administering a neutral oligonucleotide alone
CC or in conjunction with a pharmaceutical carrier), an improved method for
CC performing antisense therapy (comprising methylating CpG containing
CC oligonucleotides prior to administration to a subject), an improved
CC method for in vivo diagnoses using oligonucleotide probes comprising
CC methylating CpG containing oligonucleotides prior to administration to a
CC subject and treating or preventing a viral infection in a subject by
CC administering the immunoinhibitory oligonucleotide defined above. The
CC oligonucleotide is useful for treating, preventing or ameliorating an
CC immune system deficiency, such as systemic lupus erythematosus, sepsis,
CC tumour, cancer, or viral, fungal, bacterial or parasitic infection.
CC Compositions comprising the oligonucleotide are useful for activating a
CC subject's B cells or natural killer cells, for treating, preventing or
CC ameliorating an immune system deficiency or for vaccinating a subject.
CC The immunoinhibitory oligonucleotide is useful for treating or preventing
CC a viral infection in a subject. The oligonucleotides may also be used in
CC conjunction with a vaccine to boost a subject's immune system to effect a
CC better response from the vaccine, or for increasing the responsiveness of
CC the malignant cells to subsequent chemotherapy. The present sequence is a
CC B-cell stimulatory CpG oligonucleotide of the invention.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Query Match 74.7%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20
RESULT 27
ADQ36584
ID ADQ36584 standard; DNA; 20 BP.
XX
XX ADQ36584;
XX
XX 07-OCT-2004 (first entry)
XX

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CC dermatological, immunosuppressive and virucide activity. ADR20014-
CC ADR20040 represent the oligonucleotides describes in the disclosure of
CC the invention.
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Query Match 74.7%; Score 14.2; DB 13; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGG 20
RESULT 29
ADR28877
ID ADR28877 standard; DNA; 20 BP.
XX
AC ADR28877;
XX
DT 21-OCT-2004 (first entry)
DE CpG-containing immunostimulatory oligonucleotide ODN 1585.
XX
KW ss; immunostimulatory oligonucleotide; CpG dinucleotide;
KW transcription factor; immunoinhibitory CpG motif; B cell;
KW natural killer cell; immune system deficiency; antisense therapy;
KW viral infection; immune response; systemic lupus erythematosus; sepsis;
KW vaccine.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..3
FT /*tag= a
FT /mod_base= OTHER
FT /*note= "Phosphorothioate linkage"
FT misc_feature 9..10
FT /*tag= b
FT /*note= "CpG dinucleotide"
FT modified_base 16..20
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "Phosphorothioate linkage"
XX
PN US2004152657-A1.
XX
XX 05-AUG-2004.
XX
XX 26-FEB-2004; 2004US-00789536.
XX
XX 15-JUL-1994; 94US-00276358.
XX 07-FEB-1995; 95US-00386063.
XX 08-OCT-1999; 99US-00415142.
XX 21-OCT-2003; 2003US-00690495.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX (COLE-) COLEY PHARM GROUP INC.
XX (USSH ) US SEC HEALTH AND HUMAN SERVICES.
XX
XX Krieg AM, Klinman D, Steinberg AD;
XX WPI; 2004-624264/60.
XX
XX New oligonucleotide comprises at least one unmodified CpG dinucleotide,
XX useful for stimulating an immune response or for treating diseases
XX associated with immune system activation, e.g. systemic lupus
XX erythematosus or sepsis.
XX
XX Claim 5; SEQ ID NO 1; 19pp; English.
XX
XX The invention relates to an oligonucleotide comprising 2-100 nucleotides
CC
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CC and containing at least one unmodified CpG dinucleotide. The
CC oligonucleotide is capable of interfering with the activity of viral or
CC cellular transcription factors and containing a consensus
CC immunoinhibitory CpG motif having the formula: 5'GGXnGGG3', where X is a
CC nucleotide and n is 0-50. Also included are an oligonucleotide delivery
CC complex (comprising the oligonucleotide above and a targeting means), a
CC pharmaceutical composition (comprising the oligonucleotide above and a
CC pharmaceutical carrier), activating a subject's B cells, activating a
CC subject's natural killer cells, treating (preventing or ameliorating) an
CC immune system deficiency in a subject, vaccinating a subject, treating a
CC disease associated with an immune system activation in a subject,
CC performing antisense therapy (comprising methylating CpG containing
CC oligonucleotides prior to administration to a subject), in vivo diagnoses
CC using oligonucleotide probes comprising methylating CpG containing
CC oligonucleotides prior to administration to a subject and treating or
CC preventing a viral infection in a subject. The oligonucleotide is useful
CC for stimulating an immune response in a subject. They are also useful for
CC treating diseases associated with immune system activation including
CC systemic lupus erythematosus or sepsis, or for treating, preventing, or
CC ameliorating an immune system deficiency in a subject. The
CC oligonucleotide is also useful for treating or preventing viral
CC infection. It is also useful as a vaccine. The present sequence is an
CC immunostimulatory oligonucleotide of the invention.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Query Match 74.7%; Score 14.2; DB 13; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGG 20
RESULT 30
ADR44692
ID ADR44692 standard; DNA; 20 BP.
XX
AC ADR44692;
XX
DT 04-NOV-2004 (first entry)
DE Mitogenic CpG oligonucleotide ODN1585 used in B-cell activation.
XX
KW Immunomodulatory; CpG dinucleotide; immune system deficiency;
KW systemic lupus erythematosus; sepsis; tumour; cancer; viral infection;
KW bacterial infection; fungal infection; cytostatic; virucidal;
KW antibacterial; fungicidal; antiinflammatory; dermatological;
KW immunosuppressive; vaccine; gene therapy; phosphorothioate backbone; ss.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1..2
XX /*tag= a
XX /mod_base= OTHER
XX /*note= "Phosphorothioate backbone"
XX modified_base 16..20
XX /*tag= b
XX /mod_base= OTHER
XX /*note= "Phosphorothioate backbone"
XX
XX US2004162258-A1.
XX
XX 19-AUG-2004.
XX
XX 30-JAN-2004; 2004US-00769626.
XX
XX 15-JUL-1994; 94US-00276358.
XX 07-FEB-1995; 95US-00386063.
XX 08-OCT-1999; 99US-00415142.
XX 21-OCT-2003; 2003US-00690495.
```



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XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Krieg AM, Klinman D, Steinberg AD;
XX DR WPI; 2004-603582/58.
XX
XX PT New oligonucleotide comprises at least one unmethylated CpG dinucleotide,
XX PT useful for treating, preventing, or ameliorating an immune system
XX PT deficiency or a tumor, cancer, viral, bacterial, or fungal infection.
XX PS Disclosure; SEQ ID NO 1; 20pp; English.
XX
XX CC The present invention provides oligonucleotides comprising
XX CC immunomodulatory unmethylated CpG dinucleotide. The invention is useful
XX CC for treating, preventing and ameliorating immune system deficiencies such
XX CC as systemic lupus erythematosus and sepsis, tumour, cancer, viral,
XX CC bacterial and fungal infections. The invention acts as an cytostatic,
XX CC virucidal, antibacterial, fungicidal, antiinflammatory, dermatological
XX CC and immunosuppressive agent. The invention is also useful in the
XX CC production of vaccines and in gene therapy. The present sequence is a
XX CC mitogenic CpG oligonucleotide used in B-cell activation. Note: This
XX CC sequence is stated to be SEQ ID NO: 1 in the sequence listing. However,
XX CC this sequence differs from the sequence designated as SEQ ID NO: 1 in the
XX CC claims.
XX SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 74.7%; Score 14.2; DB 13; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db ||| ||||| ||||| |||||
2 GGGTCAACGTTTCAGGGGG 20

RESULT 31
ADR45002
ID ADR45002 standard; DNA; 20 BP.
XX AC ADR45002;
XX DT 04-NOV-2004 (first entry)
XX DE CpG oligonucleotide ODN 1585 used to stimulate B-cells.
XX KW Immune response; immune system deficiency; tumour; cancer;
XX KW viral infection; systemic lupus erythematosus; sepsis; vaccine;
XX KW gene therapy; bacterial infection; fungal infection; phosphorothioate;
XX KW ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT modified_base 1..2
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate nucleotides"
XX FT modified_base 16..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate nucleotides"
XX PN US2004162262-A1.
XX
XX PD 19-AUG-2004.
XX
XX PF 26-FEB-2004; 2004US-00789353.
XX
XX PR 15-JUL-1994; 94US-00276358.

PR 07-FEB-1995; 95US-00386063.
PR 08-OCT-1999; 99US-00415142.
PR 21-OCT-2003; 2003US-00690495.
XX
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Krieg AM, Klinman D, Steinberg AD;
XX DR WPI; 2004-603584/58.
XX
XX PT New oligonucleotide comprises at least one unmethylated CpG dinucleotide,
XX PT useful for treating, preventing, or ameliorating an immune system
XX PT deficiency or a tumor, cancer, viral, bacterial, or fungal infection.
XX PS Claim 5; SEQ ID NO 1; 19pp; English.
XX
XX CC The invention provides novel oligonucleotides containing unmethylated CpG
XX CC dinucleotides and therapeutic utilities based on their ability to
XX CC stimulate an immune response in a subject. Oligonucleotides of the
XX CC invention are useful for treating, preventing or ameliorating an immune
XX CC system deficiency or a tumour, cancer, viral, bacterial or fungal
XX CC infection. They are useful for treating diseases associated with immune
XX CC system activation including systemic lupus erythematosus or sepsis. They
XX CC are also useful as vaccines to boost subject's immune system. The
XX CC invention is also useful in gene therapy. The present sequence is a CpG
XX CC oligonucleotide used to stimulate B-cells. Note: This sequence is stated
XX CC to be the same as that shown as SEQ ID NO: 1 in page 18 of the
XX CC specification. However these sequences differ.
XX SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 74.7%; Score 14.2; DB 13; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db ||| ||||| ||||| |||||
2 GGGTCAACGTTTCAGGGGG 20

RESULT 32
ADR88228
ID ADR88228 standard; DNA; 20 BP.
XX AC ADR88228;
XX DT 18-NOV-2004 (first entry)
XX DE CpG immunomodulatory oligo, ODN 1585 used in B cell stimulation.
XX DE
XX KW CpG dinucleotide; gene therapy a; vaccine; cancer; viral infection;
XX KW fungal infection; bacterial infection; parasitic infection;
XX KW systemic lupus erythematosus; sepsis; ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT modified_base 1..3
XX FT /*tag= a
XX FT /mod_base= Phosphorothioate backbone
XX FT modified_base 15..20
XX FT /*tag= b
XX FT /mod_base= Phosphorothioate backbone
XX PN US2004171150-A1.
XX
XX PD 02-SEP-2004.
XX
XX PF 26-FEB-2004; 2004US-00787737.
XX
XX PR 15-JUL-1994; 94US-00276358.

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PR 07-FEB-1995; 95US-00386063.  
PR 09-OCT-1999; 99US-00415142.  
PR 21-OCT-2003; 2003US-00690495.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GROUP INC.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Krieg AM, Klinman D, Steinberg AD;  
PI WPI; 2004-634548/61.  
XX  
DR WPI; 2004-634548/61.  
XX  
XX New immunomodulatory oligonucleotides for preventing, treating or  
PT ameliorating diseases associated with immune system deficiency or  
PT activation, e.g. cancer, viral infection, systemic lupus erythematosus or  
PT sepsis.  
XX  
XX Claim 5; SEQ ID NO 1; 19pp; English.  
XX  
XX The present invention relates to an oligonucleotide containing at least  
CC one unmethylated CpG dinucleotide. The invention is useful in gene therapy  
CC and for preparing vaccine. The invention is also useful for preventing,  
CC treating or ameliorating diseases associated with immune system  
CC deficiency or activation such as cancer, viral, fungal, bacterial or  
CC parasitic infection, systemic lupus erythematosus or sepsis. The present  
CC sequence is a CpG immunomodulatory oligonucleotide used in B cell  
CC stimulation.  
XX  
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
Query Match 74.7%; Score 14.2; DB 13; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20  
RESULT 33  
ADS17223  
ID ADS17223 standard; DNA; 20 BP.  
XX  
XX ADS17223;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
DE ODN1, oligonucleotide used to stimulate B cells.  
XX  
XX Immunomodulator; immune system; systemic lupus erythematosus; sepsis;  
KW viral infection; vaccine; B cell; virucide; phosphorothioate backbone;  
KW ss.  
XX  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
FT modified\_base 1..3  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
FT modified\_base 15..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
XX  
XX US2004181045-A1.  
XX  
XX 16-SEP-2004.  
XX  
XX 26-FEB-2004; 2004US-00788199.  
XX  
XX 15-JUL-1994; 94US-00276358.  
PR 07-FEB-1995; 95US-00386063.

PR 08-OCT-1999; 99US-00415142.  
PR 21-OCT-2003; 2003US-00690495.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GROUP INC.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Krieg AM, Klinman D, Steinberg AD;  
PI WPI; 2004-667684/65.  
XX  
XX New oligonucleotide comprising 2-100 nucleotides and containing an  
PT unmethylated CpG dinucleotide, useful in preparing a composition for  
PT treating a disease, e.g., systemic lupus erythematosus, sepsis or viral  
PT infection.  
XX  
XX Claim 5; SEQ ID NO 1; 19pp; English.  
XX  
XX The invention relates to immunomodulatory oligonucleotides containing an  
CC unmethylated CpG dinucleotide. The oligonucleotide of the invention is  
CC useful in preparing a composition for treating a disease associated with  
CC an immune system activation, e.g. systemic lupus erythematosus, sepsis or  
CC viral infection. It is also useful to prepare vaccine. The present  
CC sequence is an immunomodulatory oligonucleotide used to stimulate B  
CC cells.  
XX  
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
Query Match 74.7%; Score 14.2; DB 13; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20  
RESULT 34  
ADU89540  
ID ADU89540 standard; DNA; 20 BP.  
XX  
XX ADU89540;  
XX  
XX 10-FEB-2005 (first entry)  
XX  
DE Allergic response suppressor oligonucleotide #224.  
XX  
XX ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;  
KW antibacterial; virucide; immunoglobulin E antagonist; allergy;  
KW immunostimulator; asthma; rhinitis; urticaria; dermatitis;  
KW bacterial infection; viral infection.  
XX  
XX Synthetic.  
XX  
XX US2004235774-A1.  
XX  
XX 25-NOV-2004.  
XX  
XX 23-APR-2004; 2004US-00831778.  
XX  
XX 03-FEB-2000; 2000US-0179991P.  
PR 02-FEB-2001; 2001US-00776479.  
XX  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
PI WPI; 2004-833006/82.  
XX  
XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
PT dermatitis, in a subject, comprises administering a first and second dose

PT of an immunostimulatory nucleic acid.  
PS Disclosure; SEQ ID NO 224; 235pp; English.  
XX  
XX The invention relates to a method of suppressing a symptom of an allergic  
CC response in a subject by administering a first and second dose of an  
CC immunostimulatory nucleic acid that comprises a nucleotide sequence  
CC comprising 5'-cg-3', and where the second dose is administered from 1 day  
CC to 8 weeks after the first dose. The methods and compositions of the  
CC present invention are useful for the treatment or prevention of asthma  
CC and allergy, including rhinitis, urticaria and atopic dermatitis, using  
CC an immunostimulatory nucleic acid alone or in combination with other  
CC medications. They can also be used in preventing bacterial and viral  
CC infections. This sequence represents an oligonucleotide used in the  
CC method of the invention.  
XX  
SQ Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;  
  
Query Match 74.7%; Score 14.2; DB 13; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTTCAGTTTGGGGG 20  
  
RESULT 35  
ADW28066  
ID ADW28066 standard; DNA; 20 BP.  
AC ADW28066;  
XX  
XX 24-MAR-2005 (first entry)  
DE Mitogenic CpG oligonucleotide ODN1585 used in B-cell stimulation.  
XX  
XX Immune modulation; immunity; immunogenicity; immune disorder; tumor;  
KW cancer; cytostatic; neoplasm; systemic lupus erythematosus; SLE;  
KW antiinflammatory; dermatological; immunosuppressive; sepsis; infection;  
KW viral infection; viricide; fungal infection; fungicide;  
KW bacterial infection; antibacterial; parasitic infection; antiparasitic;  
KW autoimmune disease; rheumatoid arthritis; antiarthritic; antirheumatic;  
KW multiple sclerosis; neuroprotective; antisense therapy; hybridization;  
KW antiviral vaccine; phosphorothioate; ss.  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..2  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
FT modified\_base 16..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
XX  
XX US2005004062-A1.  
XX  
XX 06-JAN-2005.  
XX  
XX 17-MAY-2004; 2004US-00847650.  
XX  
XX 15-JUL-1994; 94US-00276358.  
PR 07-FEB-1995; 95US-00386063.  
PR 09-OCT-1999; 99US-00415142.  
PR 21-OCT-2003; 2003US-00690495.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GROUP INC.  
PA (USDC ) US DEPT COMMERCE & NAT INST STANDARDS.  
XX  
XX

PI Krieg AM, Klinman D, Steinberg AD;  
XX WPI; 2005-065257/07.  
XX  
XX Use of an immunostimulatory oligonucleotide for boosting an immune  
PT response of a subject, or for stimulating an immune response in a  
PT subject, where increases in IFN-gamma and IL-12 expression are indicators  
PT of the immune response.  
XX  
XX Disclosure; SEQ ID NO 1; 19pp; English.  
XX  
XX The present invention relates to immunomodulatory oligonucleotides  
CC containing unmethylated CpG dinucleotides and therapeutic utilities based  
CC on their ability to stimulate an immune response in a subject. The  
CC invention is useful for treating, preventing or ameliorating immune  
CC system deficiencies such as tumor, cancer, systemic lupus erythematosus  
CC and sepsis, infections such as viral (e.g. HIV, herpes), fungal (e.g.  
CC Candida sp.) and bacterial or parasitic (e.g. Leishmania, Toxoplasma) and  
CC autoimmune diseases such as rheumatoid arthritis and multiple sclerosis.  
CC The invention is also useful in antisense therapy, as in vivo  
CC hybridization probes and as antiviral therapeutics. The present sequence  
CC is a mitogenic CpG oligonucleotide used in B-cell stimulation.  
XX  
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
  
Query Match 74.7%; Score 14.2; DB 14; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20  
  
RESULT 36  
ADV97282  
ID ADV97282 standard; DNA; 20 BP.  
AC ADV97282;  
XX  
XX 07-APR-2005 (first entry)  
DE Immunostimulatory oligonucleotide ODN 1585 SEQ ID NO:1.  
XX  
XX ss; immune modulation; pharmaceutical; immunomodulator; cytostatic;  
KW viricide; fungicide; antibacterial; antiparasitic; antiinflammatory;  
KW dermatological; immunosuppressive; antiarthritic; antirheumatic;  
KW neuroprotective; immunostimulant; immune disorder.  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..3  
FT /\*tag= a  
FT /mod\_base= phosphorothioate backbone  
FT misc\_feature 9..10  
FT /\*tag= b  
FT /note= "unmethylated CpG dinucleotide"  
FT modified\_base 15..20  
FT /\*tag= c  
FT /mod\_base= phosphorothioate backbone  
XX  
XX US2005009774-A1.  
XX  
XX 13-JAN-2005.  
XX  
XX 09-JUL-2004; 2004US-00888885.  
XX  
XX 15-JUL-1994; 94US-00276358.  
PR 07-FEB-1995; 95US-00386063.  
PR 09-OCT-1999; 99US-00415142.  
PR 21-OCT-2003; 2003US-00690495.  
XX  
XX

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PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GROUP INC.
PA (USSA ) US SEC OF ARMY.
XX
XX Krieg AM, Klinman D, Steinberg AD;
XX WPI; 2005-080553/09.
XX
XX Oral composition, useful e.g. to treat/prevent/ameliorate an immune
XX system deficiency or diseases associated with immune system activation,
XX PT comprises an immunostimulatory nucleic acid in a pharmaceutically
XX PT acceptable carrier.
XX
XX Disclosure; SEQ ID NO 1; 18pp; English.
XX
XX The invention relates to a novel pharmaceutical composition (A) for oral
XX administration comprising an immunostimulatory nucleic acid (1) (8-100
XX nucleotides in length) in a pharmaceutically acceptable carrier. The
XX immunostimulatory nucleic acid is of the formula 5'X 1 X 2 CGX 3 X 4 3'
XX (where C and G are unmethylated). The carrier comprises an emulsion. A
XX composition of the invention has immunomodulator, cytostatic, virucide,
XX fungicide, antibacterial, antiparasitic, antitumorous, antineoplastic,
XX dermatological, immunosuppressive, antiarthritic, antirheumatic,
XX neuroprotective, and immunostimulant activity. A nucleic acid of the
XX invention is useful to treat/prevent/ameliorate an immune system
XX deficiency (e.g. tumors, cancers or viral, fungal, bacterial or parasitic
XX infections) or a disease (e.g. systemic lupus erythematosus, sepsis,
XX rheumatoid arthritis and multiple sclerosis) associated with immune
XX system activation. The nucleic acids are useful as vaccine adjuvants to
XX stimulate a subject's response to a vaccine, and for antisense therapies
XX or as in vivo hybridization probes. The present sequence represents an
XX immunostimulatory oligonucleotide of the invention, ODN 1585.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 74.7%; Score 14.2; DB 14; Length 20;
XX Best Local Similarity 84.2%; Pred. No. 3.7e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 GGGGTGACGTTTCAGGGGGG 19
XX ||| |||||||||
XX Db 2 GGGTCAACGTTTCAGGGGGG 20
XX
XX RESULT 37
XX ADX87198
XX ID ADX87198 standard; DNA; 20 BP.
XX AC ADX87198;
XX
XX DT 05-MAY-2005 (first entry)
XX
XX DE B cell-stimulating oligonucleotide - SEQ ID 1.
XX
XX KW HIV infection; anti-HIV; B-lymphocyte; ss.
XX
XX OS Unidentified.
XX
XX PN US2005037985-A1.
XX
XX PD 17-FEB-2005.
XX
XX PF 25-AUG-2003; 2003US-00649584.
XX
XX PR 15-JUL-1994; 94US-00276358.
XX
XX PR 07-FEB-1995; 95US-00386063.
XX
XX PR 09-OCT-1999; 99US-00415142.
XX
XX PR 16-AUG-2001; 2001US-00931583.
XX
XX (KRIE/) KRIEG A M.
XX (KLIN/) KLINMAN D.
XX (STEL/) STEINBERG A D.
XX
PI Krieg AM, Klinman D, Steinberg AD;
XX WPI; 2005-172294/18.
XX
XX Treating a subject infected with HIV comprises administering a CpG
XX nucleic acid and an anti-HIV therapy to the subject.
XX
XX Disclosure; SEQ ID NO 1; 37pp; English.
XX
XX The invention comprises a method of treating HIV by administering a CpG
XX nucleic acid (e.g. an adjuvant-type nucleic acid or an IFN-alpha-inducing
XX CpG nucleic acid) and an anti-HIV therapy (e.g. an inhibitor of HIV
XX replication). The method of the invention is useful for the treatment and
XX prevention of HIV. The present DNA sequence represents an oligonucleotide
XX that was used to stimulate B cells.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 74.7%; Score 14.2; DB 14; Length 20;
XX Best Local Similarity 84.2%; Pred. No. 3.7e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 GGGGTGACGTTTCAGGGGGG 19
XX ||| |||||||||
XX Db 2 GGGTCAACGTTTCAGGGGGG 20
XX
XX RESULT 38
XX ADX84981
XX ID ADX84981 standard; DNA; 20 BP.
XX AC ADX84981;
XX
XX DT 05-MAY-2005 (first entry)
XX
XX DE CpG oligonucleotide ODN 1585 used to stimulate B cells.
XX
XX KW Immune modulation; immunotherapy; antisense therapy; hybridization;
XX interferon-gamma; cytokine; immune deficiency; immunostimulant;
XX immune disorder; tumor; cancer; cytostatic; neoplasm; viral infection;
XX virucide; infection; fungal infection; fungicide; bacterial infection;
XX antibacterial; parasitic infection; antiparasitic; nucleic acid vaccine;
XX leukemia; systemic lupus erythematosus; antineoplastic; dermatological;
XX immunosuppressive; sepsis; autoimmune disease; ss.
XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..2
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX
XX modified_base 16..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX
XX PN US2005037403-A1.
XX
XX PD 17-FEB-2005.
XX
XX PF 09-JUL-2004; 2004US-00888089.
XX
XX PR 15-JUL-1994; 94US-00276358.
XX
XX PR 07-FEB-1995; 95US-00386063.
XX
XX PR 09-OCT-1999; 99US-00415142.
XX
XX PR 21-OCT-2003; 2003US-00690495.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX (COLE-) COLEY PHARM GROUP INC.
XX (USDC ) US DEPT COMMERCE & NAT INST STANDARDS.
XX
XX Krieg AM, Klinman D, Steinberg AD;

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XX WPI; 2005-172254/18.  
DR Use of immunostimulatory oligonucleotide delivery complex comprising  
PT oligonucleotide linked to biodegradable delivery complex for increasing  
PT interferon-gamma levels and treating diseases associated with immune  
PT system deficiency e.g. cancer.  
XX  
PS Disclosure; SEQ ID NO 1; 19pp; English.  
XX  
PS The invention relates to a method for increasing interferon (IFN)-gamma  
CC in a subject. The method involves administering an immunostimulatory  
CC oligonucleotide/delivery complex to modulate immune response of the  
CC subject. The invention is useful for treating diseases associated with  
CC immune system deficiency e.g. tumor or cancer or viral, fungal, bacterial  
CC or parasitic infections; as vaccine; for treating leukemia, systemic  
CC lupus erythematosus, sepsis and autoimmune diseases. The present sequence  
CC is the CpG oligonucleotide used to stimulate B cells.  
XX  
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
Query Match 74.7%; Score 14.2; DB 14; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20  
RESULT 39  
ADC24305/c  
ID ADC24305 standard; DNA; 39 BP.  
XX  
AC ADC24305;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Primer, D75N, used to mutate the RTA (x)Asp(y) motif.  
XX  
KW Ricin; (x)Asp(y); primer; mutant; mutagenesis; ss;  
KW vascular leak syndrome; VLS; cancer; immunotoxin; IT; cytokine; RTA;  
KW aphasia; myalgia; fatigue; hypotension; rhabdomyolysis; MAB;  
KW ribosome inactivating protein; RIP; vaccine; graft vs. host disease;  
KW GVHD; non-Hodgkin's lymphoma; Hodgkin's lymphoma; cytostatic;  
KW immunosuppressive; myeloma; tumour; monoclonal antibody.  
XX  
OS Synthetic.  
OS Ricinus communis.  
XX  
PN US2003143193-A1.  
XX  
PD 31-JUL-2003.  
XX  
PF 29-OCT-2002; 2002US-00282935.  
XX  
PR 30-MAR-2000; 2000US-00538873.  
PR 22-SEP-2000; 2000US-00668419.  
XX  
PA (VITE/) VITETTA E S.  
PA (GHET/) GHETIE V F.  
PA (SMAL/) SMALLSHAW J E.  
PA (BALU/) BALUNA R G.  
XX  
PI Vitetta ES, Ghetie VF, Smallshaw JE, Baluna RG;  
XX WPI; 2003-744874/70.  
DR  
XX New modified proteinaceous composition, useful for treating e.g., tumors.  
PT  
PS Example 2; SEQ ID NO 18; 52pp; English.  
XX  
CC The invention discloses a new modified proteinaceous composition which

CC comprises a protein having a (x)Asp(y) sequence and at least one amino  
CC acid mutation that alters the ability of a (x)Asp(y) sequence to induce  
CC Vascular Leak Syndrome (VLS). The present invention relates to the field  
CC of physiology and cancer biology. The invention provides immunotoxins  
CC (ITs) and cytokines, methods for producing them, which have been mutated  
CC to lack amino acid sequences which induce VLS or other side effects. Also  
CC claimed is a ricin A chain toxin (RTA) with a reduced ability to promote  
CC toxicity in a patient, where at least one amino acid flanking the  
CC (x)Asp(y) sequence is altered. The toxicity in a patient is further  
CC defined as VLS, aphasia, myalgia, fatigue, hypotension or rhabdomyolysis.  
CC ITs are hybrid molecules consisting of monoclonal antibodies (MABs), or  
CC other cell binding ligands, which are biochemically or genetically linked  
CC to toxins, toxin subunits or ribosome inactivating proteins (RIPs) from  
CC plants, fungi or bacteria. The modified proteinaceous composition is  
CC useful for treating (e.g. vaccine) graft vs. host disease (GVHD), non-  
CC Hodgkin's and Hodgkin's lymphoma, myeloma and some solid tumours. The  
CC sequence presented is a primer which was used to mutate the RTA (x)Asp(y)  
CC motif.  
XX  
SQ Sequence 39 BP; 10 A; 10 C; 8 G; 11 T; 0 U; 0 Other;  
Query Match 73.7%; Score 14; DB 10; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GGTGACGTTTCAGGG 16  
Db 26 GGTGACGTTTCAGGG 13  
RESULT 40  
AAC89992  
ID AAC89992 standard; DNA; 30 BP.  
XX  
AC AAC89992;  
XX  
DT 08-MAR-2001 (first entry)  
XX  
DE Rabbit tissue factor PCR primer #4.  
XX  
KW PCR primer; DNA polymerase; reverse transcriptase; rabbit; tissue factor;  
KW ss.  
XX  
OS Oryctolagus cuniculus.  
XX  
PN WO200071739-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 19-MAY-2000; 2000WO-US013960.  
XX  
PR 22-MAY-1999; 99US-0135437P.  
XX  
PA (EPIC-) EPICENTRE TECHNOLOGIES CORP.  
XX  
PI Schanke JET;  
XX  
DR WPI; 2001-032045/04.  
XX  
PT Bacillus stearothermophilus template-dependent DNA polymerase for  
PT preparing cDNA molecule from RNA template comprises reverse transcriptase  
PT activity in the presence of magnesium ions and absence of manganese ions.  
XX  
PS Example 3; Page 22; 37pp; English.  
XX  
CC The present invention relates to a purified thermostable template-  
CC dependent DNA polymerase from Bacillus stearothermophilus comprising  
CC reverse transcriptase (RT) activity in the presence of magnesium ions at  
CC a concentration of 1 mM and in the substantial absence of manganese ions.  
CC The DNA polymerase is useful for preparing cDNA molecules from RNA  
CC templates and for amplifying a nucleic acid. The present sequence is a  
CC PCR primer for rabbit tissue factor (RTF). This sequence was used to  
CC demonstrate the activity of the DNA polymerase of the present invention

XX SQ Sequence 30 BP; 6 A; 5 C; 12 G; 7 T; 0 U; 0 Other;  
Query Match 72.6%; Score 13.8; DB 4; Length 30;  
Best Local Similarity 88.2%; Pred. No. 5.9e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GGTGACGTTTCAGGGGG 19  
DB 13 GCGCATGTTTCAGGGGG 29  
RESULT 41  
ABZ43529/c  
ID ABZ43529 standard; DNA; 41 BP.  
AC ABZ43529;  
XX 26-JUN-2003 (first entry)  
DT DT  
DE Human SULTX3 gene polymorphic site, #313.  
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FH variation replace(21,T)  
FT /tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX WO200252044-A2.  
PN 26-JUN-2003 (first entry)  
PD 04-JUL-2002.  
XX 27-DEC-2001; 2001WO-JP011592.  
XX 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX (RIKE ) RIKEN KK.  
XX Nakamura Y, Sekine A, Iida A, Saito S;  
PI WPI; 2002-583571/62.  
DR Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.  
XX Claim 23; Page 69; 2785pp; English.  
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations

CC such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. CC This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. CC Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, CC the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy  
XX SQ Sequence 41 BP; 5 A; 23 C; 2 G; 11 T; 0 U; 0 Other;  
Query Match 72.6%; Score 13.8; DB 6; Length 41;  
Best Local Similarity 88.2%; Pred. No. 6e+03; 2; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGG 17  
DB 26 GGGGTGGGGTTTCAGGGG 10  
RESULT 42  
ABZ49680/c  
ID ABZ49680 standard; DNA; 41 BP.  
XX ABZ49680;  
AC ABZ49680;  
XX 26-JUN-2003 (first entry)  
DT DT  
DE Human SULTX3 gene polymorphic site, #6462.  
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH variation replace(21,T)  
FT /tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX WO200252044-A2.  
PN 04-JUL-2002.  
XX 27-DEC-2001; 2001WO-JP011592.  
XX 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX (RIKE ) RIKEN KK.  
XX Nakamura Y, Sekine A, Iida A, Saito S;  
PI WPI; 2002-583571/62.  
DR Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.  
XX Claim 23; Page 195; 2785pp; English.

XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolising enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy  
 XX  
 SQ Sequence 41 BP; 5 A; 23 C; 2 G; 11 T; 0 U; 0 Other;  
 Query Match 72.6%; Score 13.8; DB 6; Length 41;  
 Best Local Similarity 88.2%; Pred. No. 6e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGG 17  
 ||||| |||||  
 Db 26 GGGGTGGGGTTCAGGGG 10  
 RESULT 43  
 AAD07150  
 ID AAD07150 standard; DNA; 22 BP.  
 XX  
 AC AAD07150;  
 XX  
 DT 06-AUG-2001 (first entry)  
 XX  
 DE PCR primer PR2-379 for improving priming site 19379 specificity.  
 XX  
 DE Priming site 19379; PCR; polymerase chain reaction; amplification;  
 KW branched modular primer; front module; FM; back module; BM; PCR primer;  
 KW proofreading; ss.  
 XX  
 XX Bacteriophage lambda.  
 XX  
 XX Key Location/Qualifiers  
 FH mutation 18  
 FT /\*tag= a  
 FT /mod\_base= i  
 FT mutation 19  
 FT /\*tag= b  
 FT /mod\_base= i  
 XX  
 XX US6235889-B1.  
 FN  
 XX 22-MAY-2001.  
 XX

XX 08-MAR-1999; 99US-00264466.  
 XX  
 PR 20-DEC-1991; 91US-00810898.  
 PR 06-FEB-1995; 95US-00384699.  
 PR 06-MAY-1997; 97US-00852001.  
 XX (UYCH-) UNIV CHICAGO.  
 XX  
 XX Ulanovsky L;  
 XX WPI; 2001-366426/38.  
 XX  
 XX New composition comprising front and back oligonucleotide modules, each  
 PT module has a stem and an arm segment with varying or constant sequences,  
 PT useful for amplifying nucleic acid segments such as in polymerase chain  
 PT reaction.  
 XX  
 XX Disclosure; Col 18; 32pp; English.  
 XX  
 XX The present invention relates to compositions for branched modular  
 CC primers used in methods for amplifying a nucleic acid segment. The  
 CC branched modular primer comprises of front and back oligonucleotide  
 CC modules. The front module (FM) and back module (BM) comprise of a stem  
 CC segment having a sequence that is the same from module to module and an  
 CC arm segment having a sequence that varies from module to module. The arm  
 CC of the back and front modules are annealed to a template which contains  
 CC the priming site. These modules are designed for priming sites in lambda  
 CC phage DNA. The composition is useful for amplifying a nucleic acid  
 CC segment, e.g. by polymerase chain reaction (PCR). The present sequence is  
 CC proofreading amplification primer PR2-379 used for improving  
 CC Bacteriophage lambda reverse priming site 19379 specificity  
 XX  
 SQ Sequence 22 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 2 Other;  
 Query Match 70.5%; Score 13.4; DB 4; Length 22;  
 Best Local Similarity 93.3%; Pred. No. 9.1e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 TGACGTTTCAGGGGG 19  
 ||||| |||||  
 Db 2 TGACGTTTCAGGGGTG 16  
 RESULT 44  
 AAF74944  
 ID AAF74944 standard; DNA; 22 BP.  
 XX  
 AC AAF74944;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE Bacteriophage lambda fragment PCR amplification primer SEQ ID NO:5.  
 XX  
 DE Bacteriophage lambda; PCR primer; amplification; genome mapping;  
 KW biomedical research; clinical diagnostic; ss.  
 XX  
 OS Bacteriophage lambda.  
 OS Synthetic.  
 XX  
 XX US6197556-B1.  
 FN  
 XX 06-MAR-2001.  
 XX  
 XX 06-MAY-1997; 97US-00852001.  
 XX  
 PR 20-DEC-1991; 91US-00810898.  
 PR 06-FEB-1995; 95US-00384699.  
 XX (UYCH-) UNIV CHICAGO.  
 XX  
 XX Ulanovsky L, Raja MC;  
 PI  
 XX

DR WPI; 2001-256370/26.

XX Amplifying a template nucleic acid segment, involves annealing a

PT combination of several branched and/or covered oligonucleotide modules

PT selected from a pre-synthesized library, to the template DNA.

XX

PS Disclosure; Col 18; 33pp; English.

XX

CC The present invention describes a method for amplifying a template

CC nucleic acid segment (I), comprising annealing (i) to a branched primer

CC having front (fOW) and back oligonucleotide modules with arm segments

CC complementary to a site in (I), extending the arm of fOW to form an

CC initial extension strand, annealing the strand to a reverse primer (RP),

CC extending RP to form second initial extension strand, and amplifying the

CC second strand. The method can be used for amplifying nucleic acid

CC segments, useful in genome mapping, biomedical research and clinical

CC diagnostics. The method eliminates the need for custom primer synthesis

CC in methods to amplify nucleic acid segments. The modular combination of

CC just a few oligonucleotides essentially mimics the performance of a

CC conventional, custom-made primer by matching a sequence of a priming site

CC in the template. AAF74940 to AAF74979 represent oligonucleotide sequences

CC used in the exemplification of the present invention. N.B. Any Ns given

CC in the oligonucleotide sequences represent inosine bases

XX

XX Sequence 22 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 2 Other;

XX

Query Match 70.5%; Score 13.4; DB 4; Length 22;

Best Local Similarity 93.3%; Pred. No. 9.1e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TGACGTTACGGGGGG 19

DB 2 TGACGTTACGGGGTG 16

XX

RESULT 45

ADR99754

ID ADR99754 standard; DNA; 30 BP.

XX

AC ADR99754;

XX

DT 02-DEC-2004 (first entry)

XX

DE Nucleic acid cysMR to generate evolved microorganisms.

XX

XX ss; microorganism evolution; metabolic pathway; metabolite;

KW biotransformation; NADPH-dependent enzyme; nucleic acid metabolism;

KW lipid metabolism; sugar metabolism.

XX

OS Unidentified.

XX

PN WO2004076659-A2.

XX

PD 10-SEP-2004.

XX

PF 17-FEB-2004; 2004WO-FR000354.

XX

XX 18-FEB-2003; 2003FR-00001924.

PR 14-MAY-2003; 2003FR-00005768.

PR 14-MAY-2003; 2003FR-00005769.

PR 06-NOV-2003; 2003FR-00013054.

XX

XX (META-) METABOLIC EXPLORER.

XX

XX Chateau M, Gonzalez B, Meynial-Salles I, Soucaille PNP, Zink O;

PI WPI; 2004-653418/63.

XX

XX New evolved microorganisms with altered metabolic pathways, useful e.g.

PT for production of amino acids, are selected as mutants able to grow on

PT defined media.

XX

XX Disclosure; SEQ ID NO 21; 113pp; French.

PS

XX

CC The invention relates to a method for preparing evolved microorganisms

CC (A) with modified metabolic pathways comprising: (a) genetic modification

CC of a microorganism to inhibit production or consumption of a metabolite

CC when it is grown on a defined medium, thus affecting its ability to grow;

CC (b) growing the modified organism in the defined medium so that evolution

CC can occur, optionally with addition of a co-substrate to allow evolution;

CC and (c) selecting as (A) cells able to grow on the medium, optionally in

CC presence of co-substrate. The evolved microorganisms (A), or evolved

CC proteins (I) expressed by them, are useful in biotransformation

CC processes, especially those involving NADPH-dependent enzymes,

CC particularly synthesis of amino acids (Met, Cys, Thr, Lys or Ile) but

CC also synthesis of nucleic acids or lipids, and metabolism of sugars. (A)

CC provide more efficient production of selected metabolites than parent

CC strains. This sequence represents a nucleic acid molecule used in the

CC method of the invention.

XX

XX Sequence 30 BP; 7 A; 8 C; 9 G; 6 T; 0 U; 0 Other;

XX

Query Match 70.5%; Score 13.4; DB 13; Length 30;

Best Local Similarity 93.3%; Pred. No. 9.2e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGG 15

DB 1 GGGGTGACGTTTCAGG 15

XX

RESULT 46

ADM46519/c

ID ADM46519 standard; RNA; 19 BP.

XX

AC ADM46519;

XX

DT 07-APR-2005 (first entry)

XX

DE Human survivin gene-specific siRNA sequence - SEQ ID 196.

XX

XX survivin; antisense therapy; gene silencing; cancer; cytostatic;

KW breast tumor; colon tumor; prostate tumor; lung tumor; bladder tumor;

KW ovary tumor; renal tumor; pancreas tumor; non-hodgkin lymphoma;

KW hepatocellular carcinoma; ss; siRNA; short interfering RNA;

XX RNA interference.

XX

OS Homo sapiens.

XX

PN WO2005002507-A2.

XX

PD 13-JAN-2005.

XX

PF 03-JUN-2004; 2004WO-US017490.

XX

XX 03-JUN-2003; 2003US-0475324P.

PR 11-JUL-2003; 2003US-00618553.

PR 13-APR-2004; 2004US-00823448.

XX

XX (ISIS-) ISIS PHARM INC.

PA (ELIL ) LILLY & CO ELI.

XX

XX Bhat B, Patet BK, Swayze E;

PI WPI; 2005-081840/09.

XX

XX Novel double-stranded compound, modulating expression of human survivin,

PT useful for treating condition associated with survivin expression or

PT overexpression, such as breast cancer, colon cancer, lung cancer, bladder

PT cancer.

XX

XX Example 25; SEQ ID NO 196; 159pp; English.

PS

XX The invention comprises dsRNA oligomeric sequences which are targeted to

CC the human survivin gene. The dsRNA oligomeric compounds of the invention

CC are useful for inhibiting expression of the human survivin gene, and can

CC



CC be used in the treatment of cancer, such as: hepatocellular cancer, breast cancer, colon cancer, prostate cancer, lung cancer, bladder cancer, ovarian cancer, renal cancer, glioblastoma, pancreatic cancer and non-Hodgkin's lymphoma. The present nucleic acid represents a human survivin-specific siRNA sequence of the invention.

XX SQ Sequence 19 BP; 4 A; 9 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 14; Length 19;  
Best Local Similarity 83.3%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 18  
|||:|||||:|||||  
Db 18 GGGGTGAACCTTCAGGTGG 1

RESULT 47  
ADW46518  
ID ADW46518 standard; RNA; 19 BP.

XX AC ADW46518;  
XX DT 07-APR-2005 (first entry)  
XX DE Human survivin gene-specific siRNA sequence - SEQ ID 195.

XX KW survivin; antisense therapy; gene silencing; cancer; cytostatic;  
XX KW breast tumor; colon tumor; prostate tumor; lung tumor; bladder tumor;  
XX KW ovary tumor; renal tumor; pancreas tumor; non-hodgkin lymphoma;  
XX KW hepatocellular carcinoma; ss; siRNA; short interfering RNA;  
XX KW RNA interference.

XX OS Homo sapiens.

XX PN WO2005002507-A2.

XX PD 13-JAN-2005.

XX PF 03-JUN-2004; 2004WO-US017490.

XX PR 03-JUN-2003; 2003US-0475324P.

XX PR 11-JUL-2003; 2003US-00618553.

XX PR 13-APR-2004; 2004US-00823448.

XX PA (ISIS-) ISIS PHARM INC.

XX PA (ELIL) LILLY & CO ELI.

XX PI Bhat B, Patet BK, Swayze E;

XX WPI; 2005-081840/09.

XX PT Novel double-stranded compound, modulating expression of human survivin, useful for treating condition associated with survivin expression or overexpression, such as breast cancer, colon cancer, lung cancer, bladder cancer.

XX PS Example 25; SEQ ID NO 195; 159pp; English.

XX CC The invention comprises dsRNA oligomeric sequences which are targeted to the human survivin gene. The dsRNA oligomeric compounds of the invention are useful for inhibiting expression of the human survivin gene, and can be used in the treatment of cancer, such as: hepatocellular cancer, breast cancer, colon cancer, prostate cancer, lung cancer, bladder cancer, ovarian cancer, renal cancer, glioblastoma, pancreatic cancer and non-Hodgkin's lymphoma. The present nucleic acid represents a human survivin-specific siRNA sequence of the invention.

XX SQ Sequence 19 BP; 3 A; 3 C; 9 G; 0 T; 4 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 14; Length 19;  
Best Local Similarity 66.7%; Pred. No. 1.1e+04;  
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 18  
|||:|||||:|||||  
Db 2 GGGGUGAACUCUCAGGUGG 19

RESULT 48  
AAF99395

ID AAF99395 standard; DNA; 20 BP.

XX AC AAF99395;

XX DT 12-JUN-2001 (first entry)

XX DE Immunostimulatory nucleic acid #511.

XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
XX KW immunostimulatory; tumour; viral infection; bacterial infection;  
XX KW fungal infection; parasitic infection; cancer; asthma;  
XX KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
XX OS Synthetic.

XX PN WO200122972-A2.

XX PD 05-APR-2001.

XX PF 25-SEP-2000; 2000WO-US026383.

XX PR 25-SEP-1999; 99US-0156113P.

XX PR 27-SEP-1999; 99US-0156135P.

XX PR 23-AUG-2000; 2000US-0227436P.

XX PA (IOWA) UNIV IOWA RES FOUND.

XX PA (COLE-) COLEY PHARM GMBH.

XX PI Krieg AM, Schetter C, Vollmer J;

XX WPI; 2001-273485/28.

XX PT Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.

XX PS Claim 101; Page 48; 338pp; English.

XX CC The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone

XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 4; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 18  
|||:|||||:|||||  
Db 3 GGCATGACGTTTCAGGGG 20

RESULT 49  
AAF99392

ID AAF99392 standard; DNA; 20 BP.  
 XX AAF99392;  
 AC AAF99392;  
 XX 12-JUN-2001 (first entry)  
 DT 12-JUN-2001 (first entry)  
 XX Immunostimulatory nucleic acid #508.  
 DE Immunostimulatory nucleic acid #508.  
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX Synthetic.  
 OS Synthetic.  
 PN WO200122972-A2.  
 XX WO200122972-A2.  
 PD 05-APR-2001.  
 XX 05-APR-2001.  
 XX 25-SEP-2000; 2000WO-US026383.  
 PF 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 DR Vaccinating against tumors, infectious diseases, allergies and asthma  
 XX using immunostimulatory Py-rich and TG nucleic acids.  
 PT Claim 101; Page 48; 338pp; English.  
 PS The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 69.5%; Score 13.2; DB 4; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGGG 18  
 Db |||||  
 3 GGCATGACGTTTCGGGGG 20  
 RESULT 50  
 ABS78040  
 ID ABS78040 standard; DNA; 20 BP.  
 XX ABS78040;  
 AC ABS78040;  
 XX 13-DEC-2002 (first entry)  
 DT 13-DEC-2002 (first entry)  
 XX Angiogenesis inhibitory oligonucleotide #524.  
 DE Angiogenesis inhibitory oligonucleotide #524.  
 XX

KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubecsis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophilic joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX Synthetic.  
 OS Synthetic.  
 PN WO200253141-A2.  
 XX WO200253141-A2.  
 PD 11-JUL-2002.  
 XX 11-JUL-2002.  
 PF 14-DEC-2001; 2001WO-US048458.  
 PR 14-DEC-2000; 2000US-0255534P.  
 XX (COLE-) COLEY PHARM GROUP INC.  
 PA Bratzler RL;  
 PI WPI; 2002-566690/60.  
 DR Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX Claim 2; Page 28; 276pp; English.  
 CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubecsis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma, and  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 69.5%; Score 13.2; DB 6; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGGG 18  
 Db |||||  
 3 GGCATGACGTTTCGGGGG 20  
 Search completed: February 15, 2006, 18:06:56  
 Job time : 153.207 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:07:43 ; Search time 1263.74 Seconds  
(without alignments)  
703.434 Million cell updates/sec

Title: US-09-669-187A-80

Perfect score: 19  
Sequence: 1 ggggtgacgttcaggggggg 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database :

EST.\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_est3.\*
- 4: gb\_btc.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_est7.\*
- 9: gb\_gss1.\*
- 10: gb\_gss2.\*
- 11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| C 1        | 14.2  | 74.7        | 50     | 11    | CR061079 Forward s |
| C 2        | 13.8  | 72.6        | 32     | 2     | BF568357           |
| C 3        | 13.2  | 69.5        | 46     | 9     | A2838956           |
| C 4        | 12.8  | 67.4        | 41     | 10    | BX121477           |
| C 5        | 12.6  | 66.3        | 35     | 7     | C0411608           |
| C 6        | 12.6  | 66.3        | 44     | 10    | AG215101           |
| C 7        | 12.2  | 64.2        | 28     | 1     | AA986325           |
| C 8        | 12.2  | 64.2        | 37     | 9     | A2616333           |
| C 9        | 12.2  | 64.2        | 42     | 9     | CC027439           |
| C 10       | 12.2  | 64.2        | 45     | 9     | A2307335           |
| C 11       | 11.8  | 62.1        | 19     | 9     | A2768418           |
| C 12       | 11.8  | 62.1        | 29     | 8     | CX012159           |
| C 13       | 11.8  | 62.1        | 34     | 3     | BJ035059           |
| C 14       | 11.8  | 62.1        | 41     | 9     | A2331072           |
| C 15       | 11.8  | 62.1        | 50     | 2     | BG272395           |
| C 16       | 11.6  | 61.1        | 20     | 9     | AQ074235           |
| C 17       | 11.6  | 61.1        | 25     | 9     | A2312923           |
| C 18       | 11.6  | 61.1        | 28     | 1     | A1497442           |
| C 19       | 11.6  | 61.1        | 28     | 10    | CL686485           |
| C 20       | 11.6  | 61.1        | 29     | 6     | CD029249           |
| C 21       | 11.6  | 61.1        | 30     | 9     | A2783946           |
| C 22       | 11.6  | 61.1        | 34     | 2     | B1259582           |

|       |      |      |    |    |           |       |      |      |    |    |           |           |
|-------|------|------|----|----|-----------|-------|------|------|----|----|-----------|-----------|
| c 96  | 11   | 57.9 | 49 | 10 | CZ906497  | 169   | 10.2 | 53.7 | 46 | 6  | CB884957  | CB884957  |
| c 97  | 11   | 57.9 | 50 | 1  | AUI03929  | 170   | 10.2 | 53.7 | 46 | 10 | CG571946  | CG571946  |
| c 98  | 11   | 57.9 | 50 | 1  | AUI04338  | c 171 | 10.2 | 53.7 | 47 | 1  | AA972457  | AA972457  |
| c 99  | 11   | 57.9 | 50 | 1  | AUI05978  | c 172 | 10.2 | 53.7 | 47 | 8  | R08290    | R08290    |
| c 100 | 11   | 57.9 | 50 | 1  | AUI05979  | c 173 | 10.2 | 53.7 | 47 | 9  | BZ286964  | BZ286964  |
| c 101 | 11   | 57.9 | 50 | 1  | AUI07236  | c 174 | 10.2 | 53.7 | 48 | 10 | AL760394  | AL760394  |
| c 102 | 11   | 57.9 | 50 | 1  | CZ016473  | c 175 | 10.2 | 53.7 | 49 | 1  | AW772664  | AW772664  |
| c 103 | 11   | 57.9 | 50 | 10 | BX987794  | c 176 | 10.2 | 53.7 | 49 | 8  | HI5861    | HI5861    |
| c 104 | 10.8 | 56.8 | 36 | 3  | BJ060990  | c 177 | 10.2 | 53.7 | 49 | 9  | BZ379376  | BZ379376  |
| c 105 | 10.8 | 56.8 | 43 | 5  | C00370    | c 178 | 10.2 | 53.7 | 49 | 11 | CR396950  | CR396950  |
| c 106 | 10.8 | 56.8 | 46 | 8  | D26039    | c 179 | 10.2 | 53.7 | 50 | 1  | AUI02339  | AUI02339  |
| c 107 | 10.8 | 56.8 | 47 | 8  | N44233    | c 180 | 10.2 | 53.7 | 50 | 1  | AUI04853  | AUI04853  |
| c 108 | 10.8 | 56.8 | 47 | 11 | TA195A08P | c 181 | 10.2 | 53.7 | 50 | 1  | AUI04854  | AUI04854  |
| c 109 | 10.8 | 56.8 | 50 | 1  | AUI04145  | c 182 | 10   | 52.6 | 19 | 10 | CW020460  | CW020460  |
| c 110 | 10.8 | 56.8 | 50 | 1  | AUI07408  | c 183 | 10   | 52.6 | 23 | 9  | AW527D14  | AW527D14  |
| c 111 | 10.8 | 56.8 | 50 | 1  | AUI07418  | c 184 | 10   | 52.6 | 24 | 9  | AZ314798  | AZ314798  |
| c 112 | 10.8 | 56.8 | 50 | 3  | BJ077206  | c 185 | 10   | 52.6 | 25 | 1  | AA871952  | AA871952  |
| c 113 | 10.6 | 55.8 | 22 | 1  | AUI521380 | c 186 | 10   | 52.6 | 25 | 1  | AUI363940 | AUI363940 |
| c 114 | 10.6 | 55.8 | 25 | 1  | AA878803  | c 187 | 10   | 52.6 | 25 | 1  | AI445419  | AI445419  |
| c 115 | 10.6 | 55.8 | 25 | 9  | AZ828517  | c 188 | 10   | 52.6 | 25 | 9  | AZ462642  | AZ462642  |
| c 116 | 10.6 | 55.8 | 25 | 9  | AZ981731  | c 189 | 10   | 52.6 | 25 | 9  | AZ603284  | AZ603284  |
| c 117 | 10.6 | 55.8 | 25 | 10 | CG729138  | c 190 | 10   | 52.6 | 25 | 9  | AZ794596  | AZ794596  |
| c 118 | 10.6 | 55.8 | 30 | 9  | AZ777592  | c 191 | 10   | 52.6 | 25 | 9  | AZ802728  | AZ802728  |
| c 119 | 10.6 | 55.8 | 31 | 1  | AI589323  | c 192 | 10   | 52.6 | 25 | 11 | CZ909972  | CZ909972  |
| c 120 | 10.6 | 55.8 | 32 | 10 | CZ915094  | c 193 | 10   | 52.6 | 25 | 11 | TA42C02Q  | TA42C02Q  |
| c 121 | 10.6 | 55.8 | 32 | 10 | AG224362  | c 194 | 10   | 52.6 | 26 | 1  | AA903336  | AA903336  |
| c 122 | 10.6 | 55.8 | 33 | 9  | AZ628058  | c 195 | 10   | 52.6 | 26 | 1  | AZ986927  | AZ986927  |
| c 123 | 10.6 | 55.8 | 34 | 9  | AZ431906  | c 196 | 10   | 52.6 | 28 | 9  | AZ986927  | AZ986927  |
| c 124 | 10.6 | 55.8 | 37 | 1  | AI626589  | c 197 | 10   | 52.6 | 28 | 10 | CZ917723  | CZ917723  |
| c 125 | 10.6 | 55.8 | 37 | 1  | AW250642  | c 198 | 10   | 52.6 | 28 | 9  | AZ610133  | AZ610133  |
| c 126 | 10.6 | 55.8 | 37 | 7  | CR762735  | c 199 | 10   | 52.6 | 29 | 10 | CL653182  | CL653182  |
| c 127 | 10.6 | 55.8 | 37 | 9  | AZ501429  | c 200 | 10   | 52.6 | 30 | 2  | BI223044  | BI223044  |
| c 128 | 10.6 | 55.8 | 40 | 1  | AA876140  | c 201 | 10   | 52.6 | 30 | 5  | BX624507  | BX624507  |
| c 129 | 10.6 | 55.8 | 40 | 1  | AA878861  | c 202 | 10   | 52.6 | 30 | 5  | BX624507  | BX624507  |
| c 130 | 10.6 | 55.8 | 40 | 9  | AZ806060  | c 203 | 10   | 52.6 | 31 | 1  | AA909238  | AA909238  |
| c 131 | 10.6 | 55.8 | 42 | 8  | R97402    | c 204 | 10   | 52.6 | 31 | 1  | AA910965  | AA910965  |
| c 132 | 10.6 | 55.8 | 43 | 10 | BX141236  | c 205 | 10   | 52.6 | 31 | 1  | AA933748  | AA933748  |
| c 133 | 10.6 | 55.8 | 45 | 3  | BJ015280  | c 206 | 10   | 52.6 | 31 | 1  | AI620715  | AI620715  |
| c 134 | 10.6 | 55.8 | 45 | 3  | AI355812  | c 207 | 10   | 52.6 | 31 | 1  | AI679568  | AI679568  |
| c 135 | 10.6 | 55.8 | 46 | 1  | AI677817  | c 208 | 10   | 52.6 | 31 | 1  | AI690328  | AI690328  |
| c 136 | 10.6 | 55.8 | 46 | 1  | AI809473  | c 209 | 10   | 52.6 | 31 | 9  | AZ487534  | AZ487534  |
| c 137 | 10.6 | 55.8 | 46 | 1  | AV954968  | c 210 | 10   | 52.6 | 32 | 2  | BG419594  | BG419594  |
| c 138 | 10.6 | 55.8 | 48 | 9  | AZ816555  | c 211 | 10   | 52.6 | 32 | 10 | BX947451  | BX947451  |
| c 139 | 10.6 | 55.8 | 48 | 10 | AJ598765  | c 212 | 10   | 52.6 | 33 | 9  | AZ961620  | AZ961620  |
| c 140 | 10.6 | 55.8 | 49 | 8  | CV836113  | c 213 | 10   | 52.6 | 33 | 11 | DME545578 | DME545578 |
| c 141 | 10.6 | 55.8 | 50 | 1  | AUI02260  | c 214 | 10   | 52.6 | 34 | 8  | N73483    | N73483    |
| c 142 | 10.6 | 55.8 | 50 | 1  | AUI03955  | c 215 | 10   | 52.6 | 34 | 9  | AZ659789  | AZ659789  |
| c 143 | 10.6 | 55.8 | 50 | 1  | AUI04957  | c 216 | 10   | 52.6 | 34 | 10 | CZ442563  | CZ442563  |
| c 144 | 10.6 | 55.8 | 50 | 1  | AUI04960  | c 217 | 10   | 52.6 | 35 | 9  | AZ469734  | AZ469734  |
| c 145 | 10.6 | 55.8 | 50 | 1  | AUI04965  | c 218 | 10   | 52.6 | 35 | 9  | AZ976182  | AZ976182  |
| c 146 | 10.6 | 55.8 | 50 | 1  | AUI05099  | c 219 | 10   | 52.6 | 35 | 9  | AZ871856  | AZ871856  |
| c 147 | 10.6 | 55.8 | 50 | 1  | AUI06995  | c 220 | 10   | 52.6 | 36 | 9  | AZ867309  | AZ867309  |
| c 148 | 10.4 | 54.7 | 45 | 10 | CZ468531  | c 221 | 10   | 52.6 | 36 | 11 | TA242812Q | TA242812Q |
| c 149 | 10.4 | 54.7 | 46 | 1  | AA416444  | c 222 | 10   | 52.6 | 37 | 1  | AI357425  | AI357425  |
| c 150 | 10.4 | 54.7 | 46 | 11 | CR028335  | c 223 | 10   | 52.6 | 37 | 2  | AI499210  | AI499210  |
| c 151 | 10.2 | 53.7 | 30 | 9  | AZ602612  | c 224 | 10   | 52.6 | 37 | 2  | BI080927  | BI080927  |
| c 152 | 10.2 | 53.7 | 33 | 9  | AQ026144  | c 225 | 10   | 52.6 | 37 | 9  | AZ871856  | AZ871856  |
| c 153 | 10.2 | 53.7 | 34 | 1  | AI590768  | c 226 | 10   | 52.6 | 37 | 10 | CL658108  | CL658108  |
| c 154 | 10.2 | 53.7 | 34 | 9  | AZ493518  | c 227 | 10   | 52.6 | 37 | 11 | DR11K9T   | DR11K9T   |
| c 155 | 10.2 | 53.7 | 34 | 9  | BZ661946  | c 228 | 10   | 52.6 | 38 | 2  | BE261178  | BE261178  |
| c 156 | 10.2 | 53.7 | 34 | 10 | AG201486  | c 229 | 10   | 52.6 | 38 | 3  | BI553849  | BI553849  |
| c 157 | 10.2 | 53.7 | 35 | 9  | AZ665829  | c 230 | 10   | 52.6 | 39 | 9  | BG973894  | BG973894  |
| c 158 | 10.2 | 53.7 | 35 | 2  | BF134431  | c 231 | 10   | 52.6 | 39 | 9  | AZ640839  | AZ640839  |
| c 159 | 10.2 | 53.7 | 37 | 9  | AZ455844  | c 232 | 10   | 52.6 | 39 | 9  | AZ997025  | AZ997025  |
| c 160 | 10.2 | 53.7 | 37 | 10 | CZ487169  | c 233 | 10   | 52.6 | 39 | 10 | AJ593066  | AJ593066  |
| c 161 | 10.2 | 53.7 | 37 | 10 | BX496677  | c 234 | 10   | 52.6 | 40 | 1  | AA931142  | AA931142  |
| c 162 | 10.2 | 53.7 | 38 | 10 | CZ473438  | c 235 | 10   | 52.6 | 40 | 1  | AI613303  | AI613303  |
| c 163 | 10.2 | 53.7 | 40 | 1  | AA023582  | c 236 | 10   | 52.6 | 40 | 1  | AI684941  | AI684941  |
| c 164 | 10.2 | 53.7 | 40 | 10 | CZ194944  | c 237 | 10   | 52.6 | 40 | 1  | AI745660  | AI745660  |
| c 165 | 10.2 | 53.7 | 41 | 9  | AZ588779  | c 238 | 10   | 52.6 | 40 | 1  | AV833488  | AV833488  |
| c 166 | 10.2 | 53.7 | 42 | 2  | BF139151  | c 239 | 10   | 52.6 | 40 | 7  | CO258621  | CO258621  |
| c 167 | 10.2 | 53.7 | 44 | 1  | AA792171  | c 240 | 10   | 52.6 | 40 | 7  | BX662712  | BX662712  |
| c 168 | 10.2 | 53.7 | 45 | 3  | BI663358  | c 241 | 10   | 52.6 | 41 | 1  | AV855184  | AV855184  |
| c 96  | 11   | 57.9 | 49 | 10 | CZ906497  | 169   | 10.2 | 53.7 | 46 | 6  | CB884957  | CB884957  |
| c 97  | 11   | 57.9 | 50 | 1  | AUI03929  | 170   | 10.2 | 53.7 | 46 | 10 | CG571946  | CG571946  |
| c 98  | 11   | 57.9 | 50 | 1  | AUI04338  | c 171 | 10.2 | 53.7 | 47 | 1  | AA972457  | AA972457  |
| c 99  | 11   | 57.9 | 50 | 1  | AUI05978  | c 172 | 10.2 | 53.7 | 47 | 8  | R08290    | R08290    |
| c 100 | 11   | 57.9 | 50 | 1  | AUI05979  | c 173 | 10.2 | 53.7 | 47 | 9  | BZ286964  | BZ286964  |
| c 101 | 11   | 57.9 | 50 | 1  | AUI07236  | c 174 | 10.2 | 53.7 | 48 | 10 | AL760394  | AL760394  |
| c 102 | 11   | 57.9 | 50 | 10 | CZ016473  | c 175 | 10.2 | 53.7 | 49 | 1  | AW772664  | AW772664  |
| c 103 | 11   | 57.9 | 50 | 10 | BX987794  | c 176 | 10.2 | 53.7 | 49 | 8  | HI5861    | HI5861    |
| c 104 | 10.8 | 56.8 | 36 | 3  | BJ060990  | c 177 | 10.2 | 53.7 | 49 | 9  | BZ379376  | BZ379376  |
| c 105 | 10.8 | 56.8 | 43 | 5  | C00370    | c 178 | 10.2 | 53.7 | 49 | 11 | CR396950  | CR396950  |
| c 106 | 10.8 | 56.8 | 46 | 8  | D26039    | c 179 | 10.2 | 53.7 | 50 | 1  | AUI02339  | AUI02339  |
| c 107 | 10.8 | 56.8 | 47 | 8  | N44233    | c 180 | 10.2 | 53.7 | 50 | 1  | AUI04853  | AUI04853  |
| c 108 | 10.8 | 56.8 | 47 | 11 | TA195A08P | c 181 | 10.2 | 53.7 | 50 | 1  | AUI04854  | AUI04854  |
| c 109 | 10.8 | 56.8 | 50 | 1  | AUI04145  | c 182 | 10   | 52.6 | 19 | 10 | CW020460  | CW020460  |
| c 110 | 10.8 | 56.8 | 50 | 1  | AUI07408  | c 183 | 10   | 52.6 | 23 | 9  | AW527D14  | AW527D14  |
| c 111 | 10.8 | 56.8 | 50 | 1  | AUI07418  | c 184 | 10   | 52.6 | 24 | 9  | AZ314798  | AZ314798  |
| c 112 | 10.8 | 56.8 | 50 | 3  | BJ077206  | c 185 | 10   | 52.6 | 25 | 1  | AA871952  | AA871952  |
| c 113 | 10.6 | 55.8 | 22 | 1  | AUI521380 | c 186 | 10   | 52.6 | 25 | 1  | AUI363940 | AUI363940 |
| c 114 | 10.6 | 55.8 | 25 | 1  | AA878803  | c 187 | 10   | 52.6 | 25 | 1  | AI445419  | AI445419  |
| c 115 | 10.6 | 55.8 | 25 | 9  | AZ828517  | c 188 | 10   | 52.6 | 25 | 9  | AZ462642  | AZ462642  |
| c 116 | 10.6 | 55.8 | 25 | 9  | AZ981731  | c 189 | 10   | 52.6 | 25 | 9  | AZ603284  | AZ603284  |
| c 117 | 10.6 | 55.8 | 25 | 10 | CG729138  | c 190 | 10   | 52.6 | 25 | 9  | AZ794596  | AZ794596  |
| c 118 | 10.6 | 55.8 | 30 | 9  | AZ777592  | c 191 | 10   | 52.6 | 25 | 9  | AZ802728  | AZ802728  |
| c 119 | 10.6 | 55.8 | 31 | 1  | AI589323  | c 192 | 10   | 52.6 | 25 | 11 | CZ909972  | CZ909972  |
| c 120 | 10.6 | 55.8 | 32 | 10 | CZ915094  | c 193 | 10   | 52.6 | 25 | 11 | TA42C02Q  | TA42C02Q  |
| c 121 | 10.6 | 55.8 | 32 | 10 | AG224362  | c 194 | 10   | 52.6 | 26 | 1  | AA903336  | AA903336  |
| c 122 | 10.6 | 55.8 | 33 | 9  | AZ628058  | c 195 | 10   | 52.6 | 26 | 1  | AZ986927  | AZ986927  |
| c 123 | 10.6 | 55.8 | 34 | 9  | AZ431906  | c 196 | 10   | 52.6 | 28 | 9  | AZ986927  | AZ986927  |
| c 124 | 10.6 | 55.8 | 37 | 1  | AI626589  | c 197 | 10   | 52.6 | 28 | 10 | CZ917723  | CZ917723  |
| c 125 | 10.6 | 55.8 | 37 | 1  | AW250642  | c 198 | 10   | 52.6 | 28 | 9  | AZ610133  | AZ610133  |
| c 126 | 10.6 | 55.8 | 37 | 7  | CR762735  | c 199 | 10   | 52.6 | 29 |    |           |           |



(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library. | "

```

ORIGIN
Query Match      72.6%; Score 13.8; DB 2; Length 32;
Best Local Similarity 88.2%; Pred. No. 4.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 19
    |||||
Db 23 GGTGACGTTTCAGGGG 7

RESULT 3
AZ838956
LOCUS      46 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION      2M0134D20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                  clone UUGC2M0134D20 R, genomic survey sequence.
ACCESSION      AZ838956
VERSION      AZ838956.1 GI:13008864
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0134 row: D column: 20
              Seq primer: CACACAGGAACACGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 46.
FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0134D20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1] a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

```

## ORIGIN

Query Match 69.5%; Score 13.2; DB 9; Length 46;  
Best Local Similarity 83.3%; Pred. No. 9.4e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 18  
 |||||  
Db 9 GGGTTCATGATCAGGGGG 26

## RESULT 4

BX121477/c  
LOCUS 41 bp DNA linear GSS 13-MAR-2003  
DEFINITION Danio rerio genomic clone DKEX-62P9, genomic survey sequence.

ACCESSION BX121477  
VERSION BX121477.1 GI:27952401  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 41)  
AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.

TITLE Direct Submission  
JOURNAL Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquerry@sanger.ac.uk Unpublished  
This sequence was generated from the T7 end of BAC 62P9. 62P9 is  
part of the Daniokey BAC Library created by R. Plasterk and N.V.  
keygene. Further details:  
http://www.sanger.ac.uk/Projects/D\_rerio/.

## FEATURES

source  
1..41  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-62P9"  
/tissue\_type="Testis"  
/note="vector pindigoBAC-536"

## ORIGIN

Query Match 67.4%; Score 12.8; DB 10; Length 41;  
Best Local Similarity 82.4%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGGGG 18  
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Db 39 GGGGNGCGTTCTGGGGG 23

## RESULT 5

CO411608/c  
LOCUS 35 bp mRNA linear EST 02-JUL-2004  
DEFINITION EST841993 Sequencing ESTs from loblolly pine embryos Pinus taeda

CDNA clone P1AM51 5' end, mRNA sequence.

ACCESSION CO411608  
VERSION CO411608.1 GI:49627856  
KEYWORDS EST.

SOURCE Pinus taeda (loblolly pine)

ORGANISM Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE 1 (bases 1 to 35)  
AUTHORS Buell,C.R., Zheng,L., Cowles,A. and Cairney,J.  
TITLE Sequencing of ESTs from loblolly pine embryonic libraries  
JOURNAL Unpublished (2004)  
COMMENT Contact: C. Robin Buell  
Plant Genomics Group

The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: rbuell@tigr.org  
This clone is available through TIGR. Please contact pine@tigr.org  
for further information  
Seq primer: ATT TAG GTG ACA CTA TAG.

## FEATURES

source

Location/Qualifiers  
1. .35  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/cultivar="7-56 mother tree, open-pollinated tree from,  
Lyons, Georgia, USA"  
/db\_xref="taxon:3352"  
/clone="PIALM51"  
/lab\_host="E.coli DH10B-Tona"  
/clone\_lib="Sequencing ESTs from loblolly pine embryos"  
/note="Organ: Zygotic Embryo and Megagametophyte, Somatic  
Embryo; Vector: pCMV-SPORT 6.1; Site\_1: NotI; Site\_2:  
EcoRV; tissue: Whole megagametophytes isolated from pine  
seeds; Whole embryos excised from these megagametophytes,  
whole somatic embryos and suspensor tissue from tissue  
culture, isolated from cell line A12. Pooled RNA from  
zygotic embryos, megagametophytes, and somatic embryos was  
used for library construction. Pine cones were harvested  
weekly from open-pollinated 7-56 mother trees, collections  
occurred from 7/01/02 until 10/15/02. Whole  
megagametophytes were first isolated from pine seeds, and  
whole embryos excised from these megagametophytes each was  
flash frozen. Embryo development was assessed using the  
system of Pullman et al (Pullman GS, Johnson S, Peter G,  
Cairney J, Xu N. 2003. Loblolly Pine somatic  
embryogenesis: development of a maturation medium and  
resulting embryo quality. Plant Cell Reports 21:747-758  
(http://link.springer.de/link/service/journals/00299/conte  
nts/03/00586/). For photographs see Ciavatta et al 2001.  
(Ciavatta VT, Morillon R, Pullman GS, Chrispeels M,  
Cairney J. 2001. An aquaglyceroporin is abundantly  
expressed early in the development of the suspensor and  
the embryo proper of loblolly pine (Pinus taeda L.). Plant  
Physiol. 127: 1556-1567  
(http://www.plantphysiol.org/cgi/content/full/127/4/1556))".

## ORIGIN

Query Match 66.3%; Score 12.6; DB 7; Length 35;  
Best Local Similarity 78.9%; Pred. No. 1.8e+05;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGGGGG 19  
||||| |||||  
Db 27 GGGGGGAATTTAGGGGG 9

## RESULT 6

AG215101

LOCUS

DEFINITION Drosophila melanogaster DNA, clone:NP6643-5-1, flanking P[GawB]  
transposon insertion, genomic survey sequence.

ACCESSION AG215101

VERSION AG215101.1 GI:22762101

KEYWORDS GSS.

SOURCE Drosophila melanogaster

ORGANISM

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

AUTHORS

Hayaishi, S., Ito, K., Sado, Y., Taniguchi, M., Akimoto, A., Takeuchi, H.,  
Aigaki, T., Matsuzaki, F., Nakagoshi, H., Tanimura, T., Ueda, R.,  
Uemura, T., Yoshihara, M. and Goto, S.  
GETDB, a database compiling expression patterns and molecular  
locations of a collection of Gal4 enhancer traps  
Genesis (2002) In press

## REFERENCE

2 (bases 1 to 44)

Hayaishi, S.

AUTHORS

TITLE

JOURNAL

Direct Submission

Submitted (27-AUG-2002)

Shigeo Hayaishi, RIKEN Center for

Developmental Biology, Laboratory for Morphogenetic Signaling;

Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan

(E-mail: shayaishi@cdb.riken.go.jp; Tel: 81-78-301-3184,

Fax: 81-78-301-3183)

COMMENT

This clone was isolated from genomic DNA flanking an insertion of

the P element vector P[GawB] of a Drosophila strain.

FEATURES

source

Location/Qualifiers

1. .44

/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

/strain="NP6643"

/db\_xref="taxon:7227"

/chromosome="3"

/map="64P2"

/clone="NP6643-5-1"

/note="flanking P[GawB] transposon insertion"

ORIGIN

Query Match 66.3%; Score 12.6; DB 10; Length 44;

Best Local Similarity 78.9%; Pred. No. 1.8e+05;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGGGGG 19

||||| |||||

Db 2 GGGGGGCGTGCAGCGGG 20

RESULT 7

AA986325/c

LOCUS

DEFINITION

AA986325

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:915931

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: primer name ambiguous

High quality sequence stop: 1.

Location/Qualifiers

1. .28

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL"

/db\_xref="taxon:10090"

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/clone="IMAGE:1431863"
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/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mkia"
/notes="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGCGCTTTTITTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGACTGG and 3' end
primer CGACCTGCAGCTCAGACACA."

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## ORIGIN

```

Query Match      64.2%; Score 12.2; DB 1; Length 28;
Best Local Similarity 82.4%; Pred. No. 2.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACAGGG 17
    |||||
Db 22 GGTTGAGGTTCACTGG 6

```

## RESULT 8

```

AZ616333
LOCUS
DEFINITION
M0446A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0446A08 F, genomic survey sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE

```

```

ORGANISM
Mus musculus
(house mouse)

```

```

REFERENCE
AUTHORS
Dunn,D., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

JOURNAL
Unpublished (2000)

```

```

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

```

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0446 row: A column: 08
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 37.

```

## FEATURES

```

source

```

```

1. .37
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0446A08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

```

```

/notes="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

## ORIGIN

```

Query Match      64.2%; Score 12.2; DB 9; Length 37;
Best Local Similarity 82.4%; Pred. No. 2.9e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACAGGG 17
    |||||
Db 7 GGCGTACCGTTACAGGG 23

```

## RESULT 9

```

CC027439/c
LOCUS
DEFINITION
3591_1_5_1_D10.1EL_Y_1 3591 - RescueMu Grid P Zea mays genomic,
genomic survey sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE

```

```

ORGANISM
Zea mays
Zea mays

```

```

REFERENCE
AUTHORS
Walbot,V.
TITLE
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
JOURNAL
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

```

```

Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3591_1_5_1 row: 4
Class: transposon-tagged.

```

```

Location/Qualifiers
1. .42
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3591 - RescueMu Grid P"

```

```

/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription

```

## FEATURES

```

source

```

```

1. .42
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3591 - RescueMu Grid P"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription

```



units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 64.2%; Score 12.2; DB 9; Length 42;  
Best Local Similarity 82.4%; Pred. No. 2.9e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGTGACGTTTCAGGGGG 18  
||||| ||||| ||||| |||||  
Db 17 GGGTCGCGTGCAGGGGG 1

## RESULT 10

AZ307335/c  
LOCUS  
DEFINITION LM0008K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
Clone UUGC1M0008K13 R, genomic survey sequence.

ACCESSION AZ307335  
VERSION AZ307335.1 GI:10346236  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS  
1 (bases 1 to 45)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

COMMENT  
Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0008 row: K column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 45.

## FEATURES

source

1. .45  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0008K13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gil4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 64.2%; Score 12.2; DB 9; Length 45;  
Best Local Similarity 82.4%; Pred. No. 2.9e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGG 17  
||||| ||||| ||||| |||||  
Db 20 GGGGGAATGTTTCAGGGG 4

## RESULT 11

AZ768418  
LOCUS  
DEFINITION AZ768418 19 bp DNA linear GSS 16-FEB-2001  
Clone UUGC1M0568H23 F, genomic survey sequence.

ACCESSION AZ768418  
VERSION AZ768418.1 GI:12887506  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0568 row: H column: 23

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0568H23"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 62.1%; Score 11.8; DB 9; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGG 15  
||||| |||||  
Db 4 GGGGTGAGGTTCTGG 18

## RESULT 12

CX012159  
LOCUS  
DEFINITION i057g07.b1 Whole Heart Library (DOGESTS) Canis familiaris cDNA,  
mRNA sequence.  
ACCESSION CX012159  
VERSION CX012159.1 GI:56394570  
KEYWORDS  
SOURCE  
ORGANISM Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.

## REFERENCE

1 (bases 1 to 29)  
Balijsa, V.S., Nascimento, L.U. and McCombie, W.R.  
ESTs from Canis familiaris whole heart (dog)  
Unpublished (2004)  
COMMENT  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mccombie@cshl.org.

## FEATURES

source

1..29  
Location/Qualifiers  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/dev\_stage="3 month old normal canine"  
/lab\_host="XL10 Gold"  
/clone\_lib="Whole Heart Library (DOGESTS)"  
/notes="Organ: Heart; Vector: pBluescript II SK; Site 1:  
ECORI; Site 2: XhoI; Library constructed using pBluescript  
XR kit from Stratagene. Cloned cDNA was size selected  
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and  
Medical Genetics, School of Veterinary Medicine,  
University of Pennsylvania, 3800 Spruce Street,  
Philadelphia, PA 19104-6051"

## ORIGIN

Query Match 62.1%; Score 11.8; DB 8; Length 29;  
Best Local Similarity 86.7%; Pred. No. 4.4e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTGATGTCAGGGGG 18  
||||| |||||  
Db 6 GTGATGTCAGGGGG 20

## RESULT 13

BJ035059

LOCUS  
DEFINITION BJ035059 NTBB Mochii normalized Xenopus neurula library Xenopus  
laevis cDNA clone XL031m15 5', mRNA sequence.  
ACCESSION BJ035059  
VERSION BJ035059.1 GI:117414312  
KEYWORDS  
SOURCE  
ORGANISM Xenopus laevis (African clawed frog)  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Xenopus.

REFERENCE  
AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and  
Kohata, Y.  
TITLE Expressed genes in X. laevis embryo  
JOURNAL Unpublished (2001)  
COMMENT Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp  
The information of this clone is available through the following  
URL:  
http://xenopus.nibb.ac.jp.

## FEATURES

source

1..34  
Location/Qualifiers  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="XL031m15"  
/tissue\_type="whole embryo"  
/dev\_stage="stage 15"  
/clone\_lib="NIBB Mochii normalized Xenopus neurula  
library"

## ORIGIN

Query Match 62.1%; Score 11.8; DB 3; Length 34;  
Best Local Similarity 86.7%; Pred. No. 4.5e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGG 16  
||||| |||||  
Db 17 GGCTAACGTTTCAGG 31

## RESULT 14

AZ331072/c

LOCUS

DEFINITION

AZ331072 41 bp DNA linear GSS 29-SEP-2000  
1M0056A13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0056A13 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 41)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D. Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0056 row: A column: 13  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 41.

# FEATURES

1. .41  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCIM0056A13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCIM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 62.1%; Score 11.8; DB 9; Length 41;  
 Best Local Similarity 86.7%; Pred. No. 4.5e+05;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TGACGTTTCAGGGGG 19  
 ||||| |||||  
 Db 26 TGACTTTCGGGGG 12

RESULT 15  
 BG272395  
 LOCUS  
 DEFINITION nah29f02.x1 NCI\_CGAP\_HN21 Homo sapiens cDNA clone IMAGE:4232571 3', mRNA sequence.  
 BG272395  
 ACCESSION BG272395.1 GI:12981506  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 50)  
 NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:

# REFERENCE

AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

info@image.llnl.gov  
 Seq primer: -40UP from Gibco.  
 Location/Qualifiers  
 1. .50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4232571"  
 /tissue\_type="nasopharyngeal carcinoma"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_HN21"  
 /note="Organ: head/neck; Vector: pAMP1; mRNA made from head/neck tumor, cDNA made by oligo-dT priming. Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library. cDNA Library Preparation: David B. Krizman, Ph.D."

# ORIGIN

Query Match 62.1%; Score 11.8; DB 2; Length 50;  
 Best Local Similarity 86.7%; Pred. No. 4.6e+05;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TGACGTTTCAGGGGG 19  
 ||||| |||||  
 Db 6 TGTGCTTCTCGGGGG 20

# RESULT 16

AQ074235  
 LOCUS  
 DEFINITION 21 pUC8 PstI Rice Etiolated Leaf Genomic Library Oryza sativa (indica cultivar-group) genomic clone RG152, genomic survey sequence.  
 ACCESSION AQ074235  
 VERSION AQ074235.1 GI:3435354  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM

Oryza sativa (indica cultivar-group)  
 Oryza sativa (indica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 20)  
 McCouch,S.R., Kochert,G., Yu,Z.H., Wang,Z.Y., Khush,G.S., Coffman,W.R. and Tanksley,S.D.  
 Molecular mapping of rice chromosomes  
 Theor. Appl. Genet. 76, 815-829 (1988)  
 Contact: Susan R. McCouch  
 Cornell University  
 Dept. Plant Breeding, Ithaca, NY 14853-1901, USA  
 Tel: 607 255 0420  
 Fax: 607 255 6683  
 Email: srm4@cornell.edu  
 For mapping information, additional citations and other related information concerning this probe, please refer to the RiceGenes database at  
 http://ars-genome.cornell.edu/cgi%2Dbin/WebAce/webace?db=ricegenes&class=Marker&object=RG152 DNA Sequencing was done by the DOE Plant Research Lab, Michigan State University. Informatics was done at the Computational Biology Centers, University of Minnesota.

# REFERENCE

AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

# FEATURES

1. .20  
 Location/Qualifiers  
 /organism="Oryza sativa (indica cultivar-group)"  
 /mol\_type="genomic DNA"  
 /cultivar="IR36"  
 /db\_xref="RiceGenes:RG152"  
 /db\_xref="taxon:39946"  
 /clone="RG152"

/clone lib="pUC8 PstI Rice Etiolated Leaf Genomic Library"  
 /note="vector: pUC8; Total leaf DNA was digested with the  
 restriction enzyme PstI. DH5-alpha bacterial cells were  
 then transformed with ligated plasmid. Random genomic  
 clones were given consecutive numbers (RG-#) as they were  
 prepared. The same numbers were then used to designate  
 loci in the genome as detected by genetic mapping."

## ORIGIN

Query Match 61.1%; Score 11.6; DB 9; Length 20;  
 Best Local Similarity 77.8%; Pred. No. 5.4e+05;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 18  
 |||||  
 Db 1 GGGCGACCTGCAGGGAG 18

## RESULT 17

AZ312923/c 25 bp DNA linear GSS 29-SEP-2000  
 LOCUS  
 DEFINITION  
 Clone UUGC1M0029L01 F, genomic survey sequence.

ACCESSION  
 AZ312923  
 VERSION  
 AZ312923.1 GI:10357337  
 GSS.  
 Mus musculus (house mouse)  
 SOURCE  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 25)

AUTHORS  
 Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamil C.,  
 Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T.,  
 Kelly M., Rose M., Rose R., Stokes R., Tingey A., von  
 Niederhausen A., and Wright D., Weiss R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0029 row: L column: 01  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1. .25  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0029L01"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel

## FEATURES

## source

electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 61.1%; Score 11.6; DB 9; Length 25;  
 Best Local Similarity 77.8%; Pred. No. 5.5e+05;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGG 19  
 |||||  
 Db 25 GGGTGACATCCAGAGTG 8

## RESULT 18

AI497442/c 28 bp mRNA linear EST 07-JUN-2001  
 LOCUS  
 DEFINITION  
 Fb53f02.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone  
 IMAGE:3715611 3' similar to SW:COPE\_RAT\_P23514 COATOMER BETA  
 SUBUNIT ;, mRNA sequence.

ACCESSION  
 AI497442  
 VERSION  
 AI497442.1 GI:4398445  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM

Danio rerio (zebrafish)  
 Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.

REFERENCE  
 1 (bases 1 to 28)

AUTHORS  
 Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M.,  
 Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
 Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,  
 Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
 Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

CONTACT: Stephen L. Johnson  
 Washington University School  
 of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:  
 Matthew Clark. DNA Sequencing by: Washington University Genome  
 Sequencing Center Clone Distribution: Genome Systems, St. Louis,  
 Missouri (web address: www.genomesystems.com) (email contact:  
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama  
 (web address: www.resgen.com) (email contact: info@resgen.com) and  
 Resourcenzentrum Primatendatenbank, Berlin, Germany (web address:  
 www.rzpd.de)

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Possible reversed clone: polyT not found

Seq primer: T7 ET from Amersham

High quality sequence stop: 1

POLYA=No.

## FEATURES

## source

Location/Qualifiers  
 1. .28  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:3715611"  
 /sex="mixed"  
 /tissue type="26 somite embryos, adult livers, shield  
 stage embryos"  
 /lab\_host="Xl1-blue MRF"  
 /clone\_lib="Zebrafish WashU MPIMG EST"

/note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'pgactagttctagatcgagcgccgcccctttttttttttt3']; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

## ORIGIN

Query Match 61.1%; Score 11.6; DB 1; Length 28;  
Best Local Similarity 77.8%; Pred. No. 5.5e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 18  
||||| ||| ||| |||  
Db 27 GGGGTGAGTTTGAGTGGG 10

## RESULT 19

CL686485 28 bp DNA linear GSS 09-JUL-2004  
LOCUS PRI0144b.D10.2 - PRI0144b.BR (28) Mixed stage fosmid library of P.  
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.

ACCESSION CL686485 1 GI:50194988  
VERSION CL686485.1  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.

## REFERENCE

AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
TITLE AppADB: an AcedB database for the nematode satellite organism  
Pristionchus pacificus  
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)  
PUBMED 14681447

## COMMENT

Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: raf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

## FEATURES

source  
1..28  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pEpifos-5 Fosmid vector"

## ORIGIN

Query Match 61.1%; Score 11.6; DB 10; Length 28;  
Best Local Similarity 77.8%; Pred. No. 5.5e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGG 19  
||||| ||| ||| ||| |||  
Db 7 GGGTTAGTGTCAGGGGG 24

## RESULT 20

CD029249/c 29 bp mRNA linear EST 07-MAY-2003  
LOCUS mgns012x001f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgns012x001 5', mRNA sequence.

ACCESSION CD029249 1 GI:30410705  
VERSION CD029249.1  
KEYWORDS EST.

## ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)  
Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

## REFERENCE

AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.

TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea

## JOURNAL

COMMENT Unpublished (2002)  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person;  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgns012 row: 0 column: 01  
Seq primer: T3.

## FEATURES

source  
1..29  
Location/Qualifiers  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgns012x001"  
/sex="Mat1-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea NS Uni-Zap XR Library"  
/note="Vector: phluescriptSK-; Site\_1: EcoRI; Site\_2:  
XhoI; Unidirectional cloning. EcoRI site has T3 primer and  
predominantly 5' reads. T7 primer on xhoI side of insert.  
Nitrogen starvation library. Cells were inoculated into  
minimal medium and grown for two days with shaking (150  
rpm) at room temperature. Culture was harvested, blended,  
inoculated into minimal medium as above for 24 h. Cells  
were harvested, washed with water and inoculated into  
minimal medium base lacking nitrogen source for 6 h.  
Sequences were processed by one of two methods. Where a  
full-length alignment to the M. grisea genome sequence was  
available, the EST sequence was trimmed according to the  
alignment, otherwise sequence quality was assessed using  
phredPhrap version 991019 and trimmed according to phd  
files (0.05) and for vector seqs."

## ORIGIN

Query Match 61.1%; Score 11.6; DB 6; Length 29;  
Best Local Similarity 77.8%; Pred. No. 5.6e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGG 19  
||||| ||| ||| ||| |||  
Db 21 GGGTCAGATTTCAGTGGG 4

```

RESULT 21
AZ783946/c
LOCUS          AZ783946          30 bp      DNA          linear      GSS 16-FEB-2001
DEFINITION    ZM0026B08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
               clone UUGC2M0026B08 F, genomic survey sequence.
ACCESSION     AZ783946
VERSION       AZ783946.1  GI:12919186
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 30)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL
COMMENT       Unpublished (2000)
               Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0026 row: B column: 08
               Seq primer: CGTTGTAAACGACGGCCACT
               Class: Plasmid ends
               High quality sequence stop: 30.
FEATURES             source
               1..30
                   Location/Qualifiers
                   /organism="Mus musculus"
                   /mol_type="genomic DNA"
                   /strain="C57BL/6J"
                   /db_xref="taxon:10090"
                   /clone="UUGC2M0026B08"
                   /sex="Male"
                   /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
                   /notes="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adapted DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWP42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adapted mouse DNA was annealed to
               adapted vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
ORIGIN
Query Match          61.1%; Score 11.6; DB 9; Length 30;
Best Local Similarity 77.8%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGG 18
|||||
Db 25 GGGGTGGGTGGAGGGG 8

RESULT 22
AZ759582
LOCUS          BI259582          34 bp      mRNA          linear      EST 17-JUL-2001
DEFINITION    602968347F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108146 5',
               mRNA sequence.
ACCESSION     BI259582
VERSION       BI259582.1  GI:14817058
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE     1 (bases 1 to 34)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/
               National Institutes of Health, Mammalian Gene Collection (MGC)
               Unpublished (1999)
JOURNAL
COMMENT       Contact: Robert Strausberg, Ph.D.
               Email: cgabbs@mail.nih.gov
               Tissue Procurement: ATCC
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: Incyte Genomics, Inc.
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLAM11261 row: m column: 11
               High quality sequence stop: 28.
FEATURES             source
               1..34
                   Location/Qualifiers
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:5108146"
                   /tissue_type="cervical carcinoma cell line"
                   /lab_host="DH10B"
                   /clone_lib="NIH MGC 12"
                   /notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
               Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
               Average insert size 1.4 kb. Library prepared by Life
               Technologies."
ORIGIN
Query Match          61.1%; Score 11.6; DB 2; Length 34;
Best Local Similarity 77.8%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGG 18
|||||
Db 16 GGGCAGCAGCAGCAGGGG 33

RESULT 23
AU263853/c
LOCUS          AU263853          35 bp      mRNA          linear      EST 26-APR-2004
DEFINITION    AU263853 VS Dictyostelium discoideum cDNA clone VSD330 3', mRNA
               sequence.
ACCESSION     AU263853
VERSION       AU263853.1  GI:20522851
KEYWORDS      EST.
SOURCE        Dictyostelium discoideum
ORGANISM      Dictyostelium discoideum
               Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
REFERENCE     1 (bases 1 to 35)
AUTHORS       Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H.,
               Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.
               Analyses of cDNAs from growth and slug stages of Dictyostelium
               discoideum
JOURNAL        Nucleic Acids Res. 32 (5), 1647-1653 (2004)
COMMENT       PUBLISHED
               15010511
               Contact: Hideko Urushihara

```

Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

## FEATURES

location/Qualifiers  
1..35  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clones="VSD330"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

source

## ORIGIN

Query Match 61.1%; Score 11.6; DB 1; Length 35;  
Best Local Similarity 77.8%; Pred. No. 5.6e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGGG 19

Db 18 GGGTTACTTTGGGGGGGG 1

## RESULT 24

AA986717/c

LOCUS

DEFINITION AA986717 37 bp mRNA linear EST 28-MAY-1998  
uc73e01.x1 Sugano mouse liver mlia Mus musculus cDNA clone  
IMAGE:1431288 3' similar to SW:PRP2 MOUSE P05142 PROLINE-RICH  
PROTEIN NP-2 PRECURSOR. ; mRNA sequence.

ACCESSION AA986717

VERSION AA986717.1

KEYWORDS GI:3167719

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Mus.

REFERENCE 1

AUTHORS

(Bases 1 to 37)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Seftoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:915356

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: primer name ambiguous

High quality sequence stop: 1.

location/Qualifiers

1..37

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL"

/db\_xref="taxon:10090"

/clone="IMAGE:1431288"

/sex="female"

/dev\_stage="adult"

/lab\_host="DH10B"

FEATURES source

/clone\_lib="Sugano mouse liver mlia"  
/notes="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII  
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA  
was primed with an oligo(dT) primer  
[ATGTGGCCCTTTTTTTTTTTTTT]; double-stranded cDNA was  
ligated to a DraIII adaptor [TGTGGCTACTGG]; digested  
and cloned into distinct DraIII sites of the pME18S-FL3  
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should  
be used to isolate the cDNA insert. Size selection was  
performed to exclude fragments <1.5kb. Library  
constructed by Dr. Sumio Sugano (University of Tokyo  
Institute of Medical Science). Custom primers for  
sequencing: 5' end primer CTCTGTCTCTAAAGCTGCG and 3' end  
primer CGACCTGCAGCTCGAGACA."

## ORIGIN

Query Match 61.1%; Score 11.6; DB 1; Length 37;  
Best Local Similarity 77.8%; Pred. No. 5.6e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGGG 19

Db 32 GGGTGCCCTTCGGGGGCG 15

## RESULT 25

CF291715/c

LOCUS

DEFINITION CF291715 38 bp mRNA linear EST 14-AUG-2003  
14ROOT-02-E03.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa (japonica cultivar-group) cDNA clone 14ROOT-02-E03, mRNA  
sequence.

ACCESSION CF291715

VERSION CF291715.1

KEYWORDS GI:33660748

SOURCE EST.

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1

AUTHORS

(Bases 1 to 38)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

location/Qualifiers

1..38

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="14ROOT--02-E03"

/tissue\_type="root"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice root plasmid cDNA library (14ROOT)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

## ORIGIN

Query Match 61.1%; Score 11.6; DB 6; Length 38;  
Best Local Similarity 77.8%; Pred. No. 5.6e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGGG 19

|||||

```

Db          32 GGCTGACGGCAGGGGG 15

RESULT 26
LOCUS    BI669410
DEFINITION 41 bp mRNA linear EST 12-SEP-2001
          60329295F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314750 5',
          mRNA sequence.
ACCESSION BI669410
VERSION    BI669410.1 GI:15583643
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominiidae; Homo.
REFERENCE 1 (bases 1 to 41)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabs@email.nih.gov
          Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
          cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
          Toshiyuki and Piero Carninci (RIKEN)
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM11797 row: m column: 23
          High quality sequence stop: 41.
FEATURES   source
           Location/Qualifiers
           1..41
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5314750"
            /tissue_type="hypothalamus"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC_96"
            /notes="Organ: Brain; Vector: pBluescriptR (modified
            pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
            (GTCGAG); Oligo-dT primed using primer
            5'-TTTCTTTTCTTTTCTTWN-3', size-selected for average
            insert size 2.3 kb and normalized to ROT 5. This is a
            primary library enriched for full-length clones and
            constructed using the Cap-trapper method (Carninci, in
            preparation). Library constructed by M. Brownstein
            (NIH/NHGRI, National Institutes of Health). Note: this is
            a NIH_MGC Library."
ORIGIN
Query Match 61.1%; Score 11.6; DB 3; Length 41;
Best Local Similarity 77.8%; Pred. No. 5.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 18
    ||| ||| ||| ||| ||| ||| |||
Db 9 GGGCAGACGACGAGGGGG 26

RESULT 27
LOCUS    AA948503/c
DEFINITION 43 bp mRNA linear EST 23-JUN-1998
          on53c06.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1560394 3',
          similar to SW:2F36_HUMAN P16415 ZINC FINGER PROTEIN ZFP-36 , mRNA
          sequence.
ACCESSION AA948503
VERSION    AA948503.1 GI:3109756
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominiidae; Homo.
REFERENCE 1 (bases 1 to 41)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabs@email.nih.gov
          Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
          cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
          Toshiyuki and Piero Carninci (RIKEN)
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM11797 row: m column: 23
          High quality sequence stop: 41.
FEATURES   source
           Location/Qualifiers
           1..41
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5314750"
            /tissue_type="hypothalamus"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC_96"
            /notes="Organ: Brain; Vector: pBluescriptR (modified
            pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
            (GTCGAG); Oligo-dT primed using primer
            5'-TTTCTTTTCTTTTCTTWN-3', size-selected for average
            insert size 2.3 kb and normalized to ROT 5. This is a
            primary library enriched for full-length clones and
            constructed using the Cap-trapper method (Carninci, in
            preparation). Library constructed by M. Brownstein
            (NIH/NHGRI, National Institutes of Health). Note: this is
            a NIH_MGC Library."
ORIGIN
Query Match 61.1%; Score 11.6; DB 3; Length 41;
Best Local Similarity 77.8%; Pred. No. 5.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 18
    ||| ||| ||| ||| ||| ||| |||
Db 9 GGGCAGACGACGAGGGGG 26

RESULT 28
LOCUS    BX569627
DEFINITION 44 bp mRNA linear EST 14-OCT-2003
          BX569627 Glossina morsitans morsitans adult infected gut Glossina
          morsitans morsitans cDNA clone Tse9f08_q1c, mRNA sequence.
ACCESSION BX569627.1 GI:33437816
VERSION    BX569627.1
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
           Glossina morsitans morsitans
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 44)
AUTHORS   Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
          Hamilton, J., Soares, M.B., Bonaldo, M.F., Lenane, S. and Hall, N.
          Adult midgut expressed sequence tags from the tsetse fly Glossina
          morsitans morsitans and expression analysis of putative immune
          response genes
          Genome Biol. 4 (10), R63 (2003)
JOURNAL    PUBLISHED
LOCUS      14519198
COMMENT    Contact: Hall N

```

```

REFERENCE 1 (bases 1 to 43)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
          Email: cgabs@email.nih.gov
          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 1892 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES   source
           Location/Qualifiers
           1..43
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1560394"
            /tissue_type="adenocarcinoma"
            /lab_host="DH10B"
            /clone_lib="NCI_CGAP_C08"
            /notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
            modified polylinker; 1st strand cDNA was prepared from
            colon adenocarcinoma, and was then primed with a Not I -
            oligo(dT) primer. Double-stranded cDNA was ligated to Eco
            RI adaptors (Pharmacia), digested with Not I and cloned
            into the Not I and Eco RI sites of the modified pT7T3
            vector. Library is normalized. Library was constructed by
            Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 61.1%; Score 11.6; DB 1; Length 43;
Best Local Similarity 77.8%; Pred. No. 5.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGCAGTTTCAGGGGG 19
    ||| ||| ||| ||| ||| ||| |||
Db 38 GGATGACGTTTCATTGTGG 21

RESULT 28
LOCUS    BX569627
DEFINITION 44 bp mRNA linear EST 14-OCT-2003
          BX569627 Glossina morsitans morsitans adult infected gut Glossina
          morsitans morsitans cDNA clone Tse9f08_q1c, mRNA sequence.
ACCESSION BX569627.1 GI:33437816
VERSION    BX569627.1
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
           Glossina morsitans morsitans
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 44)
AUTHORS   Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
          Hamilton, J., Soares, M.B., Bonaldo, M.F., Lenane, S. and Hall, N.
          Adult midgut expressed sequence tags from the tsetse fly Glossina
          morsitans morsitans and expression analysis of putative immune
          response genes
          Genome Biol. 4 (10), R63 (2003)
JOURNAL    PUBLISHED
LOCUS      14519198
COMMENT    Contact: Hall N

```



Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5',  
end of the cDNA all plc reads are from  
the 3' end.

## FEATURES

source  
1. .44  
Location/Qualifiers  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse9f08\_q1c"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T. brucei"

## ORIGIN

Query Match 61.1%; Score 11.6; DB 5; Length 44;  
Best Local Similarity 73.7%; Pred. No. 5.7e+05;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
||||| | |||||  
Db 7 GGGGTGAGNGAGGGGG 25

## RESULT 29

AZ648348 45 bp DNA linear GSS 14-DEC-2000  
LOCUS  
DEFINITION  
1M0517013F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0517013 F, genomic survey sequence.

ACCESSION  
AZ648348  
VERSION  
GSS.  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 45)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0517 row: 0 column: 13  
Seq primer: CGTTGTAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 45.

## FEATURES

source  
1. .45  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"

/db\_xref="taxon:10090"  
/clone="UUGC1M0517013"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (G114732114[GB|AF129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 61.1%; Score 11.6; DB 9; Length 45;  
Best Local Similarity 77.8%; Pred. No. 5.7e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 18  
||||| | |||||  
Db 11 GGGTTGAGGAGCAGGGGG 28

## RESULT 30

BI544737  
LOCUS  
DEFINITION  
603242001F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5284488 5',  
mRNA linear EST 05-SEP-2001  
BI544737  
mRNA sequence.

ACCESSION  
BI544737  
VERSION  
EST.  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 (bases 1 to 47)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Pietro Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM11719 row: a column: 01

High quality sequence stop: 47.

## FEATURES

source  
1. .47  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5284488"  
/tissue\_type="hippocampus"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_95"

/notes="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NTMNH/NHGR1, National Institutes of Health). Note: this is a NIH MGC Library."

## ORIGIN

```
Query Match      61.1%; Score 11.6; DB 3; Length 47;
Best Local Similarity 77.8%; Pred. No. 5.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 1 GGGGTGACGTTTCAGGGG 18  
db 15 GGCACAGCAGCAGGGG 32

RESULT.T 31

**Accession** JF  
**Accession** CX013593/c  
**LOCUS** 47 bp mRNA linear EST 06-DEC-2004  
**DEFINITION** i066806.b1 Whole Heart Library (DOGEST5) Canis familiaris cDNA,  
 mRNA sequence.

## REFERENCE

|           |   |
|-----------|---|
| REFERENCE | Ballal, V.S., Nascimento, L.U. and McCombie, W.R. (1998) <i>CO-41</i> |
| AUTHORS   | Ballal, V.S., Nascimento, L.U. and McCombie, W.R.                     |
| TITLE     | ESTs from <i>Canis familiaris</i> whole heart (dog)                   |
| JOURNAL   | Unpublished (2004)  |
| COMMENT   | Contact: W. Richard McCombie  |

## FEATURES

2015  
2016

```

1. 4)
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/dev_stage="3 month old normal canine"
/lab_host="X110 Gold"
(clone_lib="Whole Heart Library (DOGES)
name="Organ: Heart; Vector: plucscri
EcoRI; Site 2: XhoI; Library construct
XR kit from Stratagene. Cloned cDNA was
between 1-3 kb. Mark Haskins VMD, PhD,
Medical Genetics, School of Veterinary
University of Pennsylvania, 3800 Spruce
Philadelphia, PA 19104-6051."

```

**ORIGIN**

Query Match 61.1%; Score 11.6; DB 8; Length 47;  
Best Local Similarity 77.8%; Pred. No. 5.7e+05;  
Matches 14: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTGACGTCAGGGGG 19  
|||  
Db 47 GGCTGACCTCGAGGGGG 30  
|||

RESULT 32

AA922976/c  
LOCUS AA922976 49 bp mRNA linear EST 21-APR-1998  
DEFINITION OK77606.s1 NCI CGAP Gc4 Homo sapiens cDNA clone IMAGE:152002 3' similar to TR:Q39614 Q39614 PROLINE-RICH PROTEIN.; mRNA sequence.  
ACCESSION AA922976  
VERSION AA922976.1 GI:3070285  
KEYWORDS EST.

REFERENCE  
1 (bases 1 to 49)  
AUTHORS  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ccgap>.

cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbr/image/image.html](http://www-bio.llnl.gov/bbr/image/image.html)

Trace considered overall poor quality

ET from Amersham

High quality sequence stop: 1.

## FEATURES

source

```

1. 49
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="IMAGE:1520002"
   /tissue_type="pooled germ cell tumors"
   /lab_host="DH10B"
   /clone.lib="NCI CGAP GC4"
   /note="(vector: pT7TG3-Pac (Pharmacia)
polylinker; 1st strand cDNA was prepared
germ cell tumors, and was then primed
oligo(dT) primer. Double-stranded cDNA
RI adaptors (Pharmacia), digested with
into the Not I and Eco RI sites of the
vector. Library is normalized. Library
Rento Soares and M.Patima Bonaldo."

```

ORIGIN

Query Match 61.1%; Score 11.6; DB 1; Length 49;  
Best Local Similarity 77.8%; Pred. No. 5.7e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Q17 2 CCGTCA CATT CAGGGGG 19

RESULT 33

Accession BE615718/c  
Locus BE615718  
Definition 601279832F1 NIH MGC\_39 Homo sapiens CDNA clone IMAGE:3622110 5', mRNA sequence.  
Length 49 bp  
Library linear  
EST 24-AUG-2000

## REFERENCE

to 49)

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Straubeberg, Ph.D.  
 Email: csapbs-remail.nih.gov  
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM296 row: o column: 07.

#### FEATURES

Location/Qualifiers

1. .49

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3622110"  
 /tissue\_type="adenocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_39"  
 /note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed  
 by Ling Hong in the laboratory of Gerald M. Rubin  
 (University of California, Berkeley) using ZAP-cDNA  
 synthesis kit (Stratagene) and Superscript II RT (Life  
 Technologies)."

#### ORIGIN

Query Match 61.1%; Score 11.6; DB 2; Length 49;  
 Best Local Similarity 77.8%; Pred. No. 5.7e+05;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGG 19

Db 19 GGGTGACGCGGTTCGGGG 2

RESULT 34  
 AUI02320  
 LOCUS  
 DEFINITION AUI02320 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 ADSE01801, mRNA sequence.  
 AUI02320  
 ACCESSION  
 VERSION  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)  
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 ENBO Rep. 2 (5), 388-393 (2001)  
 11375929

COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

#### FEATURES

Location/Qualifiers

1. .50

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="ADSE01801"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

#### ORIGIN

Query Match 61.1%; Score 11.6; DB 1; Length 50;  
 Best Local Similarity 77.8%; Pred. No. 5.7e+05;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGG 19

Db 13 GCGGGACGCGTTCAGGGGAG 30

#### RESULT 35

AG204798/c

LOCUS

DEFINITION AG204798 Pan troglodytes DNA, clone: RP43-090K13.T7, genomic survey  
 sequence.

ACCESSION AG204798

VERSION AG204798.1 GI:45236973

KEYWORDS

SOURCE

ORGANISM

Pan troglodytes (chimpanzee)  
 Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Pan.

REFERENCE 1

AUTHORS

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
 BAC end sequences of Library RP-43

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 35)

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,  
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
 Direct Submission

TITLE

JOURNAL

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of  
 Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);  
 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea  
 (E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/,  
 Tel: 82-42-886-7181, Fax: 82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC  
 end was generated during the R&D process and may have higher chance  
 of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI.

Location/Qualifiers

1. .35

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="RP43-090K13.T7"

/sex="male"

/cell\_type="lymphocytes"

/clone\_lib="RP-43 Chimpanzee Male BAC Library"

#### ORIGIN

Query Match 60.0%; Score 11.4; DB 10; Length 35;  
 Best Local Similarity 92.3%; Pred. No. 7e+05;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GTGACGTTTCAGGG 16

Db 35 GTGATGTTTCAGGG 23

#### RESULT 36

```

CV933742/c
LOCUS      CV933742          36 bp      mRNA      linear      EST 25-JAN-2005
DEFINITION PM9cm_4081 mating of 88069 (A1) and 618 (A2) Phytophthora
            infestans cDNA, mRNA sequence.
ACCESSION  CV933742
VERSION     CV933742.1 GI:58123357
KEYWORDS    EST.
SOURCE      Phytophthora infestans (potato late blight agent)
ORGANISM    Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1 (bases 1 to 36)
AUTHORS     Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
            Keikar,H., Fong,A.M., Gates,K., Roberts,S., Yatskan,E., Gaffney,T.,
            Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,B.,
            Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
            Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
            Lam,S.T. and Judelson, H.S.
TITLE       Large-scale gene discovery in the oomycete Phytophthora infestans
            reveals likely components of phytopathogenicity shared with true
            fungi
JOURNAL     Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED     15782637
COMMENT     Contact: Judelson HS
            Department of Plant Pathology
            University of California
            Webber Hall, Riverside, CA 92521, USA
            Tel: 909 787 4199
            Fax: 909 787 4294
            Email: howard.judelson@ucr.edu.
FEATURES   Location/Qualifiers
            1..36
            /organism="Phytophthora infestans"
            /mol_type="mRNA"
            /strain="88069 and 618"
            /db_xref="taxon:4787"
            /sex="A1 and A2"
            /clone_lib="mating of 88069 (A1) and 618 (A2)"
            /note="Vector: pSPORT1"
ORIGIN
Query Match      60.0%; Score 11.4; DB 8; Length 36;
Best Local Similarity 92.3%; Pred. No. 7e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGGTGACGTTTCAG 14
        ||| |||||
Db      28 GGGCGACGTTTCAG 16

RESULT 37
AZ340800
LOCUS      AZ340800          22 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION IM0072G21R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
            clone UUCG1M0072G21 R, genomic survey sequence.
ACCESSION  AZ340800
VERSION     AZ340800.1 GI:10416416
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,S., Pedersen,T.,
            Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
CV933742
LOCUS      CV933742          36 bp      mRNA      linear      EST 25-JAN-2005
DEFINITION PM9cm_4081 mating of 88069 (A1) and 618 (A2) Phytophthora
            infestans cDNA, mRNA sequence.
ACCESSION  CV933742
VERSION     CV933742.1 GI:58123357
KEYWORDS    EST.
SOURCE      Phytophthora infestans (potato late blight agent)
ORGANISM    Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1 (bases 1 to 36)
AUTHORS     Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
            Keikar,H., Fong,A.M., Gates,K., Roberts,S., Yatskan,E., Gaffney,T.,
            Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,B.,
            Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
            Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
            Lam,S.T. and Judelson, H.S.
TITLE       Large-scale gene discovery in the oomycete Phytophthora infestans
            reveals likely components of phytopathogenicity shared with true
            fungi
JOURNAL     Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED     15782637
COMMENT     Contact: Judelson HS
            Department of Plant Pathology
            University of California
            Webber Hall, Riverside, CA 92521, USA
            Tel: 909 787 4199
            Fax: 909 787 4294
            Email: howard.judelson@ucr.edu.
FEATURES   Location/Qualifiers
            1..36
            /organism="Phytophthora infestans"
            /mol_type="mRNA"
            /strain="88069 and 618"
            /db_xref="taxon:4787"
            /sex="A1 and A2"
            /clone_lib="mating of 88069 (A1) and 618 (A2)"
            /note="Vector: pSPORT1"
ORIGIN
Query Match      60.0%; Score 11.4; DB 8; Length 36;
Best Local Similarity 92.3%; Pred. No. 7e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGGTGACGTTTCAG 14
        ||| |||||
Db      28 GGGCGACGTTTCAG 16

RESULT 37
AZ340800
LOCUS      AZ340800          22 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION IM0072G21R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
            clone UUCG1M0072G21 R, genomic survey sequence.
ACCESSION  AZ340800
VERSION     AZ340800.1 GI:10416416
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,S., Pedersen,T.,
            Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
CV933742/c
LOCUS      CV933742          36 bp      mRNA      linear      EST 25-JAN-2005
DEFINITION PM9cm_4081 mating of 88069 (A1) and 618 (A2) Phytophthora
            infestans cDNA, mRNA sequence.
ACCESSION  CV933742
VERSION     CV933742.1 GI:58123357
KEYWORDS    EST.
SOURCE      Phytophthora infestans (potato late blight agent)
ORGANISM    Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1 (bases 1 to 36)
AUTHORS     Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
            Keikar,H., Fong,A.M., Gates,K., Roberts,S., Yatskan,E., Gaffney,T.,
            Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,B.,
            Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
            Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
            Lam,S.T. and Judelson, H.S.
TITLE       Large-scale gene discovery in the oomycete Phytophthora infestans
            reveals likely components of phytopathogenicity shared with true
            fungi
JOURNAL     Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED     15782637
COMMENT     Contact: Judelson HS
            Department of Plant Pathology
            University of California
            Webber Hall, Riverside, CA 92521, USA
            Tel: 909 787 4199
            Fax: 909 787 4294
            Email: howard.judelson@ucr.edu.
FEATURES   Location/Qualifiers
            1..36
            /organism="Phytophthora infestans"
            /mol_type="mRNA"
            /strain="88069 and 618"
            /db_xref="taxon:4787"
            /sex="A1 and A2"
            /clone_lib="mating of 88069 (A1) and 618 (A2)"
            /note="Vector: pSPORT1"
ORIGIN
Query Match      60.0%; Score 11.4; DB 8; Length 36;
Best Local Similarity 92.3%; Pred. No. 7e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGGTGACGTTTCAG 14
        ||| |||||
Db      28 GGGCGACGTTTCAG 16

RESULT 37
AZ340800
LOCUS      AZ340800          22 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION IM0072G21R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
            clone UUCG1M0072G21 R, genomic survey sequence.
ACCESSION  AZ340800
VERSION     AZ340800.1 GI:10416416
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,S., Pedersen,T.,
            Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center

```

```

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: G column: 21
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0072G21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match      58.9%; Score 11.2; DB 9; Length 22;
Best Local Similarity 81.2%; Pred. NO. 8.6e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGGTGACGTTTCAGG 16
        ||| |||||
Db      1 GGGCTGACITTCATGG 16

RESULT 38
TA246H09Q
LOCUS      TA246H09Q          29 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 246h09, reverse sequence,
            genomic survey sequence.
ACCESSION  AL488820
VERSION     AL488820.1 GI:11864016
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
ORGANISM    Trypanosoma brucei
            Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 29)
AUTHORS     Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE       Direct Submission
JOURNAL     Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambsanger CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),

```

Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrall, Oxford University Press, 1999).

Email: nelsaye@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

#### FEATURES

Location/Qualifiers  
1..29  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="246H09"

#### ORIGIN

Query Match 58.9%; Score 11.2; DB 11; Length 29;  
Best Local Similarity 81.2%; Pred. No. 8.7e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GTGACGTTTCAGGGGG 19  
||||| ||||| |||||  
Db 9 GTGAAC TTCAGGGGG 24

#### RESULT 39

AZ483233 30 bp DNA linear GSS 05-OCT-2000  
LOCUS  
DEFINITION  
clone UUGC1M0308H16 R, genomic survey sequence.

ACCESSION  
AZ483233  
VERSION  
GI:10647043  
KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

#### ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE

AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

#### JOURNAL

COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0308 row: H column: 16  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 30.

#### FEATURES

Location/Qualifiers  
1..30  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0308H16"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 58.9%; Score 11.2; DB 9; Length 30;  
Best Local Similarity 81.2%; Pred. No. 8.7e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGGG 17  
||||| ||||| |||||  
Db 14 GGGTGATATTCATGGG 29

#### RESULT 40

CL684027 30 bp DNA linear GSS 09-JUL-2004  
LOCUS  
DEFINITION  
PRI0138b H10 2 - PRI0138b.BR (30) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION  
CL684027  
VERSION  
GI:50191937  
KEYWORDS  
GSS.

#### SOURCE

ORGANISM  
Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.

#### REFERENCE

AUTHORS  
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

TITLE  
AppaDB: an AcedB database for the nematode satellite organism

JOURNAL  
Nucleic Acids Res. 32 (1), D421-D422 (2004)

#### PUBMED

14681447

#### COMMENT

Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

#### FEATURES

Location/Qualifiers  
1..30  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
/notes="Vector: pEpifos-5 Fosmid vector"

#### ORIGIN

Query Match 58.9%; Score 11.2; DB 10; Length 30;  
Best Local Similarity 81.2%; Pred. No. 8.7e+05;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GTGACGTTTCAGGGGG 19  
||||| ||| |||||  
Db 10 GTGAAGTTTGGGGGG 25

RESULT 41  
CZ474868/c  
LOCUS  
DEFINITION  
melanogaster genomic sequence recovered from 5' end of P element,  
genomic survey sequence.

ACCESSION CZ474868 33 bp DNA linear GSS 29-APR-2005  
VERSION d06009-Sprime Exelixis P element XP insertions Drosophila  
KEYWORDS melanogaster genomic sequence recovered from 5' end of P element,  
SOURCE GSS.  
ORGANISM Drosophila melanogaster (fruit fly)

REFERENCE 1 (bases 1 to 33)  
AUTHORS Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,  
Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,  
Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,  
Greer,K., Hartouni,S.R., Howie,E., Jatkula,L., Joo,D., Killpack,K.,  
Laufer,A., Mazrotta,R., Smith,R.D., Stevens,L.M., Stuber,C.,  
Tan,L.R., Ventura,K., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,  
Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.  
TITLE A complementary transposon tool kit for Drosophila melanogaster  
using P and piggyBac

JOURNAL Nat. Genet. 36 (3), 283-287 (2004)  
PUBMED 14981521  
COMMENT Contact: Roger A Hoskins  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory  
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA  
Tel: 510 486 4015  
Fax: 510 486 6798  
Email: Rhoskins@lbl.gov  
Sequence recovery method was inverse PCR.  
Sequence orientation is forward strand relative to 5' end of P  
element.  
The P element insertion position is 26 in the 33 bases. This  
insertion position refers to the first base of the 8 base target  
recognition sequence.  
Class: transposon insertion site.

FEATURES  
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Location/Qualifiers  
1..33  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/strain="isogenic w- strain"  
/db\_xref="taxon:7227"  
/clone\_lib="Exelixis P element XP insertions"  
/notes="Vector: P element XP (GenBank accession number  
AY15149). An isogenic w- Drosophila melanogaster strain  
was mutagenized by remobilization of transposable  
elements. For the P element XP, we selected an easily  
mobilized ammunition element among inserts hopped onto the  
Biosyncy balancer. New insertions were collected in vials  
from dysgenic females using the standard chromosomal  
source of transposase, delta2-3. All lines were mapped to  
a chromosome by standard genetic methods, examined for  
homologous viability and used for recovery of flanking  
genomic sequence by inverse PCR."

ORIGIN  
Query Match 58.9%; Score 11.2; DB 10; Length 33;  
Best Local Similarity 81.2%; Pred. No. 8.8e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18  
||| ||| ||| |||||

Db 31 GGGGACCTTCTGGGGG 16

RESULT 42  
CZ294988  
LOCUS  
DEFINITION  
M090F07 GGTC Gene Trap Library GV18C05 Mus musculus cDNA clone  
M090F07, mRNA sequence.

ACCESSION CZ294988 36 bp mRNA linear GSS 22-MAR-2005  
VERSION CZ294988.1 GI:61682738  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 36)  
AUTHORS Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,  
Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.  
TITLE A large-scale, gene-driven mutagenesis approach for the functional  
analysis of the mouse genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
PUBMED 12904583  
COMMENT Contact: GGTC  
German Genetrap Consortium (GGTC)  
Email: info@genetrap.de  
FlipR0SACeoc+2 gene trap. Sequence tag generated by 5'RACE.  
Additional sequence information can be found at:  
'http://genetrap.gsf.de/project/web/new/database/result\_clone.html?  
clone\_id=M090F07'. ES cell line harboring insertion mutation of  
target gene is available at:  
'http://genetrap.gsf.de/project/web/new/order\_clones/howtoorder.htm  
1' Inhouse Sequence identifier: 18342  
Class: Gene Trap.

FEATURES  
source  
Location/Qualifiers  
1..36  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 Sv"  
/db\_xref="taxon:10090"  
/clone="M090F07"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/cell\_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"  
/clone\_lib="GGTC Gene Trap Library GV18C05"  
/note="Vector: FlipR0SACeoc+2"

ORIGIN  
Query Match 58.9%; Score 11.2; DB 10; Length 36;  
Best Local Similarity 68.4%; Pred. No. 8.8e+05;  
Matches 13; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
||||| ||| |||  
Db 4 GGGGTGCGCTCCTNNNGAGG 22

RESULT 43  
AI696220/c  
LOCUS  
DEFINITION  
tt15d10.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2240851 3',  
similar to TR:Q12799 Q12799 T-COMPLEX PROTEIN 10A. ;, mRNA  
sequence.

ACCESSION AI696220 37 bp mRNA linear EST 03-JUN-1999  
VERSION AI696220.1 GI:4984120  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 37)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarctontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
**JOURNAL** Tumor Gene Index  
**COMMENT** Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

# FEATURES

source  
 1. .37  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2240851"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DHI0B"  
 /clone\_lib="NCI\_CGAP GC6"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not 1; Site 2: Eco RI; plasmid DNA  
 from the normalized library NCI\_CGAP GC4 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneIDs  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

# ORIGIN

Query Match 58.9%; Score 11.2; DB 1; Length 37;  
 Best Local Similarity 81.2%; Pred. No. 8.8e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGG 16  
 |||||  
 Db 21 GGGCTGATGTTTCATGG 6

RESULT 44  
 C2294761  
 LOCUS 39 bp mRNA linear GSS 22-MAR-2005  
 DEFINITION M093F02 GGTC Gene Trap Library GV14C05 Mus musculus cDNA clone  
 M093F02, mRNA sequence.  
 C2294761  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)

REFERENCE  
 AUTHORS  
 Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,  
 Arnold, H.H., Schmutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.

TITLE A large-scale, gene-driven mutagenesis approach for the functional  
 analysis of the mouse genome  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
 PUBMED 12904583  
 COMMENT Contact: GGTC  
 German Genetrap Consortium (GGTC)  
 Email: info@genetrap.de  
 FlipROSAceC-2 gene trap. Sequence tag generated by 5'RACE.  
 Additional sequence information can be found at:  
 'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=M093F02'. ES cell line harboring insertion mutation of  
 target gene is available at:

'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm  
 1' Inhouse Sequence Identifier: 18341  
 Class: Gene Trap.

# FEATURES

source  
 1. .39  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Sv"  
 /db\_xref="taxon:10090"  
 /clone="M093F02"  
 /sex="Male"  
 /cell\_type="Embryonic stem cell"  
 /cell\_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"  
 /clone\_lib="GGTC Gene Trap Library GV14C05"  
 /note="Vector: FlipROSAceC-2"

# ORIGIN

Query Match 58.9%; Score 11.2; DB 10; Length 39;  
 Best Local Similarity 68.4%; Pred. No. 8.9e+05;  
 Matches 13; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGGG 19  
 |||||  
 Db 4 GGGGTGCCGTCTNNMGAGGG 22

# RESULT 45

R87616  
 LOCUS 40 bp mRNA linear EST 16-AUG-1995  
 DEFINITION YN91902.r1 Soares adult brain N2b4H855Y Homo sapiens cDNA clone  
 IMAGE:166322 5; similar to SP:S27887 S27887 NEUREXIN II-ALPHA  
 PRECURSOR -, mRNA sequence.

ACCESSION R87616  
 VERSION R87616.1 GI:946429  
 EST.  
 KEYWORDS  
 SOURCE Homo sapiens (human)

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

# REFERENCE

AUTHORS  
 1 (bases 1 to 40)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

# TITLE

JOURNAL The Washu-Merck EST Project  
 COMMENT Unpublished (1995)  
 Contact: Wilton RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 2019

High quality sequence starts: 1 High quality sequence stops: 1  
 Source: IMAGE Consortium, LLNL This clone is available royalty-free  
 through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)  
 for further information. Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Insert Length: 2019 Std Error: 0.00  
 Seq primer: M13RP1  
 High quality sequence stop: 1.

# FEATURES

source  
 1. .40  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:587017"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:166322"  
 /sex="Male"  
 /dev\_stage="55-year old"  
 /lab\_host="DHI0B (ampicillin resistant)"

/clone lib="Soares adult brain N2b4HB55v"  
 /note="Organ: brain; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

## ORIGIN

Query Match 58.9%; Score 11.2; DB 8; Length 40;  
 Best Local Similarity 81.2%; Pred. No. 8.9e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCTGAGGTTTCAGGGG 17  
 ||||| ||||| |||||

Db 10 GGCTGAGGCTCAGGGG 25

## RESULT 46

EX128210/c 41 bp DNA linear GSS 28-JAN-2003  
 LOCUS  
 DEFINITION Danio rerio genomic clone DKEY-279M17, genomic survey sequence.  
 ACCESSION EX128210  
 VERSION EX128210.1 GI:27959164  
 KEYWORDS GSS.

SOURCE Danio rerio (zebrafish)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 41)  
 Humphray,S.J., Huckle,E. and Durham,J.L.

AUTHORS Direct Submission  
 TITLE Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Unpublished

JOURNAL This sequence was generated from the SP6 end of BAC 279M17. 279M17 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:  
 http://www.sanger.ac.uk/projects/D\_rerio/.

## FEATURES

source  
 1..41  
 Location/Qualifiers  
 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKEY-279M17"  
 /tissue\_type="Testis"  
 /note="vector pindigoBAC-536"

## ORIGIN

Query Match 58.9%; Score 11.2; DB 10; Length 41;  
 Best Local Similarity 81.2%; Pred. No. 8.9e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GTGACGTTTCAGGGGG 19  
 ||||| ||||| |||||

Db 19 GTGTCGGTCGGGGGG 4

## RESULT 47

W34290/c

## LOCUS

DEFINITION

W34290 46 bp mRNA linear EST 12-SEP-1996  
 IMAGE007.r1 Soares mouse p3NNF19.5 Mus musculus cDNA clone  
 IMAGE:318828.5' similar to SW:GBG3 BOVIN P29798 GUANINE  
 NUCLEOTIDE-BINDING PROTEIN G(1)/G(3)/G(O) GAMMA-3 SUBUNIT. [1] ;  
 mRNA sequence.

## ACCESSION

W34290

## VERSION

W34290.1 GI:1316200

## KEYWORDS

EST.

## SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 46)

AUTHORS

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.

TITLE The WashU-HHMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:209444

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 1.

FEATURES

source

1..46

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:318828"

/dev\_stage="19.5 dpc total fetus"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares mouse p3NNF19.5"

/notes="Vector: pT7T3D (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5',

TGTTACCAATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. RNA was kindly provided by

Dr. Minoru Ko (Wayne State University)."

ORIGIN

Query Match 58.9%; Score 11.2; DB 8; Length 46;

Best Local Similarity 81.2%; Pred. No. 8.9e+05;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GTGACGTTTCAGGGGG 19  
 ||||| ||||| |||||

Db 21 GTGATGTTAACGGGGG 6

RESULT 48

BH802996/c

LOCUS

DEFINITION

ACCESION

VERSION

BH802996

BH802996.1 GI:20317698

48 bp DNA linear GSS 25-APR-2002  
 1008098B12.2EL.y1 1008 - RescueMu Grid I Zea mays genomic, genomic  
 survey sequence.



```

KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008098 row: 14
Class: transposon-tagged.
Location/Qualifiers
FEATURES
source
1..48
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmdb.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN
Query Match 58.9%; Score 11.2; DB 9; Length 48;
Best Local Similarity 81.2%; Pred. No. 9e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTGACGTTTCAGGGGG 18
||||| ||| |||
Db 29 GGTGACGTTCCGGGG 14

RESULT 49
CG732711 119150E01.1EL_xl 1119 - RescueMu Grid AA Zea mays genomic, genomic
LOCUS CG732711 49 bp DNA linear GSS 20-OCT-2003
DEFINITION survey sequence.
ACCESSION CG732711.1 GI:37775203
VERSION CG732711.1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 49)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences

Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 119150 row: 46
Class: transposon-tagged.
Location/Qualifiers
FEATURES
source
1..49
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match 58.9%; Score 11.2; DB 10; Length 49;
Best Local Similarity 81.2%; Pred. No. 9e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTGACGTTTCAGGGGG 18
||||| ||| |||
Db 20 GGTGACGTTGAGCTGG 35

RESULT 50
CC458057 115432.18.90.x Arabidopsis thaliana TDNA insertion lines
LOCUS CC458057 50 bp DNA linear GSS 30-MAY-2003
DEFINITION Arabidopsis thaliana genomic clone SALK_115432.18.90.x, genomic
survey sequence.
ACCESSION CC458057.1 GI:31221297
VERSION CC458057.1
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 50)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 3' end of
At5g05810.

```

Class: TDNA tagged.

FEATURES  
source  
1..50  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_115432.18.90.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN

Query Match 58.9%; Score 11.2; DB 9; Length 50;  
Best Local Similarity 81.2%; Pred. No. 9e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGG 16  
||| ||| ||| |||  
Db 29 GGGGAGATGTTAAGG 44

Search completed: February 15, 2006, 21:10:07  
Job time : 1283.74 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:56:18 ; Search time 42.7107 Seconds  
(without alignments)  
790.754 Million cell updates/sec

Title: US-09-669-187A-80  
Perfect score: 19  
Sequence: 1 ggggtgacgttcagggggg 19  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/ina/1 COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/PCRU COMB.seq:\*

7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*

8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*

9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description           |
|------------|-------|-------------|--------|----|-----------------------|
| 1          | 14.2  | 74.7        | 20     | 3  | US-08-386-063-1       |
| 2          | 14.2  | 74.7        | 20     | 3  | US-08-386-063-1       |
| 3          | 14.2  | 74.7        | 20     | 3  | US-09-082-649B-63     |
| 4          | 14.2  | 74.7        | 20     | 3  | US-09-965-101-63      |
| 5          | 14    | 73.7        | 39     | 3  | US-09-388-873-18      |
| 6          | 14    | 73.7        | 39     | 3  | US-10-282-935-18      |
| 7          | 13.4  | 70.5        | 22     | 3  | US-08-852-001-5       |
| 8          | 13.2  | 69.5        | 50     | 3  | US-10-131-827-3663    |
| 9          | 12.8  | 67.4        | 20     | 3  | US-08-666-221B-29     |
| 10         | 12.8  | 67.4        | 25     | 3  | US-09-396-196G-120261 |
| 11         | 12.8  | 67.4        | 32     | 2  | US-07-951-715A-43     |
| 12         | 12.8  | 67.4        | 32     | 2  | US-08-459-448A-43     |
| 13         | 12.8  | 67.4        | 32     | 3  | US-08-459-595A-43     |
| 14         | 12.8  | 67.4        | 32     | 3  | US-08-459-504B-43     |
| 15         | 12.8  | 67.4        | 32     | 3  | US-08-459-444-43      |
| 16         | 12.8  | 67.4        | 32     | 3  | US-09-547-422-43      |
| 17         | 12.8  | 67.4        | 32     | 3  | US-09-988-462-43      |
| 18         | 12.8  | 67.4        | 50     | 3  | US-10-131-827-4733    |
| 19         | 12.6  | 66.3        | 19     | 3  | US-09-672-126B-27     |
| 20         | 12.6  | 66.3        | 20     | 3  | US-08-738-652-12      |
| 21         | 12.6  | 66.3        | 20     | 3  | US-09-030-701-63      |
| 22         | 12.6  | 66.3        | 20     | 3  | US-08-960-774-90      |
| 23         | 12.6  | 66.3        | 20     | 3  | US-09-082-649B-52     |
| 24         | 12.6  | 66.3        | 20     | 3  | US-09-082-649B-59     |

|     |      |      |    |   |                       |                     |       |      |      |    |   |                       |                     |
|-----|------|------|----|---|-----------------------|---------------------|-------|------|------|----|---|-----------------------|---------------------|
| 98  | 11.6 | 61.1 | 26 | 2 | US-08-153-051B-33     | Sequence 33, Appl   | 171   | 11.2 | 58.9 | 25 | 3 | US-09-396-196G-104710 | Sequence 104710,    |
| 99  | 11.6 | 61.1 | 26 | 2 | US-08-060-952C-23     | Sequence 23, Appl   | C 172 | 11.2 | 58.9 | 25 | 3 | US-09-396-196G-112559 | Sequence 112559,    |
| 100 | 11.6 | 61.1 | 26 | 2 | US-08-151-477A-33     | Sequence 33, Appl   | C 173 | 11.2 | 58.9 | 25 | 3 | US-09-396-196G-112560 | Sequence 112560,    |
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| 103 | 11.6 | 61.1 | 26 | 3 | US-09-378-535-11      | Sequence 11, Appl   | C 176 | 11.2 | 58.9 | 25 | 3 | US-09-396-196G-123561 | Sequence 123561,    |
| 104 | 11.6 | 61.1 | 26 | 3 | US-09-311-784A-94     | Sequence 94, Appl   | C 177 | 11.2 | 58.9 | 26 | 3 | US-09-023-082A-108    | Sequence 108, Appl  |
| 105 | 11.6 | 61.1 | 27 | 3 | US-09-631-863A-37     | Sequence 37, Appl   | C 178 | 11.2 | 58.9 | 26 | 3 | US-09-393-554-15      | Sequence 15, Appl   |
| 106 | 11.6 | 61.1 | 28 | 3 | US-09-246-277A-6      | Sequence 6, Appl    | C 179 | 11.2 | 58.9 | 26 | 3 | US-09-218-444-29      | Sequence 29, Appl   |
| 107 | 11.6 | 61.1 | 30 | 3 | US-08-641-294-5       | Sequence 5, Appl    | C 180 | 11.2 | 58.9 | 26 | 3 | US-09-248-998-108     | Sequence 108, Appl  |
| 108 | 11.6 | 61.1 | 31 | 3 | US-09-180-109A-51     | Sequence 51, Appl   | C 181 | 11.2 | 58.9 | 26 | 3 | US-09-853-666-29      | Sequence 29, Appl   |
| 109 | 11.6 | 61.1 | 33 | 3 | US-09-170-496D-135    | Sequence 135, Appl  | C 182 | 11.2 | 58.9 | 26 | 3 | US-09-610-651-108     | Sequence 108, Appl  |
| 110 | 11.6 | 61.1 | 36 | 2 | US-08-600-783-29      | Sequence 29, Appl   | C 183 | 11.2 | 58.9 | 26 | 3 | US-09-345-373-108     | Sequence 108, Appl  |
| 111 | 11.6 | 61.1 | 36 | 2 | US-08-600-783-31      | Sequence 31, Appl   | C 184 | 11.2 | 58.9 | 26 | 3 | US-10-075-446-108     | Sequence 108, Appl  |
| 112 | 11.6 | 61.1 | 36 | 2 | US-08-600-783-33      | Sequence 33, Appl   | C 185 | 11.2 | 58.9 | 27 | 3 | US-09-688-017-342     | Sequence 342, Appl  |
| 113 | 11.6 | 61.1 | 36 | 2 | US-09-641-638-1260    | Sequence 1260, Appl | C 186 | 11.2 | 58.9 | 30 | 3 | US-08-567-200A-35     | Sequence 35, Appl   |
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| 115 | 11.6 | 61.1 | 47 | 3 | US-09-422-978-2213    | Sequence 2213, Appl | C 188 | 11.2 | 58.9 | 30 | 6 | PCT-US92-10792-29     | Sequence 29, Appl   |
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| 120 | 11.4 | 60.0 | 22 | 2 | US-08-410-779B-74     | Sequence 74, Appl   | C 193 | 11.2 | 58.9 | 45 | 3 | US-09-543-004-8       | Sequence 8, Appl    |
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ALIGNMENTS

RESULT 1
US-08-386-063-1
; Sequence 1, Application US/08386063
; Patent No. 6194388
; GENERAL INFORMATION:
; APPLICANT: Arthur M. Krieg, M.D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,063
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ARNOLD, BETH E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIZ-013CP
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid

Query Match 74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTGAGGGGG 19
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Db 2 GGGTCAACGTTGAGGGGG 20
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RESULT 2
US-08-386-063-1
; Sequence 1, Application US/08386063
; Patent No. 6194388
; GENERAL INFORMATION:
; APPLICANT: Arthur M. Krieg, M.D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,063
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ARNOLD, BETH E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIZ-013CP
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid

; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,063
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ARNOLD, BETH E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIZ-013CP
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-386-063-1

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RESULT 3
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; Sequence 63, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Kries, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
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; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
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; OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-63

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RESULT 4
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; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Kries, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-63

Query Match      74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
    ||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 5
US-09-538-873-18/c
; Sequence 18, Application US/09538873
; Patent No. 6566500
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
; TITLE OF INVENTION: SYNDROME (VLS)
; FILE REFERENCE: UTSD:603
; CURRENT APPLICATION NUMBER: US/09/538,873
; CURRENT FILING DATE: 2000-03-30
; EARLIER APPLICATION NUMBER: 60/126,826
; EARLIER FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-538-873-18

Query Match      73.7%; Score 14; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGG 16
    ||| ||||| |||||
Db 26 GGTGACGTTTCAGGG 13

RESULT 6
US-10-282-935-18/c
; Sequence 18, Application US/10282935
; Patent No. 6960652
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
; FILE REFERENCE: UTSD:884US
; CURRENT APPLICATION NUMBER: US/10/282,935
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 18  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
US-10-282-935-18

Query Match 73.7%; Score 14; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGTGACGTCAGG 16  
| | | | | | | | | | | | | | | | | |  
Db 26 GGTGACGTCAGG 13

RESULT 7  
US-08-852-001-5  
; Sequence 5, Application US/08852001  
; Patent No. 6197556  
; GENERAL INFORMATION:  
; APPLICANT: Ulanovsky, Levy  
; APPLICANT: Mugasinigalam, Raja C.  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION USING MODULAR  
; TITLE OF INVENTION: BRANCHED PRIMERS  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BRINKS, HOFER, GILSON & LIONE  
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60611-5599

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/852,001  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Martin, Alice O.  
; REGISTRATION NUMBER: 35,601  
; REFERENCE/DOCKET NUMBER: 6837/7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-321-4200  
; TELEFAX: 312-321-4299  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "primer"  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 18..19  
; OTHER INFORMATION: /product= "N = inosine"  
US-08-852-001-5

Query Match 70.5%; Score 13.4; DB 3; Length 22;  
Best Local Similarity 93.3%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TGACGTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |  
Db 2 TGACGTCAGGGGTG 16

RESULT 8  
US-10-131-827-3663  
; Sequence 3663, Application US/10131827  
; Patent No. 6905827  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Lv, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3663  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-3663

Query Match 69.5%; Score 13.2; DB 3; Length 50;  
Best Local Similarity 83.3%; Pred. No. 2.4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTCAGGGG 18  
| | | | | | | | | | | | | | | | | |  
Db 1 GCGTGCCGTTGAGGGG 18

RESULT 9  
US-08-666-221B-29/c  
; Sequence 29, Application US/08666221B  
; Patent No. 6136544  
; GENERAL INFORMATION:  
; APPLICANT: Kamboj, Rajender  
; APPLICANT: Nutt, Stephen  
; TITLE OF INVENTION: GLUTAMATE RECEPTOR (OR EAA RECEPTOR)  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/666,221B  
; FILING DATE: 20-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 016777/0308  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399

```
;
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
;
US-08-666-221B-29
;
;
; Query Match
; Best Local Similarity 67.4%; Score 12.8; DB 3; Length 20;
; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
;
; QY 2 GGGTGACGTTTCAGGGG 17
; Db 16 GGGTGATGTCAGGGG 1
;
;
; RESULT 10
; US-09-396-196G-120261/c
; Sequence 120261, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120261
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
;
US-09-396-196G-120261
;
;
; Query Match
; Best Local Similarity 67.4%; Score 12.8; DB 3; Length 25;
; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
;
; QY 2 GGGTGACGTTTCAGGGG 17
; Db 18 GGGTGAAGTTCATGGG 3
;
;
; RESULT 11
; US-07-951-715A-43/c
; Sequence 43, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
;
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
;
;
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer P5(a)"
; HYPOTHETICAL: NO
;
US-07-951-715A-43
;
; Query Match
; Best Local Similarity 67.4%; Score 12.8; DB 2; Length 32;
; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
;
; QY 3 GGTGACGTTTCAGGGGG 18
; Db 18 GGTGCGTACAGGGGG 3
;
;
; RESULT 12
; US-08-459-448A-43/c
; Sequence 43, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
;
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
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RESULT 13  
US-08-459-595A-43/c  
Sequence 43, Application US/08459595A  
Patent No. 6018104  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalin M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lydie D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

RESULT 14  
US-08-459-504B-43/c  
; Sequence 43, Application US/08459504B  
; Patent NO. 6075185  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 607518artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,504B

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/459,595

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "primer P5(a) "

HYPOTHETICAL: NO

US-08-459-504B-43

Query Match 67.4%; Score 12.8; DB 3; Length 32;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18

Db 18 GGTGCGGTACAGGGGG 3

RESULT 15

US-08-459-444-43/c

Sequence 43, Application US/08459444A

Patent No. 6121014

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,444A  
FILING DATE: 02-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer P5(a) "

HYPOTHETICAL: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-08-459-444-43

Query Match 67.4%; Score 12.8; DB 3; Length 32;

Best Local Similarity 87.5%; Pred. No. 3.7e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18

Db 18 GGTGCGGTACAGGGGG 3

RESULT 16

US-09-547-422-43/c

Sequence 43, Application US/09547422

Patent No. 6320100

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

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/
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/547,422
/ FILING DATE: 11-APR-2000
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/459,595
/ FILING DATE: 02-JUN-1995
/ APPLICATION NUMBER: US 07/951,715
/ FILING DATE: 25-SEP-1992
/ APPLICATION NUMBER: US 07/772,027
/ FILING DATE: 04-OCT-1991
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meigs, J. Timothy
/ REGISTRATION NUMBER: 38,241
/ REFERENCE/DOCKET NUMBER: S-18805H
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (919)541-8587
/ TELEFAX: (919)541-8689
/
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "primer P5(a)"
/ HYPOTHETICAL: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-547-422-43
Query Match 57.4%; Score 12.8; DB 3; Length 32;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18
Db 18 GGTGCGGTACAGGGGG 3

RESULT 17
US-09-988-462-43/c
; Sequence 43, Application US/09988462
; Patent No. 6720488
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
;
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
;
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
;
; COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/988,462
/ FILING DATE: 20-NO. 6720488-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 09/547,422
/ FILING DATE: 11-APR-2000
/ APPLICATION NUMBER: US 08/459,504
/ FILING DATE: 02-JUN-1995
/ APPLICATION NUMBER: US 07/951,715
/ FILING DATE: 25-SEP-1992
/ APPLICATION NUMBER: US 07/772,027
/ FILING DATE: 04-OCT-1991
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meigs, J. Timothy
/ REGISTRATION NUMBER: 38,241
/ REFERENCE/DOCKET NUMBER: S-18805I
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (919)541-8587
/ TELEFAX: (919)541-8689
/
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "primer P5(a)"
/ HYPOTHETICAL: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-988-462-43
Query Match 67.4%; Score 12.8; DB 3; Length 32;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18
Db 18 GGTGCGGTACAGGGGG 3

RESULT 18
US-10-131-827-4733/c
; Sequence 4733, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4733
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; US-10-131-827-4733
Query Match 67.4%; Score 12.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTGACGTTTCAGGGGG 19
Db 19 GTGACGTTTCAGGGGG 19
```

```
Db      21  GTGACGTTCTGGGAGG 6

RESULT 19
US-09-672-126B-27
; Sequence 27, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic Oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)...(13)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)...(18)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)...(19)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
US-09-672-126B-27
Query Match      66.3%; Score 12.6; DB 3; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GGGTGACGTTTCAGGGGGG 19
Db      1  GGGTCGACGTCGAGGGGGG 19

RESULT 20
US-08-738-652-12
; Sequence 12, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-12
Query Match      66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GGGTGACGTTTCAGGGGGG 19
Db      2  GGGTCAACGTTGAGGGGGG 20

RESULT 21
US-09-030-701-63
; Sequence 63, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-63
Query Match      66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GGGTGACGTTTCAGGGGGG 19
Db      2  GGGTCAACGTTGAGGGGGG 20

RESULT 22
US-08-960-774-90
; Sequence 90, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieg et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
```

```
/ FILING DATE: October 30, 1996
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haile, Lisa A.
/ REGISTRATION NUMBER: 38,347
/ REFERENCE/DOCKET NUMBER: 08918/012001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619/678-5070
/ TELEFAX: 619/678-5099
/ INFORMATION FOR SEQ ID NO: 90:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
US-08-960-774-90

Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 23
US-09-082-649B-52
/ Sequence 52, Application US/09082649B
/ Patent No. 6339068
/ GENERAL INFORMATION:
/ APPLICANT: Davis, Heather L.
/ APPLICANT: Krieg, Arthur M.
/ APPLICANT: Schorzi, Joachim
/ APPLICANT: Wu, Tong
/ TITLE OF INVENTION: Vectors and Methods for Immunization or
/ TITLE OF INVENTION: Therapeutic Protocols
/ FILE REFERENCE: C1039/7009
/ CURRENT APPLICATION NUMBER: US/09/082,649B
/ CURRENT FILING DATE: 1998-05-20
/ PRIOR APPLICATION NUMBER: US 60/047,233
/ PRIOR FILING DATE: 1997-05-20
/ PRIOR FILING DATE: 1997-05-20
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 52
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic oligonucleotide
/ NAME/KEY: misc_Feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Has a phosphorothioate backbone.
US-09-082-649B-52

Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 24
US-09-082-649B-59
/ Sequence 59, Application US/09082649B
/ Patent No. 6339068
/ GENERAL INFORMATION:
/ APPLICANT: Davis, Heather L.
```

```
/ APPLICANT: Krieg, Arthur M.
/ APPLICANT: Schorzi, Joachim
/ APPLICANT: Wu, Tong
/ TITLE OF INVENTION: Vectors and Methods for Immunization or
/ TITLE OF INVENTION: Therapeutic Protocols
/ FILE REFERENCE: C1039/7009
/ CURRENT APPLICATION NUMBER: US/09/082,649B
/ CURRENT FILING DATE: 1998-05-20
/ PRIOR APPLICATION NUMBER: US 60/047,233
/ PRIOR FILING DATE: 1997-05-20
/ PRIOR APPLICATION NUMBER: US 60/047,209
/ PRIOR FILING DATE: 1997-05-20
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 59
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic oligonucleotide
/ NAME/KEY: misc_Feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5'
/ OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages
/ OTHER INFORMATION: in between.
US-09-082-649B-59

Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 25
US-09-191-170-47
/ Sequence 47, Application US/09191170
/ Patent No. 6429199
/ GENERAL INFORMATION:
/ APPLICANT: Krieg, Arthur M.
/ APPLICANT: Hartmann, Gunther
/ TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
/ TITLE OF INVENTION: for Activating Dendritic Cells
/ FILE REFERENCE: C1039/7017
/ CURRENT APPLICATION NUMBER: US/09/191,170
/ CURRENT FILING DATE: 1998-11-13
/ EARLIER APPLICATION NUMBER: US 08/960,774
/ EARLIER FILING DATE: 1997-10-30
/ EARLIER APPLICATION NUMBER: US 08/738,652
/ EARLIER FILING DATE: 1996-10-30
/ EARLIER APPLICATION NUMBER: US 08/386,063
/ EARLIER FILING DATE: 1995-02-07
/ EARLIER APPLICATION NUMBER: US 08/276,358
/ EARLIER FILING DATE: 1994-07-15
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 47
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic oligonucleotide
US-09-191-170-47

Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTGAGGGGG 20
```

RESULT 26  
US-09-337-619-12  
; Sequence 12, Application US/09337619  
; Patent No. 6653292  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; TITLE OF INVENTION: Methods of Treating Cancer Using  
; FILE REFERENCE: C1039/7021/HCL  
; CURRENT APPLICATION NUMBER: US/09/337,619  
; CURRENT FILING DATE: 1999-06-21  
; EARLIER APPLICATION NUMBER: US 08/960,774  
; EARLIER FILING DATE: 1997-10-30  
; EARLIER APPLICATION NUMBER: US 08/738,652  
; EARLIER FILING DATE: 1996-10-30  
; EARLIER APPLICATION NUMBER: US 08/386,063  
; EARLIER FILING DATE: 1995-02-07  
; EARLIER APPLICATION NUMBER: US 08/276,358  
; EARLIER FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-337-619-12

Query Match  
Best Local Similarity 66.3%; Score 12.6; DB 3; Length 20;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 27  
US-09-965-101-52  
; Sequence 52, Application US/09965101  
; Patent No. 6821957  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Wu, Tong  
; TITLE OF INVENTION: Vectors and Methods for Immunization or  
; FILE REFERENCE: C1039/7057 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/965,101  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 09/082,649  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,233  
; PRIOR FILING DATE: 1997-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,209  
; PRIOR FILING DATE: 1997-05-20  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 52  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5',  
; OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages  
; OTHER INFORMATION: in between.  
US-09-965-101-52

Query Match  
Best Local Similarity 78.9%; Score 12.6; DB 3; Length 20;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 28  
US-09-965-101-59  
; Sequence 59, Application US/09965101  
; Patent No. 6821957  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Wu, Tong  
; TITLE OF INVENTION: Vectors and Methods for Immunization or  
; FILE REFERENCE: C1039/7057 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/965,101  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 09/082,649  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,233  
; PRIOR FILING DATE: 1997-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,209  
; PRIOR FILING DATE: 1997-05-20  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 59  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5',  
; OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages  
; OTHER INFORMATION: in between.  
US-09-965-101-59

Query Match  
Best Local Similarity 78.9%; Score 12.6; DB 3; Length 20;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 29  
US-09-672-126B-1  
; Sequence 1, Application US/09672126B  
; Patent No. 6949520  
; GENERAL INFORMATION:  
; APPLICANT: Hartmann, Gunther  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Krieg, Arthur  
; TITLE OF INVENTION: Methods Related to Immunostimulatory  
; FILE REFERENCE: C1039/7044  
; CURRENT APPLICATION NUMBER: US/09/672,126B  
; CURRENT FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/156,147  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA

```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Oligonucleotide
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(2)
/ OTHER INFORMATION: Backbone has phosphorothioate linkages.
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (3)...(14)
/ OTHER INFORMATION: Backbone has phosphodiester linkages.
/
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (15)...(19)
/ OTHER INFORMATION: Backbone has phosphorothioate linkages.
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (20)...(20)
/ OTHER INFORMATION: Backbone has phosphodiester linkages.
/
/ US-09-672-126B-1
```

```
Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||||| |||||
Db 2 GGGTCAACGTTGAGGGGG 20
```

```
RESULT 30
US-09-672-126B-5
; Sequence 5, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
/
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(20)
/ OTHER INFORMATION: Backbone has phosphorothioate linkages.
/
/ US-09-672-126B-5
```

```
Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||||| |||||
Db 2 GGGTCAACGTTGAGGGGG 20
```

```
RESULT 31
US-09-672-126B-135
; Sequence 135, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
```

```
/ APPLICANT: Hartmann, Gunther
/ APPLICANT: Bratzler, Robert L.
/ APPLICANT: Krieg, Arthur
/ TITLE OF INVENTION: Methods Related to Immunostimulatory
/ FILE REFERENCE: C1039/7044
/ CURRENT APPLICATION NUMBER: US/09/672,126B
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/156,147
/ PRIOR FILING DATE: 1999-09-29
/ NUMBER OF SEQ ID NOS: 169
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 135
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic Oligonucleotide
/
/ US-09-672-126B-135
```

```
Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||||| |||||
Db 2 GGGTCAACGTTGAGGGGG 20
```

```
RESULT 32
US-09-672-126B-136
; Sequence 136, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 136
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
/
/ US-09-672-126B-136
```

```
Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||||| |||||
Db 2 GGGTCAACGTTGAGGGGG 20
```

```
RESULT 33
US-09-672-126B-156
; Sequence 156, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 156
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
/
/ US-09-672-126B-156
```

```

; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 156
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (1)...(2)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)...(15)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)...(20)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)...(21)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
US-09-672-126B-156
```

```

Query Match          66.3%; Score 12.6; DB 3; Length 21;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 GGGGTGACGTTTCAGGGGGG 19
      ||| ||||| ||||| |||||
Db       3 GGGTCACGTTGAGGGGGG 21
```

```

RESULT 34
US-09-396-196G-78259/c
; Sequence 78259, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78259
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-78259
```

```

Query Match          66.3%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 GGGGTGACGTTTCAGGGGGG 19
      ||| ||||| ||||| |||||
Db      19 GGTGTCAGATCAGGGGAG 1
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. RESULT 35

```

US-09-672-126B-165
; Sequence 165, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 165
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-672-126B-165
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Query Match          66.3%; Score 12.6; DB 3; Length 30;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      1 GGGGTGACGTTTCAGGGGGG 19
      ||| ||||| ||||| |||||
Db       8 GGGGGAACGTTGGGGGGG 26
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```

RESULT 36
US-09-907-794A-225/c
; Sequence 225, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
```







; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 225  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide probe  
US-09-906-700-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 19 GGAGCGTCGCTCAGGGGG 1

RESULT 40  
US-09-903-603A-225/c  
; Sequence 225, Application US/09903603A  
; Patent No. 6767995  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: GNE.1618P2C12  
; CURRENT APPLICATION NUMBER: US/09/903,603A  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 225  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide probe  
US-09-903-603A-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 19 GGAGCGTCGCTCAGGGGG 1

RESULT 41  
US-09-904-920A-225/c  
; Sequence 225, Application US/09904920A  
; Patent No. 6806352  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/904,920A  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048

;  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 225  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide probe  
US-09-904-920A-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 GGGTGACCTTCAGGGGG 19  
Db 19 GGAGCGTCGCTCAGGGGG 1

RESULT 42  
US-09-909-064-225/c  
; Sequence 225, Application US/09909064  
; Patent No. 6818449  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.

;  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/909,064  
; CURRENT FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 225  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide probe  
US-09-909-064-225  
  
Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 GGGTGACCTTCAGGGGG 19  
Db 19 GGAGCGTCGCTCAGGGGG 1

RESULT 43  
US-09-905-381A-225/c  
; Sequence 225, Application US/09905381A  
; Patent No. 6818746  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/905,381A  
CURRENT FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 225  
LENGTH: 44  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: oligonucleotide probe  
US-09-905-381A-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 19 GGAGCGTCGCTCAGGGGG 1  
RESULT 44  
US-09-906-618-225/c  
; Sequence 225, Application US/09906618  
; Patent No. 6828146  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/906,618  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999





APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: GNE.1618P2C61  
CURRENT APPLICATION NUMBER: US/09/906,722A  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 225  
LENGTH: 44  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: oligonucleotide probe  
US-09-906-722A-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
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Sequence 1255, Application US/09641638  
Patent No. 6432648  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GENSET.051CPI  
CURRENT APPLICATION NUMBER: US/09/641,638  
CURRENT FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 1255  
LENGTH: 47  
TYPE: DNA  
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FEATURE:  
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LOCATION: 24  
OTHER INFORMATION: 10-387-371 : polymorphic base C or T  
US-09-641-638-1255  
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Patent No. 6794143  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GEN-T114XC2D1  
CURRENT APPLICATION NUMBER: US/10/170,097  
CURRENT FILING DATE: 2002-06-10  
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PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07



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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 251 12.6 66.3 44 3 US-09-906-646-225 Sequence 225, App  
C 252 12.6 66.3 44 3 US-09-906-700-225 Sequence 225, App  
C 253 12.6 66.3 44 3 US-09-903-786-225 Sequence 225, App  
C 254 12.6 66.3 44 3 US-09-902-903-225 Sequence 225, App  
C 255 12.6 66.3 44 3 US-09-903-749A-225 Sequence 225, App  
C 256 12.6 66.3 44 3 US-09-904-119-225 Sequence 225, App  
C 257 12.6 66.3 44 3 US-09-904-956-225 Sequence 225, App  
C 258 12.6 66.3 44 3 US-09-902-736-225 Sequence 225, App  
C 259 12.6 66.3 44 3 US-09-907-794-225 Sequence 225, App  
C 260 12.6 66.3 44 3 US-09-903-943-225 Sequence 225, App  
C 261 12.6 66.3 44 3 US-09-904-462-225 Sequence 225, App  
C 262 12.6 66.3 44 3 US-09-907-525-225 Sequence 225, App  
C 263 12.6 66.3 44 3 US-09-902-692-225 Sequence 225, App  
C 264 12.6 66.3 44 3 US-09-903-520-225 Sequence 225, App  
C 265 12.6 66.3 44 3 US-09-905-056-225 Sequence 225, App  
C 266 12.6 66.3 44 3 US-09-909-064-225 Sequence 225, App  
C 267 12.6 66.3 44 3 US-09-904-553-225 Sequence 225, App  
C 268 12.6 66.3 44 3 US-09-905-381-225 Sequence 225, App  
C 269 12.6 66.3 44 3 US-09-904-485-225 Sequence 225, App  
C 270 12.6 66.3 44 3 US-09-905-348-225 Sequence 225, App  
C 271 12.6 66.3 44 3 US-09-905-088-225 Sequence 225, App  
C 272 12.6 66.3 44 3 US-09-907-575-225 Sequence 225, App  
C 273 12.6 66.3 44 3 US-09-905-075-225 Sequence 225, App  
C 274 12.6 66.3 44 3 US-09-902-759-225 Sequence 225, App  
C 275 12.6 66.3 44 3 US-09-902-634-225 Sequence 225, App  
C 276 12.6 66.3 44 3 US-09-902-713-225 Sequence 225, App  
C 277 12.6 66.3 44 3 US-09-907-979-225 Sequence 225, App  
C 278 12.6 66.3 44 3 US-09-902-615-225 Sequence 225, App  
C 279 12.6 66.3 44 3 US-09-903-525-225 Sequence 225, App  
C 280 12.6 66.3 44 3 US-09-906-760A-225 Sequence 225, App  
C 281 12.6 66.3 44 3 US-09-903-823-225 Sequence 225, App  
C 282 12.6 66.3 44 3 US-09-907-652-225 Sequence 225, App  
C 283 12.6 66.3 44 3 US-09-902-572A-225 Sequence 225, App  
C 284 12.6 66.3 44 3 US-09-902-979-225 Sequence 225, App  
C 285 12.6 66.3 44 3 US-09-905-125-225 Sequence 225, App  
C 286 12.6 66.3 44 3 US-09-906-815A-225 Sequence 225, App  
C 287 12.6 66.3 44 3 US-09-905-449-225 Sequence 225, App  
C 288 12.6 66.3 44 3 US-09-903-806-225 Sequence 225, App  
C 289 12.6 66.3 44 3 US-09-904-992-225 Sequence 225, App  
C 290 12.6 66.3 44 3 US-09-904-838-225 Sequence 225, App  
C 291 12.6 66.3 44 3 US-09-906-777-225 Sequence 225, App  
C 292 12.6 66.3 44 3 US-09-903-603A-225 Sequence 225, App  
C 293 12.6 66.3 44 3 US-09-904-532-225 Sequence 225, App  
C 294 12.6 66.3 44 3 US-09-904-766-225 Sequence 225, App  
C 295 12.6 66.3 44 3 US-09-904-920A-225 Sequence 225, App  
C 296 12.6 66.3 44 3 US-09-904-877A-225 Sequence 225, App  
C 297 12.6 66.3 44 3 US-09-903-562-225 Sequence 225, App  
C 298 12.6 66.3 44 3 US-09-906-618-225 Sequence 225, App  
C 299 12.6 66.3 44 3 US-09-907-728-225 Sequence 225, App  
C 300 12.6 66.3 44 3 US-09-904-805-225 Sequence 225, App

## ALIGNMENTS

RESULT 1  
US-09-888-326-447  
; Sequence 447, Application US/09888326  
; Publication No. US20030026801A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Hartmann, Gunther  
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
; TITLE OF INVENTION: Cell Lysis and Treating Cancer  
; FILE REFERENCE: C1039/7052 (AWS)

; CURRENT APPLICATION NUMBER: US/09/888,326  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/213,346  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 848  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 447  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone  
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends  
US-09-888-326-447

Query Match 100.0%; Score 19; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
|||||  
Db 1 GGGGTGACGTTTCAGGGGG 19

## RESULT 2

US-09-776-479-80  
; Sequence 80, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/NAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 80  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-80

Query Match 100.0%; Score 19; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
|||||  
Db 1 GGGGTGACGTTTCAGGGGG 19

## RESULT 3

US-09-776-479-80  
; Sequence 80, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/NAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479

```

; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-80

```

```

Query Match      100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 1 GGGGTGACGTTTCAGGGGGG 19

```

```

RESULT 4
US-10-112-653-74
; Sequence 74, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-74

```

```

Query Match      100.0%; Score 19; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 1 GGGGTGACGTTTCAGGGGGG 19

```

```

RESULT 5
US-10-017-995-80
; Sequence 80, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-80

```

```

Query Match      100.0%; Score 19; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 1 GGGGTGACGTTTCAGGGGGG 19

```

```

RESULT 6
US-10-314-578-80
; Sequence 80, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-80

```

```

Query Match      100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 1 GGGGTGACGTTTCAGGGGGG 19

```

```

RESULT 7
US-10-831-778-80
; Sequence 80, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourton, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence

```

## US-10-831-778-80

Query Match 100.0%; Score 19; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |  
Db 1 GGGGTGACGTTTCAGGGGG 19

## RESULT 8

US-09-888-326-448  
; Sequence 448, Application US/09888326  
; Publication No. US20030026801A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Hartmann, Gunther  
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
; TITLE OF INVENTION: Cell Lysis and Treating Cancer  
; FILE REFERENCE: C1039/7052 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/888,326  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/213,346  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 848  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 448  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
; NAME/KEY: misc feature  
; LOCATION: (0)\_(0)  
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone  
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends  
US-09-888-326-448

Query Match 91.6%; Score 17.4; DB 3; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |  
Db 1 GGGGTGCGTTTCAGGGGG 19

## RESULT 9

US-09-776-479-82  
; Sequence 82, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Fourn, Yves  
; APPLICANT: Petersen, Deanna M.  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 82  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-82

Query Match 91.6%; Score 17.4; DB 3; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |  
Db 1 GGGGTGCGTTTCAGGGGG 19

## RESULT 10

US-09-776-479-82  
; Sequence 82, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fourn, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 82  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-82

Query Match 91.6%; Score 17.4; DB 3; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |  
Db 1 GGGGTGCGTTTCAGGGGG 19

## RESULT 11

US-10-112-653-76  
; Sequence 76, Application US/10112653  
; Publication No. US20030050268A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR  
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES  
; FILE REFERENCE: C01039/70060(AWS)  
; CURRENT APPLICATION NUMBER: US/10/112,653  
; CURRENT FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 76  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-112-653-76

Query Match 91.6%; Score 17.4; DB 5; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |

```
Db      1 GGGGTGTCGTTTCAGGGGG 19

RESULT 12
US-10-017-995-82
; Sequence 82, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-82
Query Match      91.6%; Score 17.4; DB 5; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 19
      ||||| ||||| ||||| |||||
Db      1 GGGGTGTCGTTTCAGGGGG 19

RESULT 13
US-10-314-578-82
; Sequence 82, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-82
Query Match      91.6%; Score 17.4; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 19
      ||||| ||||| ||||| |||||
Db      1 GGGGTGTCGTTTCAGGGGG 19

RESULT 14
US-10-831-778-82
; Sequence 82, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-82
Query Match      91.6%; Score 17.4; DB 8; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 19
      ||||| ||||| ||||| |||||
Db      1 GGGGTGTCGTTTCAGGGGG 19

RESULT 15
US-11-036-317-815104/c
; Sequence 815104, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 815104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-815104
Query Match      81.1%; Score 15.4; DB 10; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGG 17
      ||||| ||||| ||||| |||||
Db      21 GGGGTACGTTTCAGGGG 5

RESULT 16
US-09-415-142-1
; Sequence 1, Application US/09415142
; Publication No. US20030026782A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klimman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/09/415,142
```



```
; CURRENT FILING DATE: 1999-10-09
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Synthetic oligonucleotide
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-415-142-1

Query Match          74.7%  Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%  Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 17
US-09-888-326-449
; Sequence 449, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 449
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-449

Query Match          74.7%  Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%  Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 18
US-09-931-583-1
; Sequence 1, Application US/09931583
; Publication No. US20030050263A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred
; TITLE OF INVENTION: Methods and Products for Treating HIV Infection
; FILE REFERENCE: C1039/7053 (HCL)
; CURRENT APPLICATION NUMBER: US/09/931,583
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
```

```
; PRIOR APPLICATION NUMBER: US 09/415,142
; PRIOR FILING DATE: 1999-10-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-931-583-1

Query Match          74.7%  Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%  Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 19
US-09-776-479-224
; Sequence 224, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Synthetic Sequence
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-224

Query Match          74.7%  Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%  Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 20
US-09-776-479-224
; Sequence 224, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-224

Query Match          74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||| ||| ||| ||| |||
Db  2 GGGTTCACGTTTGGGGGG 20

RESULT 21
US-09-965-101-63
; Sequence 63, Application US/09965101
; Publication No. US20040186067A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-63

Query Match          74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||| ||| ||| ||| |||
Db  2 GGGTTCACGTTTGGGGGG 20

RESULT 22
US-10-112-653-216
; Sequence 216, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 216
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-216

Query Match          74.7%; Score 14.2; DB 5; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||| ||| ||| ||| |||
Db  2 GGGTTCACGTTTGGGGGG 20

RESULT 23
US-10-017-995-224
; Sequence 224, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-224

Query Match          74.7%; Score 14.2; DB 5; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||| ||| ||| ||| |||
Db  2 GGGTTCACGTTTGGGGGG 20

RESULT 24
US-10-314-578-224
; Sequence 224, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
```

US-10-314-578-224

Query Match 74.7%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTTCAGCTTTTCAGGGGG 20

RESULT 25

US-10-631-676-1  
; Sequence 1, Application US/10631676  
; Publication No. US20040087534A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/10/631.676  
; CURRENT FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Fast-SEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-631-676-1

Query Match 74.7%; Score 14.2; DB 7; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTTCAGCTTCAGGGGG 20

RESULT 26

US-10-789-051-1  
; Sequence 1, Application US/10789051  
; Publication No. US20040142469A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/10/789,051  
; CURRENT FILING DATE: 2004-02-26  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Fast-SEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-789-051-1

Query Match 74.7%; Score 14.2; DB 7; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19

Db 2 GGGTTCAGCTTCAGGGGG 20

RESULT 27

US-10-690-495-1  
; Sequence 1, Application US/10690495  
; Publication No. US20040143112A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/10/690,495  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Fast-SEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-690-495-1

Query Match 74.7%; Score 14.2; DB 7; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTTCAGCTTCAGGGGG 20

RESULT 28

US-10-788-191-1  
; Sequence 1, Application US/10788191  
; Publication No. US20040152656A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/10/788,191  
; CURRENT FILING DATE: 2004-02-26  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Fast-SEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-788-191-1

Query Match 74.7%; Score 14.2; DB 7; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTTCAGCTTCAGGGGG 20

RESULT 29

US-10-789-536-1  
; Sequence 1, Application US/10789536

```

; Publication No. US20040152657A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/789,536
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-789-536-1

```

```

Query Match          74.7%; Score 14.2; DB 7; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20

```

```

RESULT 30
US-10-769-626-1
; Sequence 1, Application US/10769626
; Publication No. US20040162258A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/769,626
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-769-626-1

```

```

Query Match          74.7%; Score 14.2; DB 7; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20

```

```

RESULT 31
US-10-789-353-1
; Sequence 1, Application US/10789353
; Publication No. US20040162262A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029

```

```

; CURRENT APPLICATION NUMBER: US/10/789,353
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-789-353-1

```

```

Query Match          74.7%; Score 14.2; DB 7; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20

```

```

RESULT 32
US-10-787-737-1
; Sequence 1, Application US/10787737
; Publication No. US20040171150A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/787,737
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-787-737-1

```

```

Query Match          74.7%; Score 14.2; DB 7; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20

```

```

RESULT 33
US-10-788-199-1
; Sequence 1, Application US/10788199
; Publication No. US20040181045A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/788,199
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1

```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-788-199-1

Query Match      74.7%; Score 14.2; DB 8; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19
    ||| ||||| ||||| |||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 34
US-10-831-778-224
; Sequence 224, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-224

Query Match      74.7%; Score 14.2; DB 8; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19
    ||| ||||| ||||| |||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 35
US-10-847-650-1
; Sequence 1, Application US/10847650
; Publication No. US20050004062A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/847,650
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-847-650-1

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-847-650-1

Query Match      74.7%; Score 14.2; DB 8; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19
    ||| ||||| ||||| |||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 36
US-10-888-885-1
; Sequence 1, Application US/10888885
; Publication No. US20050009774A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/888,885
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-888-885-1

Query Match      74.7%; Score 14.2; DB 8; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19
    ||| ||||| ||||| |||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 37
US-10-838-659-63
; Sequence 63, Application US/10838659
; Publication No. US20050032734A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039.70057US01
; CURRENT APPLICATION NUMBER: US/10/838,659
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 09/965,101
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-838-659-63
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US-10-838-659-63

Query Match 74.7%; Score 14.2; DB 8; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
||| ||||| |||||  
Db 2 GGGTTGACGTTTTCAGGGGGG 20

RESULT 38

US-10-888-089-1  
; Sequence 1, Application US/10888089  
; Publication No. US20050037403A1  
; GENERAL INFORMATION:  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/10/888,089  
; CURRENT FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/10/690,495  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-888-089-1

Query Match 74.7%; Score 14.2; DB 8; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCACGTTTCAGGGGGG 20

RESULT 39

US-10-649-584-1  
; Sequence 1, Application US/10649584  
; Publication No. US20050037985A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred  
; TITLE OF INVENTION: Methods and Products for Treating HIV Infection  
; FILE REFERENCE: C1039, 70084US00  
; CURRENT APPLICATION NUMBER: US/10/649,584  
; CURRENT FILING DATE: 2003-08-25  
; PRIOR APPLICATION NUMBER: US 09/931,583  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: US 08/276,358  
; PRIOR FILING DATE: 1994-07-15  
; PRIOR APPLICATION NUMBER: US 09/415,142  
; PRIOR FILING DATE: 1999-10-09  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Synthetic oligonucleotide

US-10-649-584-1

Query Match 74.7%; Score 14.2; DB 8; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCACGTTTCAGGGGGG 20

RESULT 40

US-11-067-516-1  
; Sequence 1, Application US/11067516  
; Publication No. US20050239736A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/11/067,516  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR APPLICATION NUMBER: US/10/690,495  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-067-516-1

Query Match 74.7%; Score 14.2; DB 10; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCACGTTTCAGGGGGG 20

RESULT 41

US-11-036-317-185300  
; Sequence 185300, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 185300  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-185300

Query Match 74.7%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
||| ||||| |||||

```
Db      7 GGGGAGACGTTTCATGGGCG 25

RESULT 42
US-11-036-317-282532
; Sequence 282532, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 282532
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-282532

Query Match      74.7%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 19
        ||||| ||||| ||||| |||||
Db      6 GGGGAGACGTTTCATGGGCG 24

RESULT 43
US-11-036-317-382608
; Sequence 382608, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 382608
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-382608

Query Match      74.7%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 19
        ||||| ||||| ||||| |||||
Db      6 GGGGAGACGTTTCATGGGCG 24

RESULT 44
US-11-036-317-395403
; Sequence 395403, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317

Db      3 GGGGAGACGTTTCATGGGCG 21

RESULT 45
US-11-036-317-398410
; Sequence 398410, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 398410
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-398410

Query Match      74.7%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 19
        ||||| ||||| ||||| |||||
Db      4 GGGGAGACGTTTCATGGGCG 22

RESULT 46
US-10-282-935-18/c
; Sequence 18, Application US/10282935
; Publication No. US20030143193A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETTIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; FILE REFERENCE: UTSD:884US
; CURRENT APPLICATION NUMBER: US/10/282,935
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 39
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-282-935-18

Query Match          73.7%; Score 14; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGG 16
Db 26 GGTGACGTTTCAGGG 13

RESULT 47
US-10-440-796-18/c
; Sequence 18, Application US/10440796
; Publication No. US20040009148A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SWALISHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
; TITLE OF INVENTION: SYNDROME (VLS)
; FILE REFERENCE: US20040009148A1
; CURRENT APPLICATION NUMBER: US/10/440,796
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 18
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-440-796-18

Query Match          73.7%; Score 14; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGG 16
Db 26 GGTGACGTTTCAGGG 13

RESULT 48
US-11-036-317-292133
; Sequence 292133, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 292133
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-292133
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```
Query Match          72.6%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 17
Db 8 GGGGAGACGTTTCATGG 24

RESULT 49
US-11-036-317-815105/c
; Sequence 815105, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 815105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-815105

Query Match          72.6%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 17
Db 21 GGGGTACCTTCAGGG 5

RESULT 50
US-11-036-317-822290
; Sequence 822290, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 822290
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-822290

Query Match          72.6%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGTGACGTTTCAGGG 18
Db 2 GGGGTGATGTTTCAGGG 18

Search completed: February 16, 2006, 02:34:04
Job time : 279.736 secs
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 02:03:53 ; Search time 177.124 Seconds  
(without alignments)  
98.157 Million cell updates/sec

Title: US-09-669-187A-80

Perfect score: 19

Sequence: 1 ggggtgacgttcagg9ggg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 11812030

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA.New.\*

1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*

2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*

3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*

4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*

5: /cgn2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq.\*

6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*

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11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

12: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match % | Score | Length | ID | Description            |
|------------|---------------|-------|--------|----|------------------------|
| 1          | 19            | 100.0 | 19     | 11 | US-11-127-654-74       |
| 2          | 17.4          | 91.6  | 19     | 11 | US-11-127-654-76       |
| 3          | 14.2          | 74.7  | 19     | 7  | US-10-310-914A-1228446 |
| 4          | 14.2          | 74.7  | 20     | 9  | US-11-127-797-1        |
| 5          | 14.2          | 74.7  | 20     | 9  | US-11-127-803-1        |
| 6          | 14.2          | 74.7  | 20     | 9  | US-11-128-127-1        |
| 7          | 14.2          | 74.7  | 20     | 11 | US-11-127-654-216      |
| 8          | 14            | 73.7  | 28     | 7  | US-10-310-914A-1202061 |
| 9          | 13.8          | 72.6  | 20     | 7  | US-10-310-914A-524757  |
| 10         | 13.8          | 72.6  | 20     | 7  | US-10-310-914A-895375  |
| 11         | 13.8          | 72.6  | 20     | 7  | US-10-310-914A-1185102 |
| 12         | 13.8          | 72.6  | 21     | 7  | US-10-310-914A-895439  |
| 13         | 13.8          | 72.6  | 22     | 7  | US-10-310-914A-1185206 |
| 14         | 13.8          | 72.6  | 23     | 7  | US-10-310-914A-530908  |
| 15         | 13.4          | 70.5  | 19     | 9  | US-11-101-244-1188547  |
| 16         | 13.4          | 70.5  | 19     | 10 | US-11-083-784-1188547  |
| 17         | 13.4          | 70.5  | 22     | 7  | US-10-310-914A-673587  |
| 18         | 13.2          | 69.5  | 18     | 7  | US-10-310-914A-308426  |
| 19         | 13.2          | 69.5  | 20     | 11 | US-11-127-654-498      |
| 20         | 13.2          | 69.5  | 20     | 11 | US-11-127-654-501      |
| 21         | 13.2          | 69.5  | 21     | 7  | US-10-310-914A-872061  |
| 22         | 13.2          | 69.5  | 21     | 7  | US-10-310-914A-114797  |
| 23         | 13.2          | 69.5  | 23     | 7  | US-10-310-914A-456901  |
| 24         | 13.2          | 69.5  | 23     | 7  | US-10-310-914A-518042  |
| 25         | 13.2          | 69.5  | 23     | 7  | US-10-310-914A-836953  |
| 26         | 13.2          | 69.5  | 23     | 7  | US-10-310-914A-896494  |
| 27         | 13.2          | 69.5  | 24     | 7  | US-10-310-914A-837004  |
| 28         | 13.2          | 69.5  | 25     | 11 | US-11-121-849-509542   |
| 29         | 13.2          | 69.5  | 32     | 11 | US-11-013-353-97       |
| 30         | 13.2          | 69.5  | 32     | 11 | US-11-013-353-97       |
| 31         | 12.8          | 67.4  | 18     | 7  | US-10-310-914A-1145336 |
| 32         | 12.8          | 67.4  | 19     | 7  | US-10-310-914A-966814  |
| 33         | 12.8          | 67.4  | 20     | 7  | US-10-522-362-49       |
| 34         | 12.8          | 67.4  | 20     | 7  | US-10-310-914A-746353  |
| 35         | 12.8          | 67.4  | 22     | 7  | US-10-310-914A-966777  |
| 36         | 12.8          | 67.4  | 23     | 7  | US-10-310-914A-240915  |
| 37         | 12.8          | 67.4  | 24     | 7  | US-10-310-914A-411534  |
| 38         | 12.8          | 67.4  | 25     | 7  | US-10-310-914A-1145337 |
| 39         | 12.8          | 67.4  | 25     | 11 | US-11-121-849-15921    |
| 40         | 12.8          | 67.4  | 25     | 11 | US-11-121-849-22103    |
| 41         | 12.8          | 67.4  | 25     | 11 | US-11-121-849-24138    |
| 42         | 12.8          | 67.4  | 25     | 11 | US-11-121-849-107577   |
| 43         | 12.8          | 67.4  | 25     | 11 | US-11-121-849-115643   |
| 44         | 12.8          | 67.4  | 25     | 11 | US-11-121-849-476398   |
| 45         | 12.8          | 67.4  | 25     | 11 | US-11-121-849-568167   |
| 46         | 12.8          | 67.4  | 25     | 11 | US-11-121-849-570964   |
| 47         | 12.8          | 67.4  | 32     | 6  | US-10-755-092-43       |
| 48         | 12.8          | 67.4  | 32     | 7  | US-10-939-294A-19843   |
| 49         | 12.8          | 67.4  | 50     | 11 | US-11-175-859-51905    |
| 50         | 12.6          | 66.3  | 19     | 7  | US-10-310-914A-896490  |
| 51         | 12.6          | 66.3  | 19     | 7  | US-10-310-914A-1098668 |
| 52         | 12.6          | 66.3  | 19     | 11 | US-11-127-654-930      |
| 53         | 12.6          | 66.3  | 20     | 7  | US-10-619-279-12       |
| 54         | 12.6          | 66.3  | 20     | 7  | US-10-435-656-12       |
| 55         | 12.6          | 66.3  | 20     | 7  | US-10-310-914A-142257  |
| 56         | 12.6          | 66.3  | 20     | 7  | US-10-310-914A-369058  |
| 57         | 12.6          | 66.3  | 20     | 11 | US-11-127-654-496      |
| 58         | 12.6          | 66.3  | 20     | 11 | US-11-127-654-740      |
| 59         | 12.6          | 66.3  | 20     | 11 | US-11-127-654-878      |
| 60         | 12.6          | 66.3  | 20     | 11 | US-11-127-654-923      |
| 61         | 12.6          | 66.3  | 20     | 11 | US-11-127-654-1040     |
| 62         | 12.6          | 66.3  | 20     | 11 | US-11-134-918-12       |
| 63         | 12.6          | 66.3  | 20     | 11 | US-11-031-460-12       |
| 64         | 12.6          | 66.3  | 20     | 11 | US-11-067-587-12       |
| 65         | 12.6          | 66.3  | 21     | 7  | US-10-310-914A-65931   |
| 66         | 12.6          | 66.3  | 21     | 7  | US-10-310-914A-137628  |
| 67         | 12.6          | 66.3  | 21     | 7  | US-10-310-914A-416718  |
| 68         | 12.6          | 66.3  | 21     | 7  | US-10-310-914A-1211505 |
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| 84         | 12.6          | 66.3  | 24     | 11 | US-11-127-654-495      |
| 85         | 12.6          | 66.3  | 25     | 7  | US-10-750-185-22043    |
| 86         | 12.6          | 66.3  | 25     | 7  | US-10-750-623-22043    |
| 87         | 12.6          | 66.3  | 25     | 7  | US-10-310-914A-181131  |
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| 89         | 12.6          | 66.3  | 25     | 11 | US-11-121-849-246100   |
| 90         | 12.6          | 66.3  | 26     | 7  | US-10-524-643-62       |
| 91         | 12.6          | 66.3  | 26     | 7  | US-10-524-643-62       |
| 92         | 12.6          | 66.3  | 26     | 7  | US-10-310-914A-1037101 |
| 93         | 12.6          | 66.3  | 26     | 7  | US-10-310-914A-982860  |
| 94         | 12.6          | 66.3  | 32     | 7  | US-10-939-294A-17580   |

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| C 95  | 12.6 | 66.3 | 32 | 7  | US-10-939-294A-19419    | Sequence 19419, A   | C 168 | 12.2 | 64.2 | 25 | 11 | US-11-136-527-338521   | Sequence 338521,  |
| C 96  | 12.6 | 66.3 | 50 | 11 | US-11-175-859-18833     | Sequence 18833, A   | C 169 | 12.2 | 64.2 | 26 | 7  | US-10-310-914A-477171  | Sequence 477171,  |
| C 97  | 12.4 | 65.3 | 19 | 9  | US-11-101-244-665663    | Sequence 665663,    | C 170 | 12.2 | 64.2 | 28 | 7  | US-10-310-914A-860573  | Sequence 860573,  |
| C 98  | 12.4 | 65.3 | 19 | 9  | US-11-101-244-1238420   | Sequence 1238420,   | C 171 | 12.2 | 64.2 | 30 | 7  | US-10-310-914A-550477  | Sequence 550477,  |
| C 99  | 12.4 | 65.3 | 19 | 10 | US-11-083-784-665663    | Sequence 665663,    | C 172 | 12.2 | 64.2 | 33 | 7  | US-10-209-208-33       | Sequence 33, Appl |
| C 100 | 12.4 | 65.3 | 19 | 10 | US-11-083-784-1238420   | Sequence 1238420,   | C 173 | 12.2 | 64.2 | 33 | 7  | US-10-209-208-33       | Sequence 34, Appl |
| C 101 | 12.4 | 65.3 | 20 | 11 | US-11-127-654-503       | Sequence 503, App   | C 174 | 12.2 | 64.2 | 33 | 11 | US-11-218-880-33       | Sequence 33, Appl |
| C 102 | 12.4 | 65.3 | 20 | 11 | US-11-127-654-827       | Sequence 827, App   | C 175 | 12.2 | 64.2 | 33 | 11 | US-11-218-880-34       | Sequence 34, Appl |
| C 103 | 12.4 | 65.3 | 21 | 7  | US-10-310-914A-746294   | Sequence 746294, A  | C 176 | 12.2 | 64.2 | 50 | 11 | US-11-175-859-86359    | Sequence 86359, A |
| C 104 | 12.4 | 65.3 | 23 | 7  | US-10-310-914A-1278218  | Sequence 1278218, A | C 177 | 12.2 | 64.2 | 19 | 9  | US-11-101-244-5629     | Sequence 5629, Ap |
| C 105 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-22422     | Sequence 22422, A   | C 178 | 12.2 | 63.2 | 19 | 9  | US-11-101-244-208337   | Sequence 208337,  |
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| C 107 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-58148     | Sequence 58148, A   | C 180 | 12.2 | 63.2 | 19 | 10 | US-11-083-784-208337   | Sequence 208337,  |
| C 108 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-58149     | Sequence 58149, A   | C 181 | 12.2 | 63.2 | 20 | 7  | US-10-750-185-12889    | Sequence 12889, A |
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| C 110 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-278536    | Sequence 278536,    | C 183 | 12.2 | 63.2 | 25 | 11 | US-11-121-849-12737    | Sequence 112737,  |
| C 111 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-533051    | Sequence 533051,    | C 184 | 12.2 | 63.2 | 25 | 11 | US-11-121-849-551178   | Sequence 551178,  |
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| C 113 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-533052    | Sequence 533052,    | C 186 | 12.2 | 63.2 | 50 | 11 | US-11-175-859-2042     | Sequence 2042, Ap |
| C 114 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-533053    | Sequence 533053,    | C 187 | 11.8 | 62.1 | 18 | 7  | US-10-310-914A-399938  | Sequence 399938,  |
| C 115 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-533054    | Sequence 533054,    | C 188 | 11.8 | 62.1 | 18 | 7  | US-10-310-914A-818768  | Sequence 818768,  |
| C 116 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-533882    | Sequence 533882,    | C 189 | 11.8 | 62.1 | 19 | 7  | US-10-310-914A-240911  | Sequence 240911,  |
| C 117 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-533883    | Sequence 533883,    | C 190 | 11.8 | 62.1 | 19 | 7  | US-10-310-914A-399939  | Sequence 399939,  |
| C 118 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-533884    | Sequence 533884,    | C 191 | 11.8 | 62.1 | 19 | 7  | US-10-310-914A-818916  | Sequence 818916,  |
| C 119 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-533885    | Sequence 533885,    | C 192 | 11.8 | 62.1 | 19 | 7  | US-10-310-914A-1328172 | Sequence 1328172, |
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| C 121 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-534408    | Sequence 534408,    | C 194 | 11.8 | 62.1 | 19 | 9  | US-11-101-244-631981   | Sequence 631981,  |
| C 122 | 12.4 | 65.3 | 25 | 11 | US-11-121-849-538595    | Sequence 538595,    | C 195 | 11.8 | 62.1 | 19 | 9  | US-11-101-244-1229178  | Sequence 1229178, |
| C 123 | 12.4 | 65.3 | 28 | 7  | US-10-310-914A-1201695  | Sequence 1201695,   | C 196 | 11.8 | 62.1 | 19 | 9  | US-11-101-244-1326203  | Sequence 1326203, |
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| C 125 | 12.2 | 64.2 | 18 | 7  | US-10-310-914A-1242715  | Sequence 1242715,   | C 198 | 11.8 | 62.1 | 19 | 10 | US-11-083-784-174986   | Sequence 174986,  |
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| C 128 | 12.2 | 64.2 | 19 | 7  | US-10-310-914A-394906   | Sequence 394906,    | C 201 | 11.8 | 62.1 | 19 | 10 | US-11-083-784-1316203  | Sequence 1316203, |
| C 129 | 12.2 | 64.2 | 19 | 7  | US-10-310-914A-1038534  | Sequence 1038534,   | C 202 | 11.8 | 62.1 | 19 | 10 | US-11-083-784-3522803  | Sequence 3522803, |
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| C 132 | 12.2 | 64.2 | 20 | 7  | US-10-310-914A-586723   | Sequence 586723,    | C 205 | 11.8 | 62.1 | 20 | 7  | US-10-310-914A-1145320 | Sequence 1145320, |
| C 133 | 12.2 | 64.2 | 20 | 7  | US-10-310-914A-1347887  | Sequence 1347887,   | C 206 | 11.8 | 62.1 | 20 | 7  | US-10-310-914A-1228471 | Sequence 1228471, |
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| C 135 | 12.2 | 64.2 | 21 | 7  | US-10-310-914A-404009   | Sequence 404009,    | C 208 | 11.8 | 62.1 | 21 | 7  | US-10-310-914A-317102  | Sequence 317102,  |
| C 136 | 12.2 | 64.2 | 21 | 7  | US-10-310-914A-477224   | Sequence 477224,    | C 209 | 11.8 | 62.1 | 21 | 7  | US-10-310-914A-905240  | Sequence 905240,  |
| C 137 | 12.2 | 64.2 | 21 | 7  | US-10-310-914A-509581   | Sequence 509581,    | C 210 | 11.8 | 62.1 | 21 | 7  | US-10-310-914A-1042652 | Sequence 1042652, |
| C 138 | 12.2 | 64.2 | 21 | 7  | US-10-310-914A-529206   | Sequence 529206,    | C 211 | 11.8 | 62.1 | 21 | 7  | US-10-310-914A-1168356 | Sequence 1168356, |
| C 139 | 12.2 | 64.2 | 21 | 7  | US-10-310-914A-624047   | Sequence 624047,    | C 212 | 11.8 | 62.1 | 21 | 7  | US-10-310-914A-1368477 | Sequence 1368477, |
| C 140 | 12.2 | 64.2 | 21 | 7  | US-10-310-914A-1059674  | Sequence 1059674,   | C 213 | 11.8 | 62.1 | 22 | 7  | US-10-310-914A-595017  | Sequence 595017,  |
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| C 143 | 12.2 | 64.2 | 21 | 7  | US-10-310-914A-1258075  | Sequence 1258075,   | C 216 | 11.8 | 62.1 | 22 | 7  | US-10-310-914A-905232  | Sequence 905232,  |
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| C 145 | 12.2 | 64.2 | 21 | 7  | US-10-310-914A-1314397  | Sequence 1314397,   | C 218 | 11.8 | 62.1 | 22 | 7  | US-10-310-914A-1168359 | Sequence 1168359, |
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| C 150 | 12.2 | 64.2 | 22 | 7  | US-10-310-914A-793125   | Sequence 793125,    | C 223 | 11.8 | 62.1 | 23 | 7  | US-10-310-914A-1241476 | Sequence 1241476, |
| C 151 | 12.2 | 64.2 | 23 | 7  | US-10-310-914A-57224    | Sequence 57224, A   | C 224 | 11.8 | 62.1 | 24 | 7  | US-10-310-914A-389442  | Sequence 389442,  |
| C 152 | 12.2 | 64.2 | 23 | 7  | US-10-310-914A-57225    | Sequence 57225, A   | C 225 | 11.8 | 62.1 | 24 | 7  | US-10-310-914A-433626  | Sequence 433626,  |
| C 153 | 12.2 | 64.2 | 23 | 7  | US-10-310-914A-477182   | Sequence 477182,    | C 226 | 11.8 | 62.1 | 25 | 7  | US-10-750-185-23854    | Sequence 23854, A |
| C 154 | 12.2 | 64.2 | 23 | 7  | US-10-310-914A-624007   | Sequence 624007,    | C 227 | 11.8 | 62.1 | 25 | 7  | US-10-310-914A-1042586 | Sequence 1042586, |
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ALIGNMENTS

RESULT 1  
US-11-127-654-74  
; Sequence 74, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

Sequence 667907,  
Sequence 667908,  
Sequence 13923, A  
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Sequence 94770, A  
Sequence 265957,  
Sequence 265965,  
Sequence 265981,  
Sequence 296001,  
Sequence 296022,  
Sequence 296024,  
Sequence 296028,  
Sequence 296043,  
Sequence 351683,  
Sequence 351684,  
Sequence 351693,  
Sequence 65930, A  
Sequence 1358363,  
Sequence 63104, A  
Sequence 147289,  
Sequence 369060,  
Sequence 795738,  
Sequence 873292,  
Sequence 920358,  
Sequence 1049795,  
Sequence 931, App  
Sequence 53127, A  
Sequence 63105, A  
Sequence 142175,  
Sequence 154172,  
Sequence 200792,  
Sequence 368126,  
Sequence 369887,  
Sequence 458307,  
Sequence 543421,  
Sequence 673169,  
Sequence 874575,  
Sequence 961314,  
Sequence 1021596,  
Sequence 1024378,  
Sequence 1349901,  
Sequence 1352469,  
Sequence 39373, A  
Sequence 25298, A  
Sequence 70487, A  
Sequence 954555,  
Sequence 1062633,  
Sequence 1122826,  
Sequence 1181622,  
Sequence 1211520,

; TITLE OF INVENTION: INFLAMMATORY DISEASES  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 74  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-74

Query Match 100.0%; Score 19; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
|||||  
Db 1 GGGGTGACGTTTCAGGGGG 19

RESULT 2  
US-11-127-654-76  
; Sequence 76, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

; TITLE OF INVENTION: INFLAMMATORY DISEASES  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 76  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-76

Query Match 91.6%; Score 17.4; DB 11; Length 19;  
Best Local Similarity 94.7%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
|||||  
Db 1 GGGGTGCTGTTTCAGGGGG 19

RESULT 3  
US-10-310-914A-1228446  
; Sequence 1228446, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuizat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A

;  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1228446  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1228446

Query Match 74.7%; Score 14.2; DB 7; Length 19;  
Best Local Similarity 68.4%; Pred. No. 8.1e+02;  
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19  
Db 1 GGAUGACCGUAGGGGGG 19

RESULT 4  
US-11-127-797-1  
; Sequence 1, Application US/11127797  
; Publication No. US20050245477A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/11/127,797  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US/10/690,495  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-797-1

Query Match 74.7%; Score 14.2; DB 9; Length 20;  
Best Local Similarity 84.2%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 5  
US-11-127-803-1  
; Sequence 1, Application US/11127803  
; Publication No. US20050244379A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/11/127,803  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US/10/690,495  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20

;  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-803-1

Query Match 74.7%; Score 14.2; DB 9; Length 20;  
Best Local Similarity 84.2%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 6  
US-11-128-127-1  
; Sequence 1, Application US/11128127  
; Publication No. US20050244380A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/11/128,127  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US/10/690,495  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-128-127-1

Query Match 74.7%; Score 14.2; DB 9; Length 20;  
Best Local Similarity 84.2%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 7  
US-11-127-654-216  
; Sequence 216, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 216  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-216

Query Match 74.7%; Score 14.2; DB 11; Length 20;  
Best Local Similarity 84.2%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGGTTGACGTTTGGGGG 20

## RESULT 8

US-10-310-914A-1202061/c  
; Sequence 1202061, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1202061  
; LENGTH: 28  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1202061

Query Match 73.7%; Score 14; DB 7; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGG 16  
||||| |||||  
Db 28 GGTGACGTTTCAGG 15

## RESULT 9

US-10-310-914A-524757  
; Sequence 524757, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 524757  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-524757

Query Match 72.6%; Score 13.8; DB 7; Length 20;  
Best Local Similarity 70.6%; Pred. No. 1.3e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGG 19  
||| ||||| |||||  
Db 4 GGUCAGGUUCAGGGGG 20

## RESULT 10

US-10-310-914A-895375/c  
; Sequence 895375, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 895375  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-895375

Query Match 72.6%; Score 13.8; DB 7; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 17  
||||| ||||| |||||  
Db 19 GGGTTACGTTTCAGGGG 3

## RESULT 11

US-10-310-914A-1185102  
; Sequence 1185102, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1185102  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1185102

Query Match 72.6%; Score 13.8; DB 7; Length 20;  
Best Local Similarity 70.6%; Pred. No. 1.3e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 17  
||||| ||||| |||||  
Db 2 GGGGUGCCGUUCUGGGG 18

## RESULT 12

US-10-310-914A-895439/c  
; Sequence 895439, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 895439  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human

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US-10-310-914A-895439
Query Match          72.6%; Score 13.8; DB 7; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 17
DB 20 GGGGTGACGTTTCAGGG 4

RESULT 13
US-10-310-914A-1185206
; Sequence 1185206, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1185206
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1185206
Query Match          72.6%; Score 13.8; DB 7; Length 22;
Best Local Similarity 70.8%; Pred. No. 1.3e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 17
DB 5 GGGGCGCCGUCUGGG 21

RESULT 14
US-10-310-914A-530908/c
; Sequence 530908, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 530908
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-530908
Query Match          72.6%; Score 13.8; DB 7; Length 23;
Best Local Similarity 88.2%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 17
DB 19 GGGGTGACTTTCAGGG 3

RESULT 15
US-11-101-244-1188547/c
; Sequence 1188547, Application US/1101244
; Publication No. US20050246794A1

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; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1188547
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1188547
Query Match          70.5%; Score 13.4; DB 9; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGG 16
DB 15 GGGTGACGTTTCATGG 1

RESULT 16
US-11-083-784-1188547/c
; Sequence 1188547, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1188547
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1188547
Query Match          70.5%; Score 13.4; DB 10; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGG 16
DB 15 GGGTGACGTTTCATGG 1

RESULT 17
US-10-310-914A-673587/c
; Sequence 673587, Application US/10310914A

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; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 673587
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-673587

Query Match          70.5%; Score 13.4; DB 7; Length 22;
Best Local Similarity 93.3%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 GGTGACGTTTCAGGGG 17
Db      20 GGTGACGTTTCAGGGG 6
|||||
|||||

RESULT 18
US-10-310-914A-308426/c
; Sequence 308426, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 308426
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-308426

Query Match          69.5%; Score 13.2; DB 7; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGGTGACGTTTCAGGGG 18
Db      18 GGGGTGACCTTCTTGGGG 1
|||||
|||||

RESULT 19
US-11-127-654-498
; Sequence 498, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2002-03-29
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 673587
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-673587
```

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; SEQ ID NO 498
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-498

Query Match          69.5%; Score 13.2; DB 11; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGGTGACGTTTCAGGGG 18
Db      3 GGCATGACGTTTCGGGGG 20
|||||
|||||

RESULT 20
US-11-127-654-501
; Sequence 501, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2002-03-29
; PRIOR FILING DATE: 2002-03-29
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 501
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-501

Query Match          69.5%; Score 13.2; DB 11; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGGTGACGTTTCAGGGG 18
Db      3 GGCATGACGTTTCGGGGG 20
|||||
|||||

RESULT 21
US-10-310-914A-872061
; Sequence 872061, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 872061
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-872061

Query Match          69.5%; Score 13.2; DB 7; Length 21;
```

```
Best Local Similarity 72.2%; Pred. No. 2.4e+03; Indels 3; Mismatches 3; Gaps 0;
Matches 13; Conservative 2;

QY 2 GGGTGACGTTACGGGGG 19
    |||:| | :||| |||
Db 1 GGGGAAGGUCACGGGGG 18

RESULT 22
US-10-310-914A-114797/c
; Sequence 114797, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114797
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-114797

Query Match 69.5%; Score 13.2; DB 7; Length 22;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTACGGGGG 19
    |||:| | :||| |||
Db 19 GGGTGACGCCAGGAG 2

RESULT 23
US-10-310-914A-456901/c
; Sequence 456901, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 456901
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-456901

Query Match 69.5%; Score 13.2; DB 7; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACGGGGG 18
    |||:| | :||| |||
Db 23 GGGGTGAACCTTCAGTGG 6

RESULT 24
US-10-310-914A-518042/c
; Sequence 518042, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
```

```
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 518042
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-518042

Query Match 69.5%; Score 13.2; DB 7; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACGGGGG 18
    |||:| | :||| |||
Db 20 GGGGTGACATTCATGGTG 3

RESULT 25
US-10-310-914A-836953
; Sequence 836953, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 836953
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-836953

Query Match 69.5%; Score 13.2; DB 7; Length 23;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTACGGGGG 19
    |||:| | :||| |||
Db 3 GGGUCACGUGCGGGGGG 20

RESULT 26
US-10-310-914A-896494/c
; Sequence 896494, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 896494
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-896494

Query Match 69.5%; Score 13.2; DB 7; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
```



Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGGGG 19  
|||||  
Db 23 GGGTGACGTTTCAGGGGG 6

## RESULT 27

US-10-310-914A-837004  
; Sequence 837004, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087, 0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 837004

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-837004

Query Match 69.5%; Score 13.2; DB 7; Length 24;

Best Local Similarity 66.7%; Pred. No. 2.4e+03;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGGGG 19  
|||||  
Db 7 GGGTGACGTTTCAGGGGG 24

## RESULT 28

US-10-310-914A-509542/c

; Sequence 509542, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087, 0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 509542

; LENGTH: 25

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-509542

Query Match 69.5%; Score 13.2; DB 7; Length 25;

Best Local Similarity 83.3%; Pred. No. 2.4e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 18  
|||||  
Db 21 GGGTGACGTTTCAGGGGG 4

## RESULT 29

US-11-121-849-16126

; Sequence 16126, Application US/11121849

; Publication No. US2005027080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: Microarrays

; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 16126  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-16126

Query Match 69.5%; Score 13.2; DB 11; Length 25;

Best Local Similarity 83.3%; Pred. No. 2.4e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 18  
|||||  
Db 3 GGGTGACGTTTCAGGGGG 20

## RESULT 30

US-11-012-353-97

; Sequence 97, Application US/11012353

; Publication No. US20050249730A1

; GENERAL INFORMATION:

; APPLICANT: GOETSCH, LILIANE

; APPLICANT: CORVAIA, NATHALIE

; APPLICANT: DUFLOS, ALAIN

; APPLICANT: HAEUM, JEAN-FRANCOIS

; APPLICANT: LEGER, OLIVIER

; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

; FILE REFERENCE: 017753-198

; CURRENT APPLICATION NUMBER: US/11/012,353

; CURRENT FILING DATE: 2004-12-16

; PRIOR APPLICATION NUMBER: 10/735,916

; PRIOR FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: FR 0308538

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR03/00178

; PRIOR FILING DATE: 2003-01-20

; PRIOR APPLICATION NUMBER: FR 0205753

; PRIOR FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: FR 0200653

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 0200654

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 97

; LENGTH: 32

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide

US-11-012-353-97

Query Match 69.5%; Score 13.2; DB 11; Length 32;

Best Local Similarity 83.3%; Pred. No. 2.4e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 18  
|||||  
Db 7 GGGTGACGTTTCAGGGGG 24

## RESULT 31

US-10-310-914A-1145336

; Sequence 1145336, Application US/10310914A

```
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1145336
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1145336

Query Match          67.4%; Score 12.8; DB 7; Length 18;
Best Local Similarity 75.0%; Pred. No. 3.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACGGG 16
Db 2 GGGUUGACGUACAGG 17

RESULT 32
US-10-310-914A-966814/c
; Sequence 966814, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 966814
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-966814

Query Match          67.4%; Score 12.8; DB 7; Length 19;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACGGG 16
Db 18 GGGGAGACGCTCAGG 3

RESULT 33
US-10-522-362-49
; Sequence 49, Application US/10522362
; Publication No. US20050281788A1
; GENERAL INFORMATION:
; APPLICANT: De Bari, Cosimo
; APPLICANT: Dell'Accio, Francesco
; APPLICANT: Luyten, Frank
; TITLE OF INVENTION: Compositions Comprising Muscle
; FILE REFERENCE: 50304/030001
; CURRENT APPLICATION NUMBER: US/10/522,362
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: PCT/EP03/009008
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/399,745
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 49
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: CD90 antisense primer
US-10-522-362-49

Query Match          67.4%; Score 12.8; DB 7; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTGACGTTACGGGGG 19
Db 3 GTGACGTTCTGGAGG 18

RESULT 34
US-10-310-914A-746353/c
; Sequence 746353, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 746353
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-746353

Query Match          67.4%; Score 12.8; DB 7; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACGGG 16
Db 18 GTGGGACGCTCAGG 3

RESULT 35
US-10-310-914A-966777/c
; Sequence 966777, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 966777
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-966777

Query Match          67.4%; Score 12.8; DB 7; Length 22;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 GGGGTGACGTTTCAGGG 16  
|||||  
Db 17 GGGGAGCGCTCAGGG 2

## RESULT 36

US-10-310-914A-240915/c  
; Sequence 240915, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 240915  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-240915

Query Match 67.4%; Score 12.8; DB 7; Length 23;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTGACGTTTCAGGGGG 19  
|||||  
Db 21 GTGAAGTTTCAGGGTGG 6

## RESULT 37

US-10-310-914A-411534  
; Sequence 411534, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 411534  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-411534

Query Match 67.4%; Score 12.8; DB 7; Length 24;  
Best Local Similarity 81.2%; Pred. No. 3.7e+03;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGTGACGTTTCAGGG 17  
|||||  
Db 6 GGGGAGCGGUCAGGGG 21

## RESULT 38

US-10-310-914A-1145337  
; Sequence 1145337, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1145337  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1145337

Query Match 67.4%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGG 16  
|||||  
Db 9 GGGUAGCGUACAGGG 24

## RESULT 39

US-11-121-849-15921/c  
; Sequence 15921, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 15921  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-15921

Query Match 67.4%; Score 12.8; DB 11; Length 25;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTGACGTTTCAGGGGG 18  
|||||  
Db 18 GGTGATGTTCTGGGGG 3

## RESULT 40

US-11-121-849-22103/c  
; Sequence 22103, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 22103  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-22103

Query Match 67.4%; Score 12.8; DB 11; Length 25;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY      3 GGTGACGTTTCAGGGG 18
      ||||| ||||| |||||
Db      18 GGTGATGTTCTGGGG 3

RESULT 41
US-11-121-849-24138/c
; Sequence 24138, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24138
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-24138

Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGTGACGTTTCAGGGG 18
      ||||| ||||| |||||
Db      18 GGTGATGTTCTGGGG 3

RESULT 42
US-11-121-849-107577
; Sequence 107577, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 107577
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-107577

Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGG 16
      ||||| ||||| |||||
Db      7 GGGGACGCTTCAGGG 22

RESULT 43
US-11-121-849-115643/c
; Sequence 115643, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
```

```
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115643
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-115643

Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGTGACGTTTCAGGGG 18
      ||||| ||||| |||||
Db      17 GATGACGTTTCAGGTG 2

RESULT 44
US-11-121-849-476398/c
; Sequence 476398, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 476398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-476398

Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGTGACGTTTCAGGGG 17
      ||||| ||||| |||||
Db      21 GGCTGACCTTCAGGGG 6

RESULT 45
US-11-121-849-568167/c
; Sequence 568167, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 568167
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-568167
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Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGGG 16
Db 18 GGTGTGACGTTAAGGG 3

RESULT 46
US-11-121-849-570964
; Sequence 570964, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 570964
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-570964

Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGGG 16
Db 2 GGGCTGATGTTACGGG 17

RESULT 47
US-10-755-092-43/c
; Sequence 43, Application US/10755092
; Publication No. US20060021095A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launils, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/755,092
; FILING DATE: 08-Jan-2004
```

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-Nov-2001
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer P5(a)"
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-755-092-43
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Query Match      67.4%; Score 12.8; DB 6; Length 32;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTGACGTTACGGGG 18
Db 18 GGTGCCGTACAGGGG 3
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RESULT 48
US-10-939-294A-19843
; Sequence 19843, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19843
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-19843
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Query Match      67.4%; Score 12.8; DB 7; Length 32;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGGG 16
Db 8 GGGGTGACGTTCCGGG 23
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RESULT 49  
US-11-175-859-51905/c  
; Sequence 51905, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; APPLICANT: Liu, Guoying et al.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 51905  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-51905

Query Match 67.4%; Score 12.8; DB 11; Length 50;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 16  
Db 42 GGGAGGACGTTTCAGGG 27

RESULT 50  
US-10-310-914A-896490/c  
; Sequence 896490, Application US/10310914A  
; Publication No. US2006003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 896490  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-896490

Query Match 66.3%; Score 12.6; DB 7; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
Db 19 GTGGTGACGTCGAGGGGG 1

Search completed: February 16, 2006, 02:53:00  
Job time : 181.124 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:51:58 ; Search time 575.802 Seconds  
(without alignments)  
2369.293 Million cell updates/sec

Title: US-09-669-187A-81

Perfect score: 24

Sequence: 1 ggggtccagcgtgcgcattggggg 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vl.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 24    | 100.0       | 24     | 6     | AX103889 Sequence  |
| 2          | 24    | 100.0       | 24     | 6     | AX355412 Sequence  |
| 3          | 24    | 100.0       | 24     | 6     | AX546942 Sequence  |
| 4          | 16.2  | 67.5        | 25     | 6     | AR182410 Sequence  |
| 5          | 16    | 66.7        | 30     | 6     | QB859706 Sequence  |
| 6          | 16    | 66.7        | 33     | 6     | BD263032 Trans-Spe |
| 7          | 16    | 66.7        | 33     | 6     | AR217874 Sequence  |
| 8          | 15.2  | 63.3        | 35     | 6     | AR630015 Sequence  |
| 9          | 15.2  | 63.3        | 35     | 6     | AX351117 Sequence  |
| 10         | 15    | 62.5        | 16     | 6     | AX103898 Sequence  |
| 11         | 15    | 62.5        | 16     | 6     | AX355505 Sequence  |
| 12         | 15    | 62.5        | 16     | 6     | AX546951 Sequence  |
| 13         | 15    | 62.5        | 27     | 6     | AR004426 Sequence  |
| 14         | 15    | 62.5        | 27     | 6     | I43661 Sequence 13 |
| 15         | 15    | 62.5        | 27     | 6     | I86720 Sequence 8  |
| 16         | 15    | 62.5        | 40     | 6     | AX754696 Sequence  |
| 17         | 15    | 62.5        | 50     | 8     | HSTFE3ID3          |
| 18         | 14.8  | 61.7        | 20     | 6     | AX463650 Sequence  |

|     |      |      |    |   |                    |                    |       |      |      |    |    |          |                    |
|-----|------|------|----|---|--------------------|--------------------|-------|------|------|----|----|----------|--------------------|
| 92  | 14   | 58.3 | 18 | 6 | AX040169 Sequence  | AX040169 Sequence  | c 165 | 13.8 | 57.5 | 45 | 6  | BD168552 | BD168552 Cells pro |
| 93  | 14   | 58.3 | 18 | 6 | AX040403 Sequence  | AX040403 Sequence  | 166   | 13.8 | 57.5 | 45 | 6  | AR199548 | AR199548 Sequence  |
| 94  | 14   | 58.3 | 18 | 6 | AX063576 Sequence  | AX063576 Sequence  | 167   | 13.8 | 57.5 | 45 | 6  | AR374700 | AR374700 Sequence  |
| 95  | 14   | 58.3 | 18 | 6 | AX081353 Sequence  | AX081353 Sequence  | 168   | 13.8 | 57.5 | 45 | 6  | AR409335 | AR409335 Sequence  |
| 96  | 14   | 58.3 | 18 | 6 | AX083693 Sequence  | AX083693 Sequence  | 169   | 13.8 | 57.5 | 45 | 6  | AR650967 | AR650967 Sequence  |
| 97  | 14   | 58.3 | 18 | 6 | AX088930 Sequence  | AX088930 Sequence  | 170   | 13.8 | 57.5 | 45 | 6  | AX239597 | AX239597 Sequence  |
| 98  | 14   | 58.3 | 18 | 6 | AX103809 Sequence  | AX103809 Sequence  | c 171 | 13.8 | 57.5 | 47 | 6  | AR291901 | AR291901 Sequence  |
| 99  | 14   | 58.3 | 18 | 6 | AX103862 Sequence  | AX103862 Sequence  | c 172 | 13.8 | 57.5 | 48 | 15 | AJ718919 | AJ718919 Nicotiana |
| 100 | 14   | 58.3 | 18 | 6 | AX103863 Sequence  | AX103863 Sequence  | c 173 | 13.6 | 56.7 | 21 | 6  | AR086618 | AR086618 Sequence  |
| 101 | 14   | 58.3 | 18 | 6 | AX103899 Sequence  | AX103899 Sequence  | 174   | 13.6 | 56.7 | 28 | 6  | AX766504 | AX766504 Sequence  |
| 102 | 14   | 58.3 | 18 | 6 | AX105211 Sequence  | AX105211 Sequence  | 175   | 13.6 | 56.7 | 30 | 6  | QO878195 | QO878195 Sequence  |
| 103 | 14   | 58.3 | 18 | 6 | AX135635 Sequence  | AX135635 Sequence  | c 176 | 13.6 | 56.7 | 34 | 6  | BD189694 | BD189694 A method  |
| 104 | 14   | 58.3 | 18 | 6 | AX283183 Sequence  | AX283183 Sequence  | c 177 | 13.6 | 56.7 | 34 | 6  | QO890359 | QO890359 Sequence  |
| 105 | 14   | 58.3 | 18 | 6 | AX283250 Sequence  | AX283250 Sequence  | c 178 | 13.6 | 56.7 | 34 | 6  | QO897034 | QO897034 Sequence  |
| 106 | 14   | 58.3 | 18 | 6 | AX355727 Sequence  | AX355727 Sequence  | c 179 | 13.6 | 56.7 | 35 | 6  | BD002997 | BD002997 A method  |
| 107 | 14   | 58.3 | 18 | 6 | AX355728 Sequence  | AX355728 Sequence  | c 180 | 13.6 | 56.7 | 35 | 6  | BD002999 | BD002999 A method  |
| 108 | 14   | 58.3 | 18 | 6 | AX455638 Sequence  | AX455638 Sequence  | c 181 | 13.6 | 56.7 | 36 | 6  | CS053838 | CS053838 Sequence  |
| 109 | 14   | 58.3 | 18 | 6 | AX468484 Sequence  | AX468484 Sequence  | c 182 | 13.6 | 56.7 | 36 | 6  | CS084988 | CS084988 Sequence  |
| 110 | 14   | 58.3 | 18 | 6 | AX497778 Sequence  | AX497778 Sequence  | 183   | 13.4 | 55.8 | 27 | 6  | AR477056 | AR477056 Sequence  |
| 111 | 14   | 58.3 | 18 | 6 | AX513618 Sequence  | AX513618 Sequence  | c 184 | 13.4 | 55.8 | 27 | 6  | AR477057 | AR477057 Sequence  |
| 112 | 14   | 58.3 | 18 | 6 | AX513688 Sequence  | AX513688 Sequence  | c 185 | 13.4 | 55.8 | 27 | 6  | AR606811 | AR606811 Sequence  |
| 113 | 14   | 58.3 | 18 | 6 | AX513709 Sequence  | AX513709 Sequence  | c 186 | 13.4 | 55.8 | 27 | 6  | AR606812 | AR606812 Sequence  |
| 114 | 14   | 58.3 | 18 | 6 | AX513710 Sequence  | AX513710 Sequence  | 187   | 13.4 | 55.8 | 28 | 6  | BD086016 | BD086016 Novel tac |
| 115 | 14   | 58.3 | 18 | 6 | AX537410 Sequence  | AX537410 Sequence  | 188   | 13.4 | 55.8 | 28 | 6  | BD096170 | BD096170 Novel pol |
| 116 | 14   | 58.3 | 18 | 6 | AX546862 Sequence  | AX546862 Sequence  | 189   | 13.4 | 55.8 | 30 | 6  | AX472520 | AX472520 Sequence  |
| 117 | 14   | 58.3 | 18 | 6 | AX546915 Sequence  | AX546915 Sequence  | 190   | 13.4 | 55.8 | 30 | 6  | AX476834 | AX476834 Sequence  |
| 118 | 14   | 58.3 | 18 | 6 | AX546916 Sequence  | AX546916 Sequence  | 191   | 13.4 | 55.8 | 30 | 6  | AX476857 | AX476857 Sequence  |
| 119 | 14   | 58.3 | 18 | 6 | AX546952 Sequence  | AX546952 Sequence  | 192   | 13.4 | 55.8 | 33 | 6  | AR634928 | AR634928 Sequence  |
| 120 | 14   | 58.3 | 18 | 6 | AX593887 Sequence  | AX593887 Sequence  | 193   | 13.4 | 55.8 | 33 | 6  | AX259750 | AX259750 Sequence  |
| 121 | 14   | 58.3 | 18 | 6 | AX593888 Sequence  | AX593888 Sequence  | 194   | 13.4 | 55.8 | 38 | 6  | AR050224 | AR050224 Sequence  |
| 122 | 14   | 58.3 | 18 | 6 | AX671088 Sequence  | AX671088 Sequence  | c 195 | 13.4 | 55.8 | 38 | 6  | AR050225 | AR050225 Sequence  |
| 123 | 14   | 58.3 | 18 | 6 | AX786560 Sequence  | AX786560 Sequence  | 196   | 13.4 | 55.8 | 40 | 11 | CS000590 | CS000590 Sequence  |
| 124 | 14   | 58.3 | 18 | 6 | AX797646 Sequence  | AX797646 Sequence  | c 197 | 13.4 | 55.8 | 43 | 6  | AR044090 | AR044090 Sequence  |
| 125 | 14   | 58.3 | 18 | 6 | AX797661 Sequence  | AX797661 Sequence  | c 198 | 13.4 | 55.8 | 43 | 6  | AR044094 | AR044094 Sequence  |
| 126 | 14   | 58.3 | 18 | 6 | AX957630 Sequence  | AX957630 Sequence  | c 199 | 13.4 | 55.8 | 43 | 6  | AR091711 | AR091711 Sequence  |
| 127 | 14   | 58.3 | 18 | 6 | AX957645 Sequence  | AX957645 Sequence  | c 200 | 13.4 | 55.8 | 43 | 6  | AR091715 | AR091715 Sequence  |
| 128 | 14   | 58.3 | 18 | 6 | AX957724 Sequence  | AX957724 Sequence  | c 201 | 13.4 | 55.8 | 50 | 6  | QO006768 | QO006768 Sequence  |
| 129 | 14   | 58.3 | 18 | 6 | AX957739 Sequence  | AX957739 Sequence  | c 202 | 13.4 | 55.8 | 50 | 6  | AX190187 | AX190187 Sequence  |
| 130 | 14   | 58.3 | 18 | 6 | AX958129 Sequence  | AX958129 Sequence  | c 203 | 13.4 | 55.8 | 50 | 6  | AX171490 | AX171490 Sequence  |
| 131 | 14   | 58.3 | 18 | 6 | AX958144 Sequence  | AX958144 Sequence  | c 204 | 13.2 | 55.0 | 29 | 6  | AR117364 | AR117364 Sequence  |
| 132 | 14   | 58.3 | 18 | 6 | BD009103           | BD009103 Immunosti | c 205 | 13.2 | 55.0 | 29 | 6  | AR205143 | AR205143 Sequence  |
| 133 | 14   | 58.3 | 19 | 6 | AR608704 Sequence  | AR608704 Sequence  | c 206 | 13.2 | 55.0 | 29 | 6  | AR223347 | AR223347 Sequence  |
| 134 | 14   | 58.3 | 19 | 6 | AR608705 Sequence  | AR608705 Sequence  | c 207 | 13.2 | 55.0 | 29 | 6  | AR287848 | AR287848 Sequence  |
| 135 | 14   | 58.3 | 19 | 6 | AR643614 Sequence  | AR643614 Sequence  | c 208 | 13.2 | 55.0 | 30 | 6  | AX598046 | AX598046 Sequence  |
| 136 | 14   | 58.3 | 19 | 6 | AX083694 Sequence  | AX083694 Sequence  | c 209 | 13.2 | 55.0 | 33 | 6  | B41685   | B41685 Process for |
| 137 | 14   | 58.3 | 19 | 6 | AX083695 Sequence  | AX083695 Sequence  | c 210 | 13.2 | 55.0 | 36 | 6  | CS053837 | CS053837 Sequence  |
| 138 | 14   | 58.3 | 20 | 6 | AR182888 Sequence  | AR182888 Sequence  | c 211 | 13.2 | 55.0 | 36 | 6  | CS084987 | CS084987 Sequence  |
| 139 | 14   | 58.3 | 20 | 6 | AR607451 Sequence  | AR607451 Sequence  | c 212 | 13.2 | 55.0 | 43 | 6  | AX477725 | AX477725 Sequence  |
| 140 | 14   | 58.3 | 20 | 6 | AX045387 Sequence  | AX045387 Sequence  | c 213 | 13.2 | 55.0 | 43 | 6  | AX477729 | AX477729 Sequence  |
| 141 | 14   | 58.3 | 20 | 6 | AX103895 Sequence  | AX103895 Sequence  | 214   | 13   | 54.2 | 16 | 6  | CS124138 | CS124138 Sequence  |
| 142 | 14   | 58.3 | 20 | 6 | AX355729 Sequence  | AX355729 Sequence  | 215   | 13   | 54.2 | 17 | 6  | CS124129 | CS124129 Sequence  |
| 143 | 14   | 58.3 | 20 | 6 | AX546948 Sequence  | AX546948 Sequence  | 216   | 13   | 54.2 | 18 | 6  | CS124089 | CS124089 Sequence  |
| 144 | 14   | 58.3 | 22 | 6 | A76123 Sequence 3  | A76123 Sequence 3  | 217   | 13   | 54.2 | 18 | 6  | BD008994 | BD008994 Inhibito  |
| 145 | 14   | 58.3 | 22 | 6 | A76124 Sequence 4  | A76124 Sequence 4  | 218   | 13   | 54.2 | 20 | 6  | AR052603 | AR052603 Sequence  |
| 146 | 14   | 58.3 | 23 | 6 | AR608697 Sequence  | AR608697 Sequence  | c 219 | 13   | 54.2 | 20 | 6  | AR052609 | AR052609 Sequence  |
| 147 | 14   | 58.3 | 23 | 6 | AR608698 Sequence  | AR608698 Sequence  | c 220 | 13   | 54.2 | 20 | 6  | AR176022 | AR176022 Sequence  |
| 148 | 14   | 58.3 | 23 | 6 | AX083687 Sequence  | AX083687 Sequence  | c 221 | 13   | 54.2 | 20 | 6  | AR176023 | AR176023 Sequence  |
| 149 | 14   | 58.3 | 23 | 6 | AX083688 Sequence  | AX083688 Sequence  | c 222 | 13   | 54.2 | 20 | 6  | BD187522 | BD187522 REGULATIO |
| 150 | 14   | 58.3 | 28 | 6 | AX352076 Sequence  | AX352076 Sequence  | c 223 | 13   | 54.2 | 20 | 6  | I96082   | I96082 Sequence 1  |
| 151 | 14   | 58.3 | 30 | 6 | AR116187 Sequence  | AR116187 Sequence  | c 224 | 13   | 54.2 | 20 | 6  | I96088   | I96088 Sequence 7  |
| 152 | 14   | 58.3 | 30 | 6 | AR074539 Sequence  | AR074539 Sequence  | c 225 | 13   | 54.2 | 20 | 6  | AR630667 | AR630667 Sequence  |
| 153 | 14   | 58.3 | 32 | 6 | AX513689 Sequence  | AX513689 Sequence  | c 226 | 13   | 54.2 | 20 | 6  | AR630673 | AR630673 Sequence  |
| 154 | 14   | 58.3 | 32 | 6 | AX513690 Sequence  | AX513690 Sequence  | c 227 | 13   | 54.2 | 20 | 6  | AX211669 | AX211669 Sequence  |
| 155 | 14   | 58.3 | 32 | 6 | AX513691 Sequence  | AX513691 Sequence  | c 228 | 13   | 54.2 | 20 | 6  | AX211670 | AX211670 Sequence  |
| 156 | 14   | 58.3 | 35 | 6 | AR052604 Sequence  | AR052604 Sequence  | 229   | 13   | 54.2 | 20 | 6  | AX277461 | AX277461 Sequence  |
| 157 | 14   | 58.3 | 35 | 6 | BD187517           | BD187517 REGULATIO | 230   | 13   | 54.2 | 24 | 6  | AX477295 | AX477295 Sequence  |
| 158 | 14   | 58.3 | 35 | 6 | I96083 Sequence 2  | I96083 Sequence 2  | 231   | 13   | 54.2 | 24 | 6  | AX526671 | AX526671 Sequence  |
| 159 | 14   | 58.3 | 35 | 6 | AR630668 Sequence  | AR630668 Sequence  | c 232 | 13   | 54.2 | 29 | 6  | BD057732 | BD057732 Fusion pr |
| 160 | 14   | 58.3 | 36 | 6 | BD094991           | BD094991 Apoptosis | c 233 | 13   | 54.2 | 29 | 6  | BD081562 | BD081562 Soluble s |
| 161 | 14   | 58.3 | 36 | 6 | E49826             | E49826 apoptosis-i | c 234 | 13   | 54.2 | 29 | 6  | BD170788 | BD170788 Rice sucr |
| 162 | 14   | 58.3 | 40 | 6 | AR009503 Sequence  | AR009503 Sequence  | c 235 | 13   | 54.2 | 29 | 6  | AR213673 | AR213673 Sequence  |
| 163 | 13.8 | 57.5 | 30 | 6 | AR526915 Sequence  | AR526915 Sequence  | c 236 | 13   | 54.2 | 34 | 6  | BD133294 | BD133294 Process f |
| 164 | 13.8 | 57.5 | 45 | 6 | BD056462 Novel low | BD056462 Novel low | c 237 | 13   | 54.2 | 35 | 6  | A61400   | A61400 Sequence 6  |



|       |      |      |    |   |          |                    |
|-------|------|------|----|---|----------|--------------------|
| c 238 | 13   | 54.2 | 35 | 6 | BD265504 | BD265504 Mammalian |
| c 239 | 13   | 54.2 | 35 | 6 | AR370510 | Sequence           |
| c 240 | 13   | 54.2 | 35 | 6 | AR380981 | Sequence           |
| c 241 | 13   | 54.2 | 35 | 6 | AR442709 | Sequence           |
| c 242 | 13   | 54.2 | 46 | 6 | A98793   | Sequence 26        |
| c 243 | 13   | 54.2 | 46 | 6 | AR242321 | Sequence           |
| c 244 | 13   | 54.2 | 48 | 6 | AR117273 | Sequence           |
| c 245 | 13   | 54.2 | 48 | 6 | BD087162 | Sequence           |
| c 246 | 13   | 54.2 | 48 | 6 | AR257428 | Sequence           |
| c 247 | 13   | 54.2 | 48 | 6 | AR269373 | Sequence           |
| c 248 | 13   | 54.2 | 50 | 6 | CQ008484 | Sequence           |
| c 249 | 12.8 | 53.3 | 18 | 6 | AX460270 | Sequence           |
| c 250 | 12.8 | 53.3 | 19 | 6 | AX155585 | Sequence           |
| c 251 | 12.8 | 53.3 | 20 | 6 | AX293836 | Sequence           |
| c 252 | 12.8 | 53.3 | 20 | 6 | AX296687 | Sequence           |
| c 253 | 12.8 | 53.3 | 23 | 6 | I27136   | Sequence 32        |
| c 254 | 12.8 | 53.3 | 24 | 6 | I27121   | Sequence 17        |
| c 255 | 12.8 | 53.3 | 24 | 6 | AX289203 | Sequence           |
| c 256 | 12.8 | 53.3 | 24 | 6 | AX292054 | Sequence           |
| c 257 | 12.8 | 53.3 | 24 | 6 | AX444476 | Sequence           |
| c 258 | 12.8 | 53.3 | 25 | 6 | AX751162 | Sequence           |
| c 259 | 12.8 | 53.3 | 25 | 6 | AX751163 | Sequence           |
| c 260 | 12.8 | 53.3 | 26 | 6 | AR228693 | Sequence           |
| c 261 | 12.8 | 53.3 | 29 | 6 | AR117362 | Sequence           |
| c 262 | 12.8 | 53.3 | 29 | 6 | AR205141 | Sequence           |
| c 263 | 12.8 | 53.3 | 29 | 6 | AR223345 | Sequence           |
| c 264 | 12.8 | 53.3 | 29 | 6 | AR287846 | Sequence           |
| c 265 | 12.8 | 53.3 | 30 | 6 | AX166282 | Sequence           |
| c 266 | 12.8 | 53.3 | 31 | 6 | I19522   | Sequence 4         |
| c 267 | 12.8 | 53.3 | 31 | 6 | AX148321 | Sequence           |
| c 268 | 12.8 | 53.3 | 31 | 6 | BD017439 | Transgeni          |
| c 269 | 12.8 | 53.3 | 33 | 6 | E09065   | DNA encodin        |
| c 270 | 12.8 | 53.3 | 36 | 6 | BD188836 | Hybrid pr          |
| c 271 | 12.8 | 53.3 | 36 | 6 | BD188838 | Hybrid pr          |
| c 272 | 12.8 | 53.3 | 36 | 6 | BD188841 | Hybrid pr          |
| c 273 | 12.8 | 53.3 | 36 | 6 | BD188843 | Hybrid pr          |
| c 274 | 12.8 | 53.3 | 36 | 6 | BD188845 | Hybrid pr          |
| c 275 | 12.8 | 53.3 | 39 | 6 | BD233542 | Targeted           |
| c 276 | 12.8 | 53.3 | 39 | 6 | AR435711 | Sequence           |
| c 277 | 12.8 | 53.3 | 39 | 6 | AX006837 | Sequence           |
| c 278 | 12.8 | 53.3 | 39 | 6 | AX463645 | Sequence           |
| c 279 | 12.8 | 53.3 | 39 | 6 | AX463653 | Sequence           |
| c 280 | 12.8 | 53.3 | 41 | 6 | CS063847 | Sequence           |
| c 281 | 12.8 | 53.3 | 41 | 6 | AX699916 | Sequence           |
| c 282 | 12.8 | 53.3 | 43 | 6 | AX286326 | Sequence           |
| c 283 | 12.8 | 53.3 | 49 | 6 | AX528867 | Sequence           |
| c 284 | 12.8 | 53.3 | 50 | 6 | CQ002429 | Sequence           |
| c 285 | 12.8 | 53.3 | 50 | 6 | CQ003647 | Sequence           |
| c 286 | 12.8 | 53.3 | 50 | 6 | CQ003696 | Sequence           |
| c 287 | 12.8 | 53.3 | 50 | 6 | CQ006015 | Sequence           |
| c 288 | 12.8 | 53.3 | 50 | 6 | CQ009000 | Sequence           |
| c 289 | 12.8 | 53.3 | 50 | 6 | AX157284 | Sequence           |
| c 290 | 12.6 | 52.5 | 20 | 6 | AR170368 | Sequence           |
| c 291 | 12.6 | 52.5 | 20 | 6 | BD075110 | MAGE-3 pe          |
| c 292 | 12.6 | 52.5 | 20 | 6 | BD084642 | RNAse L a          |
| c 293 | 12.6 | 52.5 | 20 | 6 | BD233818 | Transcrip          |
| c 294 | 12.6 | 52.5 | 20 | 6 | BD237168 | MAGE-A3 p          |
| c 295 | 12.6 | 52.5 | 20 | 6 | CS103773 | Sequence           |
| c 296 | 12.6 | 52.5 | 20 | 6 | AR221344 | Sequence           |
| c 297 | 12.6 | 52.5 | 20 | 6 | AR234713 | Sequence           |
| c 298 | 12.6 | 52.5 | 20 | 6 | AR241179 | Sequence           |
| c 299 | 12.6 | 52.5 | 20 | 6 | AR277764 | Sequence           |
| c 300 | 12.6 | 52.5 | 20 | 6 | AR492423 | Sequence           |

RESULT 1

AX103889

LOCUS

AX103889

DEFINITION

Sequence 81 from Patent WO0122972.

ACCESSION

AX103889

ALIGNMENTS

AX103889

AX103889

24 bp

DNA

linear

PAT 30-APR-2001

VERSION

AX103889.1

GI:13920086

KEYWORDS

synthetic construct

SOURCE

synthetic construct

ORGANISM

other sequences; artificial sequences.

REFERENCE

1

AUTHORS

Krieg,A.M., Schetter,C. and Vollmer,J.C.

TITLE

Immunostimulatory nucleic acids

JOURNAL

Patent: WO 012972-A 81 05-APR-2001;

UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical

GmbH (DE)

FEATURES

Location/Qualifiers

source

1..24

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

ORIGIN

Query Match

100.0%;

Score 24;

DB 6;

Length 24;

Best Local Similarity

100.0%;

Pred. No. 33;

Matches

24;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1

GGGGTCCAGCGTGGCCCATGGGG

24

|||||

Db

1

GGGGTCCAGCGTGGCCCATGGGG

24

|||||

RESULT 2

AX355412

LOCUS

AX355412

DEFINITION

Sequence 440 from Patent WO0197843.

ACCESSION

AX355412

VERSION

AX355412.1

GI:18620080

KEYWORDS

synthetic construct

SOURCE

synthetic construct

ORGANISM

other sequences; artificial sequences.

REFERENCE

1

AUTHORS

Weiner,G. and Hartmann,G.

TITLE

Methods for enhancing antibody-induced cell lysis and treating

JOURNAL

Patent: WO 0197843-A 440 27-DEC-2001;

UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES

Location/Qualifiers

source

1..24

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="Synthetic oligonucleotide

chimeric phosphorothioate/phosphodiester backbone with

phosphorothioate at 5' and 3' ends"

ORIGIN

Query Match

100.0%;

Score 24;

DB 6;

Length 24;

Best Local Similarity

100.0%;

Pred. No. 33;

Matches

24;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1

GGGGTCCAGCGTGGCCCATGGGG

24

|||||

Db

1

GGGGTCCAGCGTGGCCCATGGGG

24

|||||

RESULT 3

AX546942

LOCUS

AX546942

DEFINITION

Sequence 81 from Patent WO02053141.

ACCESSION

AX546942

VERSION

AX546942.1

GI:25812086

KEYWORDS

synthetic construct

SOURCE

synthetic construct

ORGANISM

other sequences; artificial sequences.

REFERENCE

1

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AUTHORS      Bratzler,R.I.
TITLE         Inhibition of angiogenesis by nucleic acids
JOURNAL       Patent: WO 02053141-A 81.11-JUL-2002;
              Coley Pharmaceutical Group, Inc. (US)
FEATURES      source
              1. .24
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic Sequence"

ORIGIN
Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGTCCAGCGTGGCCCATGGGG 24
        |||||
Db      1 GGGGTCCAGCGTGGCCCATGGGG 24

RESULT 4
AR182410
LOCUS      AR182410                25 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6338850.
ACCESSION  AR182410
VERSION     AR182410.1 GI:20225617
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Jevnikar,A.M., Ma,S. and Stiller,C.R.
TITLE       Methods and products for controlling the immune response of a
            mammal to glutamic acid decarboxylase
JOURNAL     Patent: US 6338850-A 1 15-JAN-2002;
            Location/Qualifiers
FEATURES    source
            1. .25
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            /mol_type="unassigned DNA"

ORIGIN
Query Match      67.5%; Score 16.2; DB 6; Length 25;
Best Local Similarity 85.7%; Pred. No. 5.2e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GGGTCCAGCGTGGCCCATGGG 22
        |||||
Db      2 GGATCCGGCGCGCCCATGGG 22

RESULT 5
CQ859706/c
LOCUS      CQ859706                30 bp      DNA      linear      PAT 10-SEP-2004
DEFINITION Sequence 2 from Patent WO2004072225.
ACCESSION  CQ859706
VERSION     CQ859706.1 GI:51981619
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    .
REFERENCE   1
AUTHORS     Sharon,A. and Goldstein-Barhoom,S.
TITLE       Transgenic fungi expressing bcl-2 and methods of using bcl-2 or
            portions thereof for improving biomass production, survival,
            longevity, stress resistance and pathogenicity of fungi
JOURNAL     Patent: WO 2004072225-A 2 26-AUG-2004;
            Ramot at Tel Aviv University Ltd. (IL)
            Location/Qualifiers
FEATURES    source
            1. .30
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

AUTHORS      Bratzler,R.I.
TITLE         Inhibition of angiogenesis by nucleic acids
JOURNAL       Patent: WO 02053141-A 81.11-JUL-2002;
              Coley Pharmaceutical Group, Inc. (US)
FEATURES      source
              1. .24
              /organism="synthetic construct"
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              /db_xref="taxon:32630"
              /note="Synthetic Sequence"

ORIGIN
Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGTCCAGCGTGGCCCATGGGG 24
        |||||
Db      1 GGGGTCCAGCGTGGCCCATGGGG 24

RESULT 6
BD263032/c
LOCUS      BD263032                33 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Trans-species transfer of apoptotic genes and transgenic plants
            developed thereby.
ACCESSION  BD263032
VERSION     BD263032.1 GI:33072800
KEYWORDS    JP 2002538769-A/5.
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1 (bases 1 to 33)
            Dickman,M.B.
REFERENCE   1
AUTHORS     Dickman,M.B.
TITLE       Trans-species transfer of apoptotic genes and transgenic plants
            developed thereby
JOURNAL     Patent: JP 2002538769-A 5 19-NOV-2002;
            UNIVERSITY OF NEBRASKA LINCOLN
            OS Artificial Sequence
            PN JP 2002538769-A/5
            PD 19-NOV-2002
            PF 29-OCT-1999 JP 2000579763
            PR 30-OCT-1998 US 60/106321,09-JUN-1999 US 60/138303 PI
            MARTIN B DICKMAN
JOURNAL     PC A01H57/00,C12N5/10,C12N15/09,C12Q1/68//(C12N5/10,C12R1:91), PC
            C12N15/00,
            PC C12N5/00, (C12N5/00,C12R1:91)
            CC PCR primer
            FH Key
            FT source
            Location/Qualifiers
            1. .33
            /organism='Artificial Sequence'.

FEATURES      source
              1. .33
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

ORIGIN
Query Match      66.7%; Score 16; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCATGG 21
        |||||
Db      33 CCAGCGTGGCCCATGG 18

RESULT 7
AR217874/c
LOCUS      AR217874                33 bp      DNA      linear      PAT 25-SEP-2002
DEFINITION Sequence 11 from patent US 6417002.
ACCESSION  AR217874
VERSION     AR217874.1 GI:23317768
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
            1 (bases 1 to 33)
REFERENCE   1
AUTHORS     Horlick,R.A. and Chelsky,D.
TITLE       Method for maintenance and selection of episomes
JOURNAL     Patent: US 6417002-A 11 09-JUL-2002;
            PharmacoPeia, Inc.; Cranbury, NJ
```

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FEATURES
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    Location/Qualifiers
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ORIGIN
Query Match
Best Local Similarity 66.7%; Score 16; DB 6; Length 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CCAGCGTGGCCATGG 21
    |||||
Db 27 CCAGCGTGGCCATGG 12
    |||||
RESULT 8
AR630015/c
LOCUS
DEFINITION Sequence 69 from patent US 6838556.
ACCESSION AR630015
VERSION AR630015.1 GI:59762210
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 35)
  Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
  Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
  Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
  Promoters for regulated gene expression
  Patent: US 6838556-A 69 04-JAN-2005;
  Genelabs Technologies, Inc.; Redwood City, CA
FEATURES
  source
    Location/Qualifiers
      1..35
        /organism="unknown"
        /mol_type="genomic DNA"
ORIGIN
Query Match
Best Local Similarity 63.3%; Score 15.2; DB 6; Length 35;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGGTCCAGCGTGGCCATGG 21
    |||||
Db 28 GGGTCCAGCGGAGCCATGG 9
    |||||
RESULT 9
AX351117/c
LOCUS
DEFINITION Sequence 69 from Patent WO0194600.
ACCESSION AX351117
VERSION AX351117.1 GI:18616471
KEYWORDS
SOURCE
ORGANISM
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
  Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
  Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
  Sheppard,L.T., Lim,M.Y. and Bruice,T.W.
  Promoters for regulated gene expression
  Patent: WO 0194600-A 69 13-DEC-2001;
  GENELABS TECHNOLOGIES, INC. (US)
FEATURES
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Query Match
Best Local Similarity 63.3%; Score 15.2; DB 6; Length 35;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGGTCCAGCGTGGCCATGG 21
    |||||
Db 28 GGGTCCAGCGGAGCCATGG 9
    |||||
RESULT 9
AX351117/c
LOCUS
DEFINITION Sequence 69 from Patent WO0197843.
ACCESSION AX351117
VERSION AX351117.1 GI:18620173
KEYWORDS
SOURCE
ORGANISM
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
  Weiner,G. and Hartmann,G.
  Methods for enhancing antibody-induced cell lysis and treating
  cancer
  Patent: WO 0197843-A 533 27-DEC-2001;
  UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
  source
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      1..16
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        /mol_type="unassigned DNA"
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        /notes="Synthetic oligonucleotide
        chimeric phosphorothioate/phosphodiester backbone with
        phosphorothioate at 5' and 3' ends"
ORIGIN
Query Match
Best Local Similarity 62.5%; Score 15; DB 6; Length 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TCCAGCGTGGCCAT 19
    |||||
Db 1 TCCAGCGTGGCCAT 15
    |||||
RESULT 10
AX103898
LOCUS
DEFINITION Sequence 90 from Patent WO0122972.
ACCESSION AX103898
VERSION AX103898.1 GI:13920095
KEYWORDS
SOURCE
ORGANISM
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
  Krieg,A.M., Schetter,C. and Vollmer,J.C.
  Immunostimulatory nucleic acids
  Patent: WO 0122972-A 90 05-APR-2001;
  UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
  GmbH (DE)
FEATURES
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ORIGIN
Query Match
Best Local Similarity 62.5%; Score 15; DB 6; Length 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TCCAGCGTGGCCAT 19
    |||||
Db 1 TCCAGCGTGGCCAT 15
    |||||
RESULT 11
AX355505
LOCUS
DEFINITION Sequence 533 from Patent WO0197843.
ACCESSION AX355505
VERSION AX355505.1 GI:18620173
KEYWORDS
SOURCE
ORGANISM
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
  Weiner,G. and Hartmann,G.
  Methods for enhancing antibody-induced cell lysis and treating
  cancer
  Patent: WO 0197843-A 533 27-DEC-2001;
  UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
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    Location/Qualifiers
      1..16
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /notes="Synthetic oligonucleotide
        chimeric phosphorothioate/phosphodiester backbone with
        phosphorothioate at 5' and 3' ends"
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TCCAGCGTGGCCAT 19
    |||||
Db 1 TCCAGCGTGGCCAT 15
    |||||
```

[illegible]



[illegible]

LOCUS BD002993 35 bp DNA linear PAT 31-JAN-2002  
DEFINITION A method for determining DNA methyltransferase.  
ACCESSION BD002993  
VERSION BD002993.1 GI:18630954  
KEYWORDS JP 2000232889-A/2.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Aonuma, M.  
TITLE A method for determining DNA methyltransferase  
JOURNAL Patent: JP 2000232889-A 2 29-AUG-2000;  
COMMENT DAIICHI PHARMACEUTICAL CO LTD  
OS Artificial Sequence  
PN JP 2000232889-A/2  
PD 29-AUG-2000  
PF 30-JUL-1999 JP 1999216640  
PR MASASHI AONUMA  
PI C12N15/09, C12N9/10, C12N11/14, C12Q1/48, C12N15/00 CC  
PC Location/Qualifiers  
FH Key 1..35  
FT source /organism='Artificial Sequence'.  
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source 1..35  
/organism="synthetic construct"  
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ORIGIN  
Query Match 60.0%; Score 14.4; DB 6; Length 35;  
Best Local Similarity 75.0%; Pred. No. 2.7e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 26 GCGGCTCGCGTGGCCAGCGGG 3  
RESULT 26  
LOCUS BD002995/c 35 bp DNA linear PAT 31-JAN-2002  
DEFINITION A method for determining DNA methyltransferase.  
ACCESSION BD002995  
VERSION BD002995.1 GI:18630956  
KEYWORDS JP 2000232889-A/4.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Aonuma, M.  
TITLE A method for determining DNA methyltransferase  
JOURNAL Patent: JP 2000232889-A 4 29-AUG-2000;  
COMMENT DAIICHI PHARMACEUTICAL CO LTD  
OS Artificial Sequence  
PN JP 2000232889-A/4  
PD 29-AUG-2000  
PF 30-JUL-1999 JP 1999216640  
PR MASASHI AONUMA  
PI C12N15/09, C12N9/10, C12N11/14, C12Q1/48, C12N15/00 CC  
PC Location/Qualifiers  
FH Key 1..35  
FT source /organism='Artificial Sequence'.  
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ORIGIN  
Query Match 60.0%; Score 14.4; DB 6; Length 35;  
Best Local Similarity 75.0%; Pred. No. 2.7e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 26 GCGGCTCGCGTGGCCAGCGGG 3  
RESULT 26  
LOCUS BD002995/c 35 bp DNA linear PAT 31-JAN-2002  
DEFINITION A method for determining DNA methyltransferase.  
ACCESSION BD002995  
VERSION BD002995.1 GI:18630956  
KEYWORDS JP 2000232889-A/4.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Aonuma, M.  
TITLE A method for determining DNA methyltransferase  
JOURNAL Patent: JP 2000232889-A 4 29-AUG-2000;  
COMMENT DAIICHI PHARMACEUTICAL CO LTD  
OS Artificial Sequence  
PN JP 2000232889-A/4  
PD 29-AUG-2000  
PF 30-JUL-1999 JP 1999216640  
PR MASASHI AONUMA  
PI C12N15/09, C12N9/10, C12N11/14, C12Q1/48, C12N15/00 CC  
PC Location/Qualifiers  
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/mol\_type="genomic DNA"  
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Query Match 60.0%; Score 14.4; DB 6; Length 35;  
Best Local Similarity 75.0%; Pred. No. 2.7e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 26 GCGGCTCGCGTGGCCAGCGGG 3

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 26 GCGGCTCGCGTGGCCAGCGGG 3  
RESULT 27  
LOCUS CQ008520/c 50 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 7160 from Patent WO0147944.  
ACCESSION CQ008520  
VERSION CQ008520.1 GI:41015226  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0147944-A 7160 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES  
source 1..50  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
misc\_feature 25..26  
/note="Nucleotide deleted between bases 25 and 26"  
Accession number cg40388639"  
ORIGIN  
Query Match 60.0%; Score 14.4; DB 6; Length 50;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 33 GGGGCCAGCCGTTGGCATGGGG 10  
RESULT 28  
LOCUS BD194701 19 bp DNA linear PAT 17-JUL-2003  
DEFINITION Lineage-restricted neuronal precursors.  
ACCESSION BD194701  
VERSION BD194701.1 GI:33004447  
KEYWORDS JP 2002515071-A/14.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Rao, M.S., Proschel, M.M. and Kalyani, A.J.  
TITLE Lineage-restricted neuronal precursors  
JOURNAL Patent: JP 2002515071-A 14 21-MAY-2002;  
UNIVERSITY OF UTAH RESEARCH FOUNDATION  
COMMENT OS Rattus norvegicus (rat)  
PN JP 2002515071-A/14  
PD 21-MAY-2002  
PF 03-JUL-1998 JP 1999507430  
PR 04-JUL-1997 US 08/909435, 02-JUL-1998 US 09/109858 PI  
MAHENDRA S RAO, MARGOT MAYER PROSCHEL, ANJALI J KALYANI PC  
A61K48/00, A61K35/30, C12N5/00, C12N5/06, C12N5/08 CC  
Lineage-restricted neuronal precursors  
FH Key Location/Qualifiers  
FT source 1..19  
/organism="Rattus norvegicus (rat)".  
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Location/Qualifiers

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            /db_xref="taxon:10116"

ORIGIN
Query Match      59.2%; Score 14.2; DB 6; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  3  GGTCCAGCGTGGCCATGG 21
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Db  1  GGTCCAGCAATTGGCCATGG 19

RESULT 29
AR580293
LOCUS      AR580293
DEFINITION Sequence 14 from patent US 6787353.
ACCESSION AR580293
VERSION    AR580293.1 GI:56610412
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Rao,M.S., Mayer-Proschel,M. and Kalyani,A.J.
TITLE      Lineage-restricted neuronal precursors and methods of isolation
JOURNAL    Patent: US 6787353-A 14 07-SEP-2004;
           University of Utah Research Foundation; Salt Lake City, UT
FEATURES   source
            Location/Qualifiers
            1. .19
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            /mol_type="genomic DNA"

ORIGIN
Query Match      59.2%; Score 14.2; DB 6; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  3  GGTCCAGCGTGGCCATGG 21
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Db  1  GGTCCAGCAATTGGCCATGG 19

RESULT 30
AX839895/c
LOCUS      AX839895
DEFINITION Sequence 9 from Patent EPI348964.
ACCESSION AX839895
VERSION    AX839895.1 GI:39978426
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Cochran,S.Y., Yamagami,K.M. and Ohashi,Y.M.
TITLE      Schizophrenia related gene
JOURNAL    Patent: EP 1348964-A 9 01-OCT-2003;
           Mitsubishi Pharma Corporation (JP)
FEATURES   source
            Location/Qualifiers
            1. .45
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: oligonucleotide
            (45mer) used for in s i t u hybridization for Kv3.3 mRNA"

ORIGIN
Query Match      59.2%; Score 14.2; DB 6; Length 45;
Best Local Similarity 84.2%; Pred. No. 3.1e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy  4  GTCCAGCGTGGCCATGG 22
      |||||  |||||
Db  37 GTTCAGCGGCGCCAGGG 19

RESULT 31
I96090
LOCUS      I96090
DEFINITION Sequence 9 from patent US 5734033.
ACCESSION I96090
VERSION    I96090.1 GI:3940560
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Reed,J.
TITLE      Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL    Patent: US 5734033-A 9 31-MAR-1998;
           Location/Qualifiers
FEATURES   source
            Location/Qualifiers
            1. .17
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            /mol_type="unassigned DNA"

ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6  CCAGCGTGGCCAT 19
      |||||  |||||
Db  4  CCAGCGTGGCCAT 17

RESULT 32
I96091
LOCUS      I96091
DEFINITION Sequence 10 from patent US 5734033.
ACCESSION I96091
VERSION    I96091.1 GI:3940561
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Reed,J.
TITLE      Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL    Patent: US 5734033-A 10 31-MAR-1998;
           Location/Qualifiers
FEATURES   source
            Location/Qualifiers
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Query Match      58.3%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6  CCAGCGTGGCCAT 19
      |||||  |||||
Db  1  CCAGCGTGGCCAT 14

RESULT 33
AR052619
LOCUS      AR052619
DEFINITION Sequence 17 from patent US 5831066.
ACCESSION AR052619
VERSION    AR052619.1 GI:5975983
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Reed,J.
TITLE      Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL    Patent: US 5734033-A 10 31-MAR-1998;
           Location/Qualifiers
FEATURES   source
            Location/Qualifiers
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            /mol_type="unassigned DNA"

ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6  CCAGCGTGGCCAT 19
      |||||  |||||
Db  1  CCAGCGTGGCCAT 14

RESULT 33
AR052619
LOCUS      AR052619
DEFINITION Sequence 17 from patent US 5831066.
ACCESSION AR052619
VERSION    AR052619.1 GI:5975983
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Reed,J.
TITLE      Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL    Patent: US 5734033-A 10 31-MAR-1998;
           Location/Qualifiers
FEATURES   source
            Location/Qualifiers
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ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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REFERENCE 1 (bases 1 to 18)
AUTHORS   Reed,J.C.
TITLE     Regulation of bcl-2 gene expression
JOURNAL   Patent: US 5831066-A 17 03-NOV-1998;
FEATURES  Location/Qualifiers
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            /mol_type="unassigned DNA"
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Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19
|||||
Db
5 CCAGCGTGGCCCAT 18

RESULT 34
AR052624      AR052624      18 bp      DNA      linear      PAT 29-SEP-1999
LOCUS
DEFINITION     Sequence 24 from patent US 5831066.
ACCESSION     AR052624
VERSION       AR052624.1 GI:5975988
KEYWORDS
SOURCE        Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Reed,J.C.
TITLE          Regulation of bcl-2 gene expression
JOURNAL        Patent: US 5831066-A 24 03-NOV-1998;
FEATURES       Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19
|||||
Db
5 CCAGCGTGGCCCAT 18

RESULT 35
AR116926      AR116926      18 bp      DNA      linear      PAT 16-MAY-2001
LOCUS
DEFINITION     Sequence 1 from patent US 6140051.
ACCESSION     AR116926
VERSION       AR116926.1 GI:14097832
KEYWORDS
SOURCE        Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Brown,L.R. and Xu,C.
TITLE          Fluorescent dibenzazole derivatives and methods related thereto
JOURNAL        Patent: US 6140051-A 1 31-OCT-2000;
FEATURES       Location/Qualifiers
          source
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Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19

REFERENCE 1 (bases 1 to 18)
AUTHORS   Reed,J.C.
TITLE     Regulation of bcl-2 gene expression
JOURNAL   Patent: US 5831066-A 24 03-NOV-1998;
FEATURES  Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19
|||||
Db
5 CCAGCGTGGCCCAT 18

RESULT 36
AR140496      AR140496      18 bp      DNA      linear      PAT 16-JUN-2001
LOCUS
DEFINITION     Sequence 55 from patent US 6207646.
ACCESSION     AR140496
VERSION       AR140496.1 GI:14482992
KEYWORDS
SOURCE        Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.
TITLE          Immunostimulatory nucleic acid molecules
JOURNAL        Patent: US 6207646-A 55 27-MAR-2001;
FEATURES       Location/Qualifiers
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ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19
|||||
Db
5 CCAGCGTGGCCCAT 18

RESULT 37
AR146347      AR146347      18 bp      DNA      linear      PAT 08-AUG-2001
LOCUS
DEFINITION     Sequence 59 from patent US 6218371.
ACCESSION     AR146347
VERSION       AR146347.1 GI:15109536
KEYWORDS
SOURCE        Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Krieg,A.M. and Weiner,G.
TITLE          Methods and products for stimulating the immune system using
JOURNAL        immunotherapeutic oligonucleotides and cytokines
JOURNAL        Patent: US 6218371-A 59 17-APR-2001;
FEATURES       Location/Qualifiers
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            /mol_type="unassigned DNA"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19
|||||
Db
5 CCAGCGTGGCCCAT 18

RESULT 38
AR146392      AR146392      18 bp      DNA      linear      PAT 08-AUG-2001
LOCUS
DEFINITION     Sequence 104 from patent US 6218371.
ACCESSION     AR146392
VERSION       AR146392.1 GI:15109581
KEYWORDS
SOURCE        Unknown.
ORGANISM       Unclassified.
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REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Weiner,G.
TITLE Methods and products for stimulating the immune system using
JOURNAL immunotherapeutic oligonucleotides and cytokines
PATENT: US 6218371-A 104 17-APR-2001;
FEATURES
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            /mol_type="unassigned DNA"
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Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CCAGCGTGC GCCAT 19
Db 5 CCAGCGTGC GCCAT 18
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RESULT 39
LOCUS AR154716 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 45 from patent US 6239116.
ACCESSION AR154716
VERSION AR154716.1 GI:15122769
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Kline,J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 45 29-MAY-2001;
FEATURES
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            /mol_type="unassigned DNA"
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Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CCAGCGTGC GCCAT 19
Db 5 CCAGCGTGC GCCAT 18
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RESULT 40
LOCUS AR167448 18 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 14 from patent US 6287591.
ACCESSION AR167448
VERSION AR167448.1 GI:17903228
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sample,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansell,S.M.,
Cullis,P., Scherrer,P. and Debever,D.
TITLE Charged therapeutic agents encapsulated in lipid particles
containing four lipid components
JOURNAL Patent: US 6287591-A 14 11-SEP-2001;
FEATURES
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ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CCAGCGTGC GCCAT 19
Db 5 CCAGCGTGC GCCAT 18
|||||
RESULT 41
LOCUS BD069938 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Use of nucleic acids containing unhyethylated CPG dinucleotide in
the treatment of LPS-associated disorders.
ACCESSION BD069938
VERSION BD069938.1 GI:22615541
KEYWORDS JP 2001513776-A/27.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schwartz,D.A. and Krieg,A.M.
TITLE Use of nucleic acids containing unhyethylated CPG dinucleotide in
the treatment of LPS-associated disorders
JOURNAL Patent: JP 2001513776-A 27 04-SEP-2001;
COMMENT UNIVERSITY OF IOWA RESEARCH FOUNDATION
OS Artificial Sequence
PN JP 2001513776-A/27
PD 04-SEP-2001
PF 25-FEB-1998 JP 1998537810
PR 28-FEB-1997 US 60/039405
PI DAVID A SCHWARTZ,ARTHUR M KRIEG
PC A61K49/00,C07H21/02,C07H21/04,A01N43/04
CC synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1..18
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            /mol_type="genomic DNA"
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Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CCAGCGTGC GCCAT 19
Db 5 CCAGCGTGC GCCAT 18
|||||
RESULT 42
LOCUS BD076451 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Combined antisense library.
ACCESSION BD076451
VERSION BD076451.1 GI:22622054
KEYWORDS JP 2001519170-A/45.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Riley,T.A., Brown,B.D. and Arnold,L.J.
TITLE Combined antisense library
JOURNAL Patent: JP 2001519170-A 45 23-OCT-2001;
COMMENT OASIS BIOSCIENCES INC
OS Artificial Sequence
PN JP 2001519170-A/45
PD 23-OCT-2001
PF 28-SEP-1998 JP 2000515030
PR 02-OCT-1997 US 60/060673,18-AUG-1998 US
TIMOTHY A RILEY,BOB D BROWN,D LYLE J ARNOLD
PC C12Q1/68,C07H21/04,C12N15/09,C12P19/34,C12N15/00 CC

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synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1..18
/organism="Artificial Sequence".

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    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18

RESULT 43
BD080525/c
LOCUS BD080525 18 bp RNA linear PAT 27-AUG-2002
DEFINITION Ribonucleoside-derivative and method for preparing the same.
ACCESSION BD080525
VERSION BD080525.1 GI:22626128
KEYWORDS JP 2001515087-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pitsch,S., Weiss,P.A. and Jenny,L.
TITLE Ribonucleoside-derivative and method for preparing the same
JOURNAL Patent: JP 2001515087-A 4 18-SEP-2001;
COMMENT STEFAN PITTSCH,PATRICK A WEISS,LUZI JENNY
OS Artificial Sequence
PN JP 2001515087-A/4
PD 18-SEP-2001
PF 17-AUG-1998 JP 2000509723
PI STEFAN PITTSCH,PATRICK A WEISS,LUZI JENNY
PC C07H19/06,C07F7/18,C07H19/16,C07H21/02,C07H23/00 CC
Description of Artificial Sequence:synthetic polynucleotide FH
Key Location/Qualifiers
FT source 1..18
/organism="Artificial Sequence".

FEATURES
    source Location/Qualifiers
    1..18
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    /mol_type="genomic RNA"
    /db_xref="taxon:32630"

ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19
Db 14 CCAGCGTGGCCCAT 1

RESULT 44
BD106497
LOCUS BD106497 18 bp DNA linear PAT 18-SEP-2002
DEFINITION High efficiency encapsulation of charged therapeutic agents in lipid vesicles.
ACCESSION BD106497
VERSION BD106497.1 GI:23201315
KEYWORDS JP 2002501511-A/14.
SOURCE Chlamydia sp.
ORGANISM Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

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REFERENCE 1 (bases 1 to 18)
AUTHORS Sample,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansel,S.M.,
Cullis,P., Scherrer,P. and Debever,D.S.
TITLE High efficiency encapsulation of charged therapeutic agents in lipid vesicles
JOURNAL Patent: JP 2002501511-A 14 15-JAN-2002;
INEX PHARMACEUTICALS CORP
COMMENT PN JP 2002501511-A/14
PD 15-JAN-2002
PF 14-MAY-1998 JP 1998548646
PI SEAN C SEMPLER,SANDRA K KLIMUK,TROY HARASYM,MICHAEL J HOPE, PI
STEVEN M ANSELL,
PI PIETER CULLIS,PETER SCHERRER,DAN SUITE DEBEVER PC A61K9/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
    source Location/Qualifiers
    1..18
    /organism="Chlamydia sp."
    /mol_type="genomic DNA"
    /db_xref="taxon:35827"

ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18

RESULT 45
BD187532
LOCUS BD187532 18 bp DNA linear PAT 17-JUL-2003
DEFINITION REGULATION OF bcl-2 GENE EXPRESSION.
ACCESSION BD187532
VERSION BD187532.1 GI:32997271
KEYWORDS JP 2003026609-A/17.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Reed,J.C.
TITLE REGULATION OF bcl-2 GENE EXPRESSION
JOURNAL Patent: JP 2003026609-A 17 29-JAN-2003;
COMMENT John C REED
OS Artificial Sequence
PN JP 2003026609-A/17
PD 29-JAN-2003
PF 19-JUN-2002 JP 2002178753
PR 20-SEP-1993 US 08/124256
PI John C Reed
CC Description of Artificial Sequence: Designed DNA based on bcl-2 gene
FH Key Location/Qualifiers.
    source Location/Qualifiers
    1..18
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18

RESULT 46

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BD190420  
LOCUS BD190420 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Microemulsions with Adsorbed Macromolecules and Microparticles.  
ACCESSION BD190420  
VERSION BD190420.1 GI:33000159  
KEYWORDS JP 2002537102-A/4.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Barackman,J., Simph,M., Ugozoli,M., Kazazu,J., Donnelly,J.,  
Ott,G.S. and Ohagan,D.  
TITLE Microemulsions with Adsorbed Macromolecules and Microparticles  
JOURNAL Patent: JP 2002537102-A 4 05-NOV-2002;  
Chiron Corporation  
COMMENT OS Artificial Sequence  
PN JP 2002537102-A/4  
PD 05-NOV-2002  
PF 09-FEB-2000 JP 2000600618  
PR 29-JUL-1999 US 60/146391,28-OCT-1999 US 60/161997, PR  
26-FEB-1999 US 60/121858  
PI john barackman,manmohan simph,mildred ugozoli,jina kazazu,john  
donnelly,  
PI gary s ott,derek ohagan  
CC Oligonucleotide Location/Qualifiers.  
FH Key Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
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Query Match 58.3%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.4e+05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 CCAGCGTGGCCCAT 19  
Db 5 CCAGCGTGGCCCAT 18  
RESULT 47  
LOCUS BD192469 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Compositions and methods for the delivery of oligonucleotides via  
the alimentary canal.  
ACCESSION BD192469  
VERSION BD192469.1 GI:33002208  
KEYWORDS JP 2002510319-A/34.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Teng,C.L. and Hardee,G.  
TITLE Compositions and methods for the delivery of oligonucleotides via  
the alimentary canal  
JOURNAL Patent: JP 2002510319-A 34 02-APR-2002;  
ISIS PHARMACEUTICALS INC  
COMMENT OS Artificial Sequence  
PN JP 2002510319-A/34  
PD 02-APR-2002  
PF 01-JUL-1998 JP 1999507295  
PR 01-JUL-1997 US 08/886829  
PI CHING LEOU TENG,GREG HARDEE  
PC C1201/68,A61K9/127,A61K48/00,C07H21/04  
CC Description of Artificial Sequence: Novel Sequence FH Key  
Location/Qualifiers.  
FEATURES  
source  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"

/db\_xref="taxon:32630"  
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Query Match 58.3%; Score 14; DB 6; Length 18;  
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REFERENCE 1 (bases 1 to 18)  
AUTHORS Wagner,H. and Lipford,G.  
TITLE Method of controlling hematopoiesis by using CpG oligonucleotide  
JOURNAL Patent: JP 2002514397-A 59 21-MAY-2002;  
CORY PHARMACEUTICALS GMBH,CORY PHARMACEUTICALS GROUP INC  
COMMENT OS Artificial Sequence  
PN JP 2002514397-A/59  
PD 21-MAY-2002  
PF 14-MAY-1999 JP 2000547969  
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HERMANN WAGNER,GRAYSON LIPFORD  
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ACCESSION BD205614  
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REFERENCE 1 (bases 1 to 18)  
AUTHORS Wagner,H. and Lipford,G.  
TITLE Method of controlling hematopoiesis by using CpG oligonucleotide  
JOURNAL Patent: JP 2002514397-A 104 21-MAY-2002;  
CORY PHARMACEUTICALS GMBH,CORY PHARMACEUTICALS GROUP INC  
COMMENT OS Artificial Sequence  
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ACCESSION BD222609  
VERSION BD222609.1 GI:33032379  
KEYWORDS JP 2002522510-A/1.  
SOURCE Quillaja saponaria  
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rosids; eurosids I; Fabales; Quillajaaceae; Quillaja.  
1 (bases 1 to 18)  
REFERENCE Kersil,C.A.  
AUTHORS Compositions of CPG and saponin adjuvants and uses thereof  
TITLE Patent: JP 2002522510-A 1 23-JUL-2002;  
JOURNAL AQUILA BIOPHARMACEUTICALS INC  
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-09-669-187A-81

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Searched: 4996997 seqs, 3332346308 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 144 | 14 | 58.3 | 18 | 10 | ADF82829  | Adf82829 Immunosti | 217 | 14   | 58.3 | 30 | 3  | AAC63979 | Aac63979 Icelandic |
| 145 | 14 | 58.3 | 18 | 10 | ADG68147  | Adg68147 Umethylya | 218 | 14   | 58.3 | 32 | 14 | AE828476 | Aeb28476 Phosphodi |
| 146 | 14 | 58.3 | 18 | 10 | ACF36817  | Acf36817 Immunosti | 219 | 14   | 58.3 | 35 | 2  | AAQ86644 | Aaq86644 Bcl-2 tra |
| 147 | 14 | 58.3 | 18 | 10 | ABX76040  | Abx76040 Immunosti | 220 | 14   | 58.3 | 35 | 2  | AAV19652 | Aav19652 Human bcl |
| 148 | 14 | 58.3 | 18 | 10 | ACA58705  | Aca58705 Gastric u | 221 | 14   | 58.3 | 35 | 6  | ABK90265 | Abk90265 Bcl-2-tar |
| 149 | 14 | 58.3 | 18 | 11 | ADM41180  | Adm41180 Human ant | 222 | 14   | 58.3 | 35 | 6  | ABQ78523 | Abq78523 Antisense |
| 150 | 14 | 58.3 | 18 | 12 | ADE90170  | Ade90170 Human bcl | 223 | 14   | 58.3 | 35 | 6  | ABL54150 | AbL54150 Bcl-2 ant |
| 151 | 14 | 58.3 | 18 | 12 | ADE39674  | Ade39674 Oligonucl | 224 | 14   | 58.3 | 35 | 13 | ADT93919 | Adt93919 Antisense |
| 152 | 14 | 58.3 | 18 | 12 | ADP39689  | Adp39689 Oligonucl | 225 | 14   | 58.3 | 35 | 14 | ADW13831 | Adw13831 Bcl-2 gen |
| 153 | 14 | 58.3 | 18 | 12 | ADF42925  | Adf42925 Methylate | 226 | 14   | 58.3 | 36 | 4  | AAH45307 | Aah45307 Human Bcl |
| 154 | 14 | 58.3 | 18 | 12 | ADF42910  | Adf42910 Methylate | 227 | 14   | 58.3 | 36 | 10 | ADM10311 | Adm10311 Human epi |
| 155 | 14 | 58.3 | 18 | 12 | ADT01087  | Adt01087 Immunosti | 228 | 14   | 58.3 | 40 | 2  | AAQ53418 | Aaq53418 Human dop |
| 156 | 14 | 58.3 | 18 | 12 | ADL64033  | AdL64033 Cpg DNA o | 229 | 14   | 58.3 | 40 | 12 | ADO70419 | Ado70419 Human Bcl |
| 157 | 14 | 58.3 | 18 | 12 | ADL63958  | AdL63958 Cpg DNA o | 230 | 14   | 58.3 | 40 | 12 | ADO70436 | Ado70436 Human Bcl |
| 158 | 14 | 58.3 | 18 | 12 | ADL97920  | AdL97920 Immunosti | 231 | 14   | 58.3 | 50 | 6  | ABZ04678 | Abz04678 Human leu |
| 159 | 14 | 58.3 | 18 | 12 | ADN11025  | Adn11025 Cpg oligo | 232 | 13.8 | 57.5 | 30 | 3  | AAZ46938 | Aaz46938 Human sac |
| 160 | 14 | 58.3 | 18 | 12 | ADM99056  | Adm99056 Immunosti | 233 | 13.8 | 57.5 | 45 | 5  | AAH26512 | Aah26512 Low densi |
| 161 | 14 | 58.3 | 18 | 12 | ADQ04772  | Ado04772 Cpg oligo | 234 | 13.8 | 57.5 | 45 | 6  | ABK70067 | Abk70067 Antibody  |
| 162 | 14 | 58.3 | 18 | 12 | ADQ07602  | Adq07602 Umethylya | 235 | 13.8 | 57.5 | 45 | 10 | ADL18019 | Adl18019 Anti-lect |
| 163 | 14 | 58.3 | 18 | 12 | ADP86189  | Adp86189 Cpg immun | 236 | 13.8 | 57.5 | 45 | 11 | ADL35283 | Adl35283 Anti-Fcga |
| 164 | 14 | 58.3 | 18 | 12 | ADQ26939  | Adq26939 Human Bcl | 237 | 13.8 | 57.5 | 47 | 3  | AAZ69280 | Aaz69280 Human map |
| 165 | 14 | 58.3 | 18 | 12 | ADQ07472  | Adq07472 Immunosti | 238 | 13.6 | 56.7 | 21 | 2  | AAZ59612 | Aat59612 Human cys |



|  |               |  |
|--|---------------|--|
| 12-JUN-2001  | (first entry) |  |
| Immunostimulatory nucleic acid #72.  |               |  |
| Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.  |               |  |
| Synthetic.   |               |  |
| WO200122972-A2.  |               |  |
| 05-APR-2001.   |               |  |
| 25-SEP-2000; 2000WO-US026383.  |               |  |
| 25-SEP-1999; 99US-0156113P.  |               |  |
| 27-SEP-1999; 99US-0156135P.  |               |  |
| 23-AUG-2000; 2000US-0227436P.  |               |  |
| (IOWA ) UNIV IOWA RES FOUND.   |               |  |
| (COLE-) COLEY PHARM GMBH.  |               |  |
| Krieg AM, Schetter C, Vollmer J;   |               |  |
| WPI; 2001-273485/28.   |               |  |
| Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.  |               |  |
| Disclosure; Page 40; 338pp; English.   |               |  |
| The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone |               |  |
| Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;   |               |  |
| Query Match 100.0%; Score 24; DB 4; Length 24;   |               |  |
| Best Local Similarity 100.0%; Pred. No. 0.58;  |               |  |
| Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |               |  |
| QY 1 GGGGTCACGCGGCCCATGGGG 24  |               |  |
|  |               |  |
| Db 1 GGGGTCACGCGGCCCATGGGG 24  |               |  |
|  |               |  |
| RESULT 2   |               |  |
| ABST77597  |               |  |
| ID ABST77597 standard; DNA; 24 BP.   |               |  |
| XX ABST77597;  |               |  |
| AC ABST77597;  |               |  |
| XX 13-DEC-2002 (first entry)   |               |  |
| XX   |               |  |
| XX Angiogenesis inhibitory oligonucleotide #81.  |               |  |
| XX   |               |  |
| XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  |               |  |
| KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  |               |  |
| XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;   |               |  |
| KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;   |               |  |
| XX   |               |  |

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophilic joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX Synthetic.  
 OS  
 XX  
 PN WO200253141-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 XX 14-DEC-2001; 2001WO-US048458.  
 XX  
 XX 14-DEC-2000; 2000US-0255534P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 XX  
 XX Bratzler RL;  
 XX  
 XX WPI; 2002-566690/60.  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX  
 XX Claim 2; Page 21; 276pp; English.  
 XX  
 CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX  
 XX Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 24; DB 6; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.58;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGTCCAGCGTGGCCATGGGG 24  
 |||||  
 DB 1 GGGGTCCAGCGTGGCCATGGGG 24  
 |||||  
 RESULT 3  
 ABL39036  
 ID ABL39036 standard; DNA; 24 BP.  
 XX  
 AC ABL39036;  
 XX  
 DT 16-APR-2002 (first entry)  
 XX  
 XX Immunostimulatory nucleic acid SEQ ID NO: 440.  
 DE  
 XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO200197843-A2.  
 PN  
 XX 27-DEC-2001.  
 PD  
 XX 22-JUN-2001; 2001WO-US020154.  
 PF  
 XX

PR 22-JUN-2000; 2000US-0213346P.  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA  
 XX Weiner G, Hartmann G;  
 PI  
 XX WPI; 2002-154611/20.  
 DR  
 XX  
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
 PT administering immunostimulatory nucleic acids that induce expression of  
 PT cell surface antigens and antibodies to a subject having or at risk of  
 PT developing cancer.  
 XX  
 XX Disclosure; Page 207; 312pp; English.  
 XX  
 CC The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for  
 CC treating or preventing cancer such as basal cell carcinoma, bladder  
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
 CC present sequence is an immunostimulatory oligonucleotide described in the  
 CC exemplification of the invention  
 XX  
 XX Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 24; DB 6; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.58;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGTCCAGCGTGGCCATGGGG 24  
 |||||  
 DB 1 GGGGTCCAGCGTGGCCATGGGG 24  
 |||||  
 RESULT 4  
 ACD99389  
 ID ACD99389 standard; DNA; 24 BP.  
 XX  
 AC ACD99389;  
 XX  
 DT 25-SEP-2003 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #75.  
 XX  
 XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX US2003050268-A1.  
 PN  
 XX 13-MAR-2003.  
 PD  
 XX 29-MAR-2002; 2002US-00112653.  
 PF  
 XX 29-MAR-2001; 2001US-0279642P.  
 XX  
 XX (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX  
 XX Krieg AM, Berg DJ;  
 PI  
 XX WPI; 2003-521815/49.  
 DR  
 XX

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX  
XX  
PS Disclosure; Page 10; 229pp; English.  
XX  
CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
XX Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 24; DB 9; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGTCCAGCGTGGCCATGGGG 24  
Db 1 GGGGTCCAGCGTGGCCATGGGG 24  
RESULT 5  
ADB36458  
ID ADB36458 standard; DNA; 24 BP.  
XX  
XX AC ADB36458;  
XX  
XX DT 04-DEC-2003 (first entry)  
XX  
XX DE Immunostimulatory nucleic acid #72.  
XX  
XX KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX  
XX OS Synthetic.  
XX  
XX PN US2003087848-A1.  
XX  
XX PD 08-MAY-2003.  
XX  
XX PF 02-FEB-2001; 2001US-00776479.  
XX  
XX PR 03-FEB-2000; 2000US-0179991P.  
XX  
XX PA (BRAT/) BRATZLER R L.  
XX  
XX PA (PETE/) PETERSEN D M.  
XX  
XX PA (FOUR/) FOURON Y.  
XX  
XX PI Bratzler RL, Petersen DM, Fouron Y;  
XX  
XX WPI; 2003-657977/62.  
XX  
XX PT Treating and/or preventing allergy or asthma using an immunostimulatory  
XX nucleic acid alone or in combination with an asthma/allergy medicament.  
XX  
XX PS Disclosure; Page 6; 221pp; English.  
XX  
XX CC The invention relates to a method of treating or preventing allergy or  
XX asthma which comprises administering to a subject a poly-G nucleic acid  
XX in an aerosol formulation. The methods and compositions of the present  
XX invention are useful for diagnosing and/or treating asthma and allergy  
XX especially in a hypo-responsive subject. The present sequence represents  
XX an immunostimulatory nucleic acid of the invention.  
XX  
XX SQ Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 24; DB 9; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGTCCAGCGTGGCCATGGGG 24  
Db 1 GGGGTCCAGCGTGGCCATGGGG 24  
RESULT 6  
ADU89397  
ID ADU89397 standard; DNA; 24 BP.  
XX  
XX AC ADU89397;  
XX  
XX DT 10-FEB-2005 (first entry)  
XX  
XX DE Allergic response suppressor oligonucleotide #81.  
XX  
XX KW ss; antiaesthetic; antiallergic; dermatological; antiinflammatory;  
KW antibacterial; virucide; immunoglobulin E antagonist; allergy;  
KW immunostimulatory; asthma; rhinitis; urticaria; dermatitis;  
KW bacterial infection; viral infection.  
XX  
XX OS Synthetic.  
XX  
XX PN US2004235774-A1.  
XX  
XX PD 25-NOV-2004.  
XX  
XX PF 23-APR-2004; 2004US-00831778.  
XX  
XX PR 03-FEB-2000; 2000US-0179991P.  
XX  
XX PR 02-FEB-2001; 2001US-00776479.  
XX  
XX PA (BRAT/) BRATZLER R L.  
XX  
XX PA (PETE/) PETERSEN D M.  
XX  
XX PA (FOUR/) FOURON Y.  
XX  
XX PI Bratzler RL, Petersen DM, Fouron Y;  
XX  
XX WPI; 2004-833006/82.  
XX  
XX PT Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
XX dermatitis, in a subject, comprises administering a first and second dose  
XX of an immunostimulatory nucleic acid.  
XX  
XX PS Disclosure; SEQ ID NO 81; 235pp; English.  
XX  
XX CC The invention relates to a method of suppressing a symptom of an allergic  
XX response in a subject by administering a first and second dose of an  
XX immunostimulatory nucleic acid that comprises a nucleotide sequence  
XX comprising 5'-cg-3', and where the second dose is administered from 1 day  
XX to 8 weeks after the first dose. The methods and compositions of the  
XX present invention are useful for the treatment or prevention of asthma  
XX and allergy, including rhinitis, urticaria and atopic dermatitis, using  
XX an immunostimulatory nucleic acid alone or in combination with other  
XX medicaments. They can also be used in preventing bacterial and viral  
XX infections. This sequence represents an oligonucleotide used in the  
XX method of the invention.  
XX  
XX SQ Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 24; DB 13; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGTCCAGCGTGGCCATGGGG 24  
Db 1 GGGGTCCAGCGTGGCCATGGGG 24  
RESULT 7  
AAQ86577  
ID AAQ86577 standard; DNA; 26 BP.

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGTCCAGCGTGGCCATGGGG 24  
Db 1 GGGGTCCAGCGTGGCCATGGGG 24

RESULT 6  
ADU89397  
ID ADU89397 standard; DNA; 24 BP.

XX  
XX AC ADU89397;  
XX  
XX DT 10-FEB-2005 (first entry)  
XX

XX Allergic response suppressor oligonucleotide #81.

XX ss; antiaesthetic; antiallergic; dermatological; antiinflammatory;  
KW antibacterial; virucide; immunoglobulin E antagonist; allergy;  
KW immunostimulatory; asthma; rhinitis; urticaria; dermatitis;  
KW bacterial infection; viral infection.

XX Synthetic.

XX US2004235774-A1.

XX 25-NOV-2004.

XX 23-APR-2004; 2004US-00831778.

XX 03-FEB-2000; 2000US-0179991P.

XX 02-FEB-2001; 2001US-00776479.

XX (BRAT/) BRATZLER R L.

XX (PETE/) PETERSEN D M.

XX (FOUR/) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;

XX WPI; 2004-833006/82.

XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
XX dermatitis, in a subject, comprises administering a first and second dose  
XX of an immunostimulatory nucleic acid.

XX Disclosure; SEQ ID NO 81; 235pp; English.

XX The invention relates to a method of suppressing a symptom of an allergic  
XX response in a subject by administering a first and second dose of an  
XX immunostimulatory nucleic acid that comprises a nucleotide sequence  
XX comprising 5'-cg-3', and where the second dose is administered from 1 day  
XX to 8 weeks after the first dose. The methods and compositions of the  
XX present invention are useful for the treatment or prevention of asthma  
XX and allergy, including rhinitis, urticaria and atopic dermatitis, using  
XX an immunostimulatory nucleic acid alone or in combination with other  
XX medicaments. They can also be used in preventing bacterial and viral  
XX infections. This sequence represents an oligonucleotide used in the  
XX method of the invention.

XX Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 13; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.58;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCATGGGG 24

Db 1 GGGGTCCAGCGTGGCCATGGGG 24

RESULT 7

AAQ86577

ID AAQ86577 standard; DNA; 26 BP.

```

XX AC AAQ86577;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 25-SEP-1995 (first entry)
XX DE Alpha-amylase signal sequence primer.
XX DE
XX KW Barley; Hordeum vulgare; alpha-amylase; signal peptide; PCR; primer;
XX KW polymerase chain reaction; major histocompatibility complex; MHC;
XX KW transgenic plant; allograft rejection suppression; plasmid pSM155;
XX KW tobacco; Nicotiana tabacum; ss.
XX OS Synthetic.
XX OS
XX PN WO9508347-A1.
XX PD
XX PD 30-MAR-1995.
XX PF 21-SEP-1994; 94WO-CA000530.
XX PR 21-SEP-1993; 93GB-00019429.
XX PA (UNLO ) UNIV HOSPITAL LONDON HEALTH ASSOC.
XX PI Jevnikar AM, Ma S, Stiller CR;
XX WPI; 1995-139392/18.
XX DR
XX PT Expressing a mammalian antigen in transformed plants to provide a source
XX PT of plant material - for oral or enteral admin. to a mammal to produce
XX PT tolerance to the antigen.
XX PS Example 2; Page 17; 41pp; English.
XX CC The signal sequence was isolated from barley alpha-amylase cDNA by PCR
XX CC using the primers given in AAQ86577-78. The product was cloned into
XX CC pBluescriptII together with a mouse MHC II alpha chain mature peptide-
XX CC encoding sequence to obtain plasmid pSM155, for expression in tobacco cv.
XX CC SRI transformants. (Updated on 25-MAR-2003 to correct PN field.) (Updated
XX CC on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 26 BP; 4 A; 8 C; 12 G; 2 T; 0 U; 0 Other;
Query Match 71.7%; Score 17.2; DB 2; Length 26;
Best Local Similarity 86.4%; Pred. No. 5.e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGGTCCAGCGTGGCCCATGGG 23
Db 2 GGATCCGGCGCGCCCATGGG 23
RESULT 8
ID ADR29366/c
XX AC ADR29366;
XX DT 18-NOV-2004 (first entry)
XX DE Human Bcl-2 PCR primer SEQ ID NO:2.
XX KW filamentous fungus; Bcl-2; herbicide;
XX KW Colletotrichum gloeosporioides f.sp. aescynomene; food production;
XX KW drug production; paper; pulp industry; agriculture; bioremediation;
XX KW human; PCR; primer; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2004072225-A2.
XX
XX PD 26-AUG-2004.
XX PF 10-FEB-2004; 2004WO-IL000132.
XX PR 12-FEB-2003; 2003US-0446513P.
XX PA (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
XX PI Sharon A, Goldstein-Barhoom S;
XX WPI; 2004-625842/60.
XX DR
XX PT Novel filamentous fungus having exogenous polynucleotide expressing Bcl-2
XX PT polypeptide, and exhibiting accelerated growth compared to wild-type
XX PT filamentous fungus, useful for eradicating unwanted weed growing in crop
XX PT field.
XX PS Disclosure; SEQ ID NO 2; 57pp; English.
XX CC The present invention describes a filamentous fungus (I) comprising an
XX CC exogenous polynucleotide capable of expressing a Bcl-2 polypeptide or its
XX CC active portion, and exhibiting accelerated growth as compared to a wild-
XX CC type filamentous fungus. Also described: (1) enhancing (M1) growth of
XX CC filamentous fungus, involving providing the filamentous fungus with a Bcl
XX CC -2 polypeptide or its active portion, and so enhancing the growth of the
XX CC filamentous fungus; (2) enhancing (M2) the viability and/or pathogenicity
XX CC of a filamentous fungus stored at sub-optimal temperature; (3) increasing
XX CC (M3) the resistance of a filamentous fungus to stress; (4) a fungal
XX CC culture medium (II) suitable for growth of fungus, comprising Bcl-2
XX CC polypeptide or its active portion and a carbon source; and (5) a
XX CC filamentous fungus comprising a first exogenous polynucleotide encoding
XX CC Bcl-2 or its active portion, and a second exogenous polynucleotide
XX CC encoding a suicide gene. Bcl-2 has herbicide activities, (I) is
XX CC Colletotrichum gloeosporioides f.sp. aescynomene. (M1) is useful for
XX CC eradicating an unwanted weed growing in a crop field, which involves
XX CC spreading (I) in the crop field which is pathogenic to the unwanted weed.
XX CC The filamentous fungi are useful in industrial applications, such as food
XX CC and drug production, paper and pulp industry, agriculture and
XX CC bioremediation. (I) remains viable in storage for a time period longer
XX CC than the wild-type filamentous fungus when grown on solid media. (I)
XX CC exhibits increased resistance to temperature, oxidative and/or radiation
XX CC stress, as compared to the wild-type filamentous fungus. The present
XX CC sequence represents a PCR primer for the human Bcl-2 gene, which is used
XX CC in the exemplification of the present invention.
XX SQ Sequence 30 BP; 7 A; 8 C; 13 G; 2 T; 0 U; 0 Other;
Query Match 66.7%; Score 16; DB 13; Length 30;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CCAGCGTGGCCCATGG 21
Db 20 CCAGCGTGGCCCATGG 5
RESULT 9
ID AAA50259/c
XX AC AAA50259;
XX DT 07-NOV-2000 (first entry)
XX DE Bcl2 gene 5' PCR primer.
XX KW Bcl2 gene; human; episome; transfection; selection; gene therapy;
XX KW PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200047778-A1.
XX

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PD 17-AUG-2000.
XX
XX
PF 11-FEB-2000; 2000WO-US003547.
XX
XX 11-FEB-1999; 99US-00249585.
XX
XX (PHAR-) PHARMACOPEIA INC.
XX
XX Horlick RA, Chelsky D;
XX
XX WPI; 2000-515062/46.
XX
XX Stably transfecting eukaryotic cells with at least one episome for the
XX production of a desired protein in vitro and for gene therapy.
XX
XX Example 1; Page 29; 53pp; English.
XX
XX The present 5' primer was used with the 3' primer given in AAA50260 for
XX the PCR amplification of Bcl2 DNA, introducing a 5' BsiWI site and a 3'
XX NheI site. The PCR product was incorporated into an episome to
XX demonstrate a method of the invention. The method relates to the
XX maintenance and selection of episomes in transfecting eukaryotic cells
XX in vitro or in vivo, e.g. for gene therapy. It involves transfecting the
XX cells with an episome under conditions in which cells that survive are
XX successfully transfecting with the episome. The resulting cells express a
XX first protein whose expression causes cell death and a second protein
XX whose expression prevents cell death resulting from expression of the
XX first protein. In an example of the method, bcl2 and bad, and dff45 and
XX cide-1, were used as kill antagonist and kill agonist pairs in episomes
XX used to transfect 293E cells. The method allows the rapid establishment
XX of eukaryotic cells that stably and reliably express a gene of interest
XX
XX Sequence 33 BP; 9 A; 9 C; 10 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 16; DB 3; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 CCAGCGTGGCCATGG 21
XX Db 27 CCAGCGTGGCCATGG 12
XX
XX RESULT 10
XX AAA48984/c
XX ID AAA48984 standard; DNA; 33 BP.
XX AC AAA48984;
XX XX
XX DT 28-NOV-2000 (first entry)
XX XX
XX DE Mutagenic PCR primer Bcl2-5 targeted to anti-apoptotic gene bcl-2.
XX XX
XX KW Apoptosis; bcl-2; resistance; bacterial; viral; pathogens; PCR primer;
XX KW human; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200026391-A2.
XX XX
XX PD 11-MAY-2000.
XX XX
XX PF 29-OCT-1999; 99WO-US025522.
XX XX
XX PR 30-OCT-1998; 98US-0106321P.
XX PR 09-JUN-1999; 99US-013803P.
XX XX
XX PA (UYNE-) UNIV NEBRASKA-LINCOLN.
XX XX
XX FI Dickman MB;
XX XX
XX WPI; 2000-365634/31.
XX
XX

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PT Transgenic plants with improved resistance characteristics comprising
PT nucleic acids encoding apoptotic proteins.
XX
XX Example 3; Page 58; 109pp; English.
XX
XX The present invention relates to the use of apoptotic genes in the the
XX production of transgenic plants with improved resistance characteristics.
XX The present sequence is the mutagenic PCR primer Bcl2-5. This primer was
XX used with primer Bcl2-3 (AAA48985) to introduce a 5' NcoI site and a 3'
XX XbaI site in the human apoptotic gene bcl-2. Specifically the primer
XX introduced an Ala residue between the Met (position 1) and His (position
XX 2) residues of the native protein. The altered bcl-2 sequence was used in
XX the creation of the final vector used to transform plants. The improved
XX resistance characteristics of the plants helps protect against bacterial,
XX viral and other pathogens. Resistance to abiotic challenges may also be
XX conferred
XX
XX Sequence 33 BP; 3 A; 9 C; 12 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 16; DB 3; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 CCAGCGTGGCCATGG 21
XX Db 33 CCAGCGTGGCCATGG 18
XX
XX RESULT 11
XX ABK29920/c
XX ID ABK29920 standard; DNA; 35 BP.
XX XX
XX AC ABK29920;
XX XX
XX DT 23-APR-2002 (first entry)
XX XX
XX DE Human epidermal growth factor receptor 2 (Her2), primer #2.
XX XX
XX KW Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
XX KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
XX KW vanH promoter; androgen receptor promoter; AR promoter;
XX KW human epidermal growth factor receptor 2 promoter; her2 promoter;
XX KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
XX KW colon cancer; immunological disorder; prostate cancer; cytostatic;
XX KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;
XX KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;
XX KW gene expression modulator; multiple sclerosis; MS;
XX KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
XX KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
XX KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
XX KW transgenic; ds.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200194600-A2.
XX XX
XX PD 13-DEC-2001.
XX XX
XX PF 06-JUN-2001; 2001WO-US018343.
XX XX
XX PR 06-JUN-2000; 2000US-0209549P.
XX XX
XX PA (GENE-) GENELABS TECHNOLOGIES INC.
XX XX
XX PI Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
XX PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
XX PI Lim MY, Bruce TW;
XX XX
XX DR WPI; 2002-130595/17.
XX XX
XX PT New nucleic acid regulatory sequences, which are able to regulate
XX PT expression of a gene operably linked to a promoter, useful for regulating
XX PT the expression of transgenes and for treating e.g., cancer and

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CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth.  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubecosis, Osler-Webber Syndrome, myocardial angioneitis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX

SQ Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 62.5%; Score 15; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
 Db 1 TCCAGCGTGC GCCAT 15

RESULT 14  
 ABL39111  
 ID ABL39111 standard; DNA; 16 BP.  
 XX  
 AC ABL39111;  
 XX  
 DT 16-APR-2002 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid SEQ ID NO: 533.  
 XX  
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200197843-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 22-JUN-2001; 2001WO-US020154.  
 XX  
 PR 22-JUN-2000; 2000US-0213346P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 PI Weiner G, Hartmann G;  
 XX  
 DR WPI; 2002-154611/20.  
 XX

XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
 PT administering immunostimulatory nucleic acids that induce expression of  
 PT cell surface antigens and antibodies to a subject having or at risk of  
 PT developing cancer.  
 XX

PS Disclosure; Page 231; 312pp; English.

XX The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for  
 CC treating or preventing cancer such as basal cell carcinoma, bladder  
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The

CC present sequence is an immunostimulatory oligonucleotide described in the  
 CC exemplification of the invention

SQ Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 62.5%; Score 15; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
 Db 1 TCCAGCGTGC GCCAT 15

RESULT 15  
 ACD99398  
 ID ACD99398 standard; DNA; 16 BP.  
 XX  
 AC ACD99398;  
 XX  
 DT 25-SEP-2003 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #84.  
 XX  
 KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003050268-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 29-MAR-2002; 2002US-00112653.  
 XX  
 PR 29-MAR-2001; 2001US-0279642P.  
 XX  
 PA (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX  
 PI Krieg AM, Berg DJ;  
 XX  
 DR WPI; 2003-521815/49.  
 XX

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX

PS Disclosure; Page 10; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 XX

SQ Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 9; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
 Db 1 TCCAGCGTGC GCCAT 15

RESULT 16

```
ADB36467
ID  ADB36467 standard; DNA; 16 BP.
XX
XX  ADB36467;
AC
XX
XX  04-DEC-2003 (first entry)
DT
XX
XX  Immunostimulatory nucleic acid #81.
DE
XX
XX  ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW  hypo-responsive subject; immunostimulatory.
KW
XX
XX  Synthetic.
OS
XX
XX  US2003087848-A1.
FN
XX
XX  08-MAY-2003.
PD
XX
XX  02-FEB-2001; 2001US-00776479.
PF
XX
XX  03-FEB-2000; 2000US-0179991P.
PR
XX
XX  (BRAT/) BRATZLER R L.
PA  (PETE/) PETERSEN D M.
PA  (FOUR/) FOURON Y.
XX
XX  Bratzler RL, Petersen DM, Fouron Y;
FI  WPI; 2003-657977/62.
XX
XX  Treating and/or preventing allergy or asthma using an immunostimulatory
DR  nucleic acid alone or in combination with an asthma/allergy medicament.
XX
XX  Disclosure; Page 6; 221pp; English.
PS
XX  The invention relates to a method of treating or preventing allergy or
CC  asthma which comprises administering to a subject a poly-G nucleic acid
CC  in an aerosol formulation. The methods and compositions of the present
CC  invention are useful for diagnosing and/or treating asthma and allergy
CC  especially in a hypo-responsive subject. The present sequence represents
CC  an immunostimulatory nucleic acid of the invention.
XX
XX  Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 62.5%; Score 15; DB 9; Length 16;
XX  Best Local Similarity 100.0%; Pred. No. 5.4e+03;
XX  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  Qy 5 TCCAGCGTGGCCCAT 19
XX  Db 1 TCCAGCGTGGCCCAT 15
XX
XX  RESULT 17
XX  ADU89406
XX  ID  ADU89406 standard; DNA; 16 BP.
XX
XX  AC  ADU89406;
XX
XX  10-FEB-2005 (first entry)
DT
XX
XX  Allergic response suppressor oligonucleotide #90.
DE
XX
XX  ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;
KW  antibacterial; virucide; immunoglobulin E antagonist; allergy;
KW  immunostimulator; asthma; rhinitis; urticaria; dermatitis;
KW  bacterial infection; viral infection.
XX
XX  Synthetic.
OS
XX
XX  US2004235774-A1.
FN
XX
XX  25-NOV-2004.
PD
XX
XX  23-APR-2004; 2004US-00831778.
XX
XX  03-FEB-2000; 2000US-0179991P.
PR  02-FEB-2001; 2001US-00776479.
XX
XX  (BRAT/) BRATZLER R L.
PA  (PETE/) PETERSEN D M.
PA  (FOUR/) FOURON Y.
XX
XX  Bratzler RL, Petersen DM, Fouron Y;
FI  WPI; 2004-833006/82.
XX
XX  Suppressing allergies, including asthma, rhinitis, urticaria and atopic
PT  dermatitis, in a subject, comprises administering a first and second dose
PT  of an immunostimulatory nucleic acid.
XX
XX  Disclosure; SEQ ID NO 90; 235pp; English.
PS
XX  The invention relates to a method of suppressing a symptom of an allergic
CC  response in a subject by administering a first and second dose of an
CC  immunostimulatory nucleic acid that comprises a nucleotide sequence
CC  comprising 5'-cg-3', and where the second dose is administered from 1 day
CC  to 8 weeks after the first dose. The methods and compositions of the
CC  present invention are useful for the treatment or prevention of asthma
CC  and allergy, including rhinitis, urticaria and atopic dermatitis, using
CC  an immunostimulatory nucleic acid alone or in combination with other
CC  medicaments. This can also be used in preventing bacterial and viral
CC  infections. This sequence represents an oligonucleotide used in the
CC  method of the invention.
XX
XX  Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 62.5%; Score 15; DB 13; Length 16;
XX  Best Local Similarity 100.0%; Pred. No. 5.4e+03;
XX  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  Qy 5 TCCAGCGTGGCCCAT 19
XX  Db 1 TCCAGCGTGGCCCAT 15
XX
XX  RESULT 18
XX  ACI96181/c
XX  ID  ACI96181 standard; DNA; 25 BP.
XX
XX  AC  ACI96181;
XX
XX  14-OCT-2003 (first entry)
DT
XX
XX  Human microarray DNA oligonucleotide SEQ ID NO 96172.
DE
XX
XX  EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW  genetic variation; biallelic marker; polymorphism; human;
KW  cross-species comparison.
XX
XX  Homo sapiens.
OS
XX
XX  US2003104410-A1.
FN
XX
XX  05-JUN-2003.
PD
XX
XX  15-MAR-2002; 2002US-00098263.
PF
XX
XX  16-MAR-2001; 2001US-0276759P.
PR
XX
XX  (AFFY-) AFFYMETRIX INC.
XX
XX  Mittmann MP;
PI
XX
XX  WPI; 2003-567953/53.
DR
XX
```



PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 96172; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying allelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX SQ Sequence 25 BP; 3 A; 9 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 9; Length 25;  
 Best Local Similarity 78.3%; Pred. No. 5.5e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GGGTCCAGCTGCGCCATGGG 23  
 ||||| ||||| ||||| |||||  
 Db 24 GGATCCACAGTCCGCCACGGG 2

RESULT 19

AAT18388/c

ID AAT18388 standard; DNA; 27 BP.

XX AAT18388;

XX 08-DEC-1996 (first entry)

XX Human Bcl-2 forward DNA primer.

XX Fas-associated protein; tumour necrosis factor receptor; PTP-BAS;  
 KW apoptosis; FAP; cell surface protein; autoimmune disease; HIV virus;  
 KW hybridoma; cell death; DNA primer; PCR; polymerase chain reaction; ss.

XX Synthetic.

XX WO9534661-A1.

XX 21-DEC-1995.

XX 14-JUN-1995; 95WO-US007583.

XX 14-JUN-1994; 94US-00259514.

XX 27-MAR-1995; 95US-00410804.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Reed JC, Sato T;

XX WPI; 1996-049689/05.

XX New Fas associated proteins PTP-BAS types 4 and 5 - involved in

PT programmed cell death, used for modulating apoptosis, e.g. for treating  
 PT cancer, and for identifying other modulators.

XX Disclosure; Page 42; 84pp; English.

XX The cDNA sequence encoding the cytoplasmic domain of human Fas (AA 191-  
 CC 335) was modified by PCR mutagenesis using this primer along with the  
 CC corresponding reverse primer (AAT18389) and another forward (AAT18386)  
 CC and reverse (AAT18387) primer set. It was then subcloned in frame into  
 CC plasmid pEG202 to produce plasmid pEG/Fas(191-135). The cDNA sequence for  
 CC the cytoplasmic domain of human Fas was then subcloned into the EcoRI  
 CC site of pEG202, in-frame with the upstream LexA sequences

XX SQ Sequence 27 BP; 7 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 2; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CCACGCTGCGCCATG 20  
 ||||| ||||| ||||| |||||  
 Db 21 CCACGCTGCGCCATG 7

RESULT 20

ADY71779

ID ADY71779 standard; DNA; 28 BP.

XX ADY71779;

XX 02-JUN-2005 (first entry)

XX Signal sequence-containing oligonucleotide #5.

XX Cellular transport; ss.

XX Synthetic.

XX WO2005024033-A2.

XX 17-MAR-2005.

XX 10-SEP-2004; 2004WO-EP010162.

XX 11-SEP-2003; 2003EP-00020437.

XX (UYSC-) UNIV SCHLESWIG-HOLSTEIN.

XX Sczakiel G, Hopert A, Wuensche W, Overhoff M;

XX WPI; 2005-223387/23.

XX New nucleic acid promoting transmembrane transport of nucleic acids,  
 PT useful for treating genetically based disorders.

XX Example 3; Page 11; 23pp; English.

XX The invention relates to a nucleic acid comprising a first nucleotide  
 CC sequence having at least one signal sequence unit or a mixture of units,  
 CC the signal sequence causing a transmembrane transport of the nucleic acid  
 CC in a biological system. The invention also relates to a vector containing  
 CC the nucleic acid, a host organism containing at least the nucleic acid or  
 CC the vector, a method of producing the nucleic acid or the vector, a  
 CC pharmaceutical composition comprising the nucleic acid, the vector or the  
 CC host organism and optionally a pharmaceutical carrier and/or diluent or  
 CC a kit comprising the nucleic acid, the vector or the host organism. The  
 CC nucleotide sequence further contains at least one second nucleotide  
 CC linked and/or forming a complex with the first and/or second nucleotide  
 CC sequence, where the covalently linked and/or complexed components are  
 CC biologically active. The nucleic acid, vector or host organism is useful  
 CC for preparing a pharmaceutical composition for treating genetically based  
 CC disorders. This sequence represents a signal sequence-containing

CC oligonucleotide used in the scope of the invention.

XX Sequence 28 BP; 3 A; 9 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 14; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCATG 20

Db 5 CCAGCGTGGCCCATG 19

RESULT 21

ADY71781  
ID ADY71781 standard; DNA; 28 BP.

XX AC ADY71781;

XX 02-JUN-2005 (first entry)

XX Control oligonucleotide #18.

XX Cellular transport; ss.

XX Synthetic.

XX W02005024033-A2.

XX 17-MAR-2005.

XX 10-SEP-2004; 2004WO-EP010162.

XX 11-SEP-2003; 2003EP-00020437.

XX (UYSC-) UNIV SCHLESWIG-HOLSTEIN.

XX Sczakiel G, Hopert A, Wuensche W, Overhoff M;

XX WPI; 2005-223387/23.

XX New nucleic acid promoting transmembrane transport of nucleic acids,  
PT useful for treating genetically based disorders.

XX Example 3; Page 11; 23pp; English.

XX The invention relates to a nucleic acid comprising a first nucleotide  
CC sequence having at least one signal sequence unit or a mixture of units,  
CC the signal sequence causing a transmembrane transport of the nucleic acid  
CC in a biological system. The invention also relates to a vector containing  
CC the nucleic acid, a host organism containing at least the nucleic acid or  
CC the vector, a method of producing the nucleic acid or the vector, a  
CC pharmaceutical composition comprising the nucleic acid, the vector or the  
CC host organism and optionally a pharmaceutical carrier and/or diluent and  
CC a kit comprising the nucleic acid, the vector or the host organism. The  
CC nucleotide sequence further contains at least one second nucleotide  
CC sequence to be transported and/or one or more components covalently  
CC linked and/or forming a complex with the first and/or second nucleotide  
CC sequence, where the covalently linked and/or complexed components are  
CC biologically active. The nucleic acid, vector or host organism is useful  
CC for preparing a pharmaceutical composition for treating genetically based  
CC disorders. This sequence represents an oligonucleotide used in the scope  
CC of the invention.

XX Sequence 28 BP; 6 A; 10 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 14; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCATG 20

Db 5 CCAGCGTGGCCCATG 19

RESULT 22

ADF70717/c  
ID ADF70717 standard; DNA; 40 BP.

XX AC ADF70717;

XX 12-FEB-2004 (first entry)

XX Human dopamine transporter enhancer SEQ ID NO:1.

XX human; ds; dopamine transporter; DAT; enhancer; expression vector;  
KW reporter gene; antiparkinsonian; neuroleptic; antidepressant;  
KW Parkinson's disease; schizophrenia.

XX Homo sapiens.

XX GB2381525-A.

XX 07-MAY-2003.

XX 01-NOV-2001; 2001GB-00026268.

XX 01-NOV-2001; 2001GB-00026268.

XX (TCS-) TCS CELLWORKS LTD.

XX Quinn J;

XX WPI; 2003-432825/41.

XX Novel expression vector comprising reporter gene and a reporter gene-  
PT transcription promoting enhancer sequence that has a variable number of  
PT tandem repeat and is found in 3'non-coding region of human dopamine  
PT transporter.

XX Claim 1; SEQ ID NO 1; 52pp; English.

XX The invention relates to a novel expression vector comprising an enhancer  
CC sequence and a reporter gene. The enhancer sequence comprises a variable  
CC number of tandem repeat (VNTR) and is found in the 3' non-coding region  
CC of the human dopamine transporter (DAT) gene. The enhancer sequence is  
CC capable of promoting the transcription of the reporter gene. An  
CC expression vector of the invention has antiparkinsonian, neuroleptic, and  
CC antidepressant activity, and may act as a dopamine transporter gene  
CC expression regulator, that increases or decreases dopamine levels. The  
CC expression vector is useful for identifying a compound capable of  
CC regulating the expression of a target gene (preferably human dopamine  
CC transporter gene) that comprises an enhancer sequence. A compound of the  
CC invention is useful for treating Parkinson's disease and schizophrenia  
CC that are associated with reduced and increased levels of dopamine,  
CC respectively. The present sequence is used in the exemplification of the  
CC invention.

XX Sequence 40 BP; 8 A; 15 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 10; Length 40;  
Best Local Similarity 78.3%; Pred. No. 5.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCCATGGGG 23

Db 32 GGGGCCCTGCATGCGTCTCTGGGG 10

RESULT 23

ABN86431  
ID ABN86431 standard; DNA; 20 BP.

XX AC ABN86431;

XX 21-OCT-2002 (first entry)

```
XX DE Translational consensus WAP-EPO with NotI modification sequence.
XX KW Therapeutic; erythropoietin; EPO; transgenic; WAP; ss.
XX OS Synthetic.
XX PN EP1217072-A2.
XX PD 26-JUN-2002.
XX PP 07-DEC-2001; 2001EP-00128498.
XX PR 07-DEC-2000; 2000CZ-00004569.
XX PA (BIOP-) BIOPHARM VU BIOFARMACIE A VETERINARNICH.
XX PI Mikus T, Maly P;
XX DR WPI; 2002-550408/59.
XX PT Preparing vectors for therapeutic protein production in transgenic
XX PT animals, based on utilization of modified translational Kozak consensus
XX PT to connect promoter regulatory sequences with coding structural gene
XX PT fragments.
XX PS Disclosure; Fig 1; 32pp; English.
XX CC The invention relates to the preparation of an expression vector for the
XX CC therapeutic protein production, characterized by the utilization of
XX CC sequence motifs for restriction endonucleases NotI or NcoI to connect the
XX CC gene segments (including promoter regulatory regions) with the gene
XX CC segments (including structural fragments of the gene coding the required
XX CC protein). The method is useful for preparing an expression vector for
XX CC therapeutic protein production, in particular human erythropoietin (EPO).
XX CC The vector produced by the method is useful for EPO expression in
XX CC suitable transfected eukaryotic cells or in the mammary gland of
XX CC transgenic organisms. The present sequence represents a translational
XX CC consensus WAP-EPO sequence with NotI modification
XX SQ Sequence 20 BP; 3 A; 7 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 61.7%; Score 14.8; DB 6; Length 20;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 CCAGCGTGGCCCATGGGG 23
Db 3 CCAGCGCGCCCATGGGG 20
RESULT 24
ACI35454
ID ACI35454 standard; DNA; 25 BP.
XX AC ACI35454;
XX DT 13-OCT-2003 (first entry)
XX DE Human microarray DNA oligonucleotide SEQ ID NO 35445.
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS Homo sapiens.
XX PN US2003104410-A1.
XX PD 05-JUN-2003.
XX PF 15-MAR-2002; 2002US-00098263.
XX PR 15-MAR-2002; 2002US-00098263.
XX XX
PR 16-MAR-2001; 2001US-0276759P.
XX PA (AFFY-) AFFYMETRIX INC.
XX PI Mittmann MP;
XX XX WPI; 2003-567953/53.
XX XX New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX PS Claim 1; SEQ ID NO 35445; 9pp; English.
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, perfect mismatch, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying biallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX SQ Sequence 25 BP; 2 A; 7 C; 9 G; 7 T; 0 U; 0 Other;
Query Match 60.8%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 GTCCAGCGTGGCCCATGGGG 24
Db 1 GTCCACTGTGCTCCATGGGTG 21
RESULT 25
ACI87918
ID ACI87918 standard; DNA; 25 BP.
XX AC ACI87918;
XX DT 14-OCT-2003 (first entry)
XX DE Human microarray DNA oligonucleotide SEQ ID NO 87909.
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS Homo sapiens.
XX PN US2003104410-A1.
XX PD 05-JUN-2003.
XX PF 15-MAR-2002; 2002US-00098263.
XX PR 16-MAR-2001; 2001US-0276759P.
XX XX
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DR WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 87293; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 3 A; 7 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 60.8%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 GTCCAGCGTGCAGCCATGGGG 24
DB 3 GTCCACTGTGCTCCATGGGTG 23
RESULT 28
AAA30408
ID AAA30408 standard; DNA; 47 BP.
XX
XX AAA30408;
XX
XX 15-SEP-2003 (revised)
DT 11-SEP-2000 (first entry)
XX
XX EGF sequence biotinylated PCR primer Anchor1M8f.
XX
XX Phage display; biopanning; fusion protein; antibacterial;
KW ligand internalisation; cell transduction; library screening;
KW gene therapy; PCR primer; ss.
XX
XX Enterobacteria phage M13.
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /note= "biotinylated"
XX
XX WO200029555-A1.
XX
XX 25-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025361.
XX
XX 17-NOV-1998; 98US-00193445.
PR 17-NOV-1998; 98US-00195379.
XX
PR 26-FEB-1999; 99US-00258689.
XX
XX (SELE-) SELECTIVE GENETICS INC.
XX
XX Larocca D, Baird A, Kassner P;
XX
XX WPI; 2000-387775/33.
XX
XX Selecting internalized ligands displayed on a genetic package by
PT contacting them with a cell, where each package carries a gene encoding a
PT detectable product expressed on internalization, useful for identifying
PT ligands for gene therapy.
XX
XX Example 19; Page 65; 112pp; English.
XX
XX The present sequence is a PCR primer used to amplify the EGF sequence in
CC COS cells infected with non-targeted M13 phage and EGF-phage. The
CC amplification primers have sequences located on each side of the EGF
CC sequence in the gene III coding sequence. The PCR products were digested
CC with restriction endonucleases and ligated into a new phage vector and
CC used to transform competent bacterial cells by electroporation. Plaques
CC were analysed via PCR using oligonucleotides which included the present
CC sequence. Four rounds of selection were sufficient to enrich the targeted
CC EGF-phage to 100%. This selection procedure is a useful example of a
CC novel method of selecting internalising ligands displayed on a genetic
CC package. The package carries a gene encoding a detectable product
CC expressed on internalisation. The method is referred to as Ligand
CC Identification via Expression or LIVE (RTM). The method identifies
CC ligands that may be useful as antibacterial agents or in gene therapy.
CC The method is also useful for studying protein-protein interactions that
CC lead to cell transduction and identifying cells which are transduced by
CC the ligands. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 47 BP; 6 A; 10 C; 18 G; 13 T; 0 U; 0 Other;
Query Match 60.8%; Score 14.6; DB 3; Length 47;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGGGTCCAGCGTGCAGCCATGG 21
DB 10 GGGTTCCTCCGCTGGCGATGG 30
RESULT 29
ADD14864
ID ADD14864 standard; DNA; 47 BP.
XX
XX ADD14864;
XX
XX 01-JAN-2004 (first entry)
DT
XX
XX Ligand gene III fusion PCR primer #1.
XX
XX Transgene expression; gene delivery; anti-bacterial agent; cancer;
KW restenosis; antibacterial; cytostatic; vasotrophic; PCR; primer; ss.
XX
XX Synthetic.
XX
XX US2002068272-A1.
XX
XX 06-JUN-2002.
XX
XX 24-MAY-2001; 2001US-00866073.
XX
XX 29-OCT-1999; 99WO-US025361.
XX
XX (LARO/) LARocca D.
XX (KASS/) KASSNER P.
XX (BAIR/) BAIRD A.
XX
XX Larocca D, Kassner P, Baird A;
XX
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```

DR WPI; 2003-776567/73.
XX
PT Genetic package display method useful for detecting and identifying
PT protein-protein interactions that facilitate internalization and
PT transgene expression.
XX
PS Example 19; Page 24; 47pp; English.
XX
CC The invention relates to a method for selecting ligands that internalise
CC and facilitate transgene expression, comprising displaying on a phage
CC carrying a transgene encoding a detectable product, and recovering a
CC nucleic acid molecule encoding the ligands from the cell expressing the
CC detectable product. The methods are useful in selecting and identifying
CC ligands displayed on a phage that internalise and facilitate transgene
CC expression, and also in identifying transduction facilitating peptides.
CC Internalising ligands identified by the methods are useful in gene
CC delivery methods and as anti-bacterial agents. The ligands and anti-
CC ligands identified are useful in the treatment of e.g., cancer and
CC restenosis. The method is also useful in that it allows identification of
CC molecules that are targets for new discovery. This sequence represents a
CC PCR primer used to amplify a ligand gene III fusion of the invention.
XX
SQ Sequence 47 BP; 6 A; 10 C; 18 G; 13 T; 0 U; 0 Other;
Query Match 60.8%; Score 14.6; DB 10; Length 47;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GGGTCCAGCGTCGCCATGG 21
Db ||||| ||||| |||||
10 GGGTCCCGCGTGGCGATGG 30
RESULT 30
ADP86181
ID ADP86181 standard; DNA; 18 BP.
XX
AC ADP86181;
XX
DT 09-SEP-2004 (first entry)
XX
DE CpG immunostimulatory oligonucleotide #52.
XX
KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW viral infection; bacterial infection; cancer; lymphoma;
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS Unidentified.
XX
PH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PN WO2004053104-A2.
XX
PD 24-JUN-2004.
XX
PF 11-DEC-2003; 2003WO-US039775.
XX
PR 11-DEC-2002; 2002US-0432409P.
XX
PR 25-SEP-2003; 2003US-0506108P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;
XX
XX WPI; 2004-487902/46.
XX
DR New oligonucleotides, useful for treating allergy or asthma, viral and
XX bacterial infections, and cancer, e.g. biliary tract cancer, breast
XX
PT bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT cancer, cervical cancer.
XX
PS Example; SEQ ID NO 52; 104pp; English.
XX
CC The invention relates to a class of CpG immunostimulatory
CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC are useful for stimulating an immune response. Oligonucleotides and
CC compositions of the invention are useful for treating allergy or asthma,
CC viral and bacterial infections and cancer e.g. biliary tract cancer,
CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC testicular cancer, as well as other carcinomas and sarcomas. The
CC invention is also useful in gene therapy. The present sequence is a CpG
CC immunostimulatory oligonucleotide.
XX
SQ Sequence 18 BP; 2 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 60.0%; Score 14.4; DB 12; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GTCGAGCGTGGCCAT 19
Db ||||| ||||| |||||
3 GTCGAGCGTGGCCAT 18
RESULT 31
ADP86182
ID ADP86182 standard; DNA; 18 BP.
XX
AC ADP86182;
XX
DT 09-SEP-2004 (first entry)
XX
DE CpG immunostimulatory oligonucleotide #53.
XX
KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW viral infection; bacterial infection; cancer; lymphoma;
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS Unidentified.
XX
PH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PN WO2004053104-A2.
XX
PD 24-JUN-2004.
XX
PF 11-DEC-2003; 2003WO-US039775.
XX
PR 11-DEC-2002; 2002US-0432409P.
XX
PR 25-SEP-2003; 2003US-0506108P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;
XX
XX WPI; 2004-487902/46.
XX
DR New oligonucleotides, useful for treating allergy or asthma, viral and
XX bacterial infections, and cancer, e.g. biliary tract cancer, breast
XX

```

PT cancer, cervical cancer.

PS Example; SEQ ID NO 53; 104pp; English.

XX The invention relates to a class of CpG immunostimulatory oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that are useful for stimulating an immune response. Oligonucleotides and compositions of the invention are useful for treating allergy or asthma, viral and bacterial infections and cancer e.g. biliary tract cancer, breast cancer, cervical cancer, choriocarcinoma, colon cancer, endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms, liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma, neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer, Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer, testicular cancer, as well as other carcinomas and sarcomas. The invention is also useful in gene therapy. The present sequence is a CpG immunostimulatory oligonucleotide.

XX Sequence 18 BP; 2 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 12; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GTCCAGCGTGGCCCAT 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 3 GCCCAGCGTGGCCCAT 18

RESULT 32  
ADW88846/C

ID ADW88846 standard; DNA; 26 BP.

XX AC ADW88846;

XX 21-APR-2005 (first entry)

XX Human Bcl-2 RT-PCR primer Bcl-2up.

XX cytostatic; gene therapy; apoptosis modulation; pharmaceutical; cancer;  
KW cytosstatic; neoplasm; Bcl-2; reverse transcriptase PCR; RT-PCR; primer;  
KW ss.

XX Homo sapiens.

OS WO2005012357-A1.

XX 10-FEB-2005.

XX 30-JUL-2004; 2004WO-GB003326.

XX 31-JUL-2003; 2003GB-00017988.

XX (MILM/) MILMER J.

XX Milmer J, Jiang M;

XX WPI; 2005-123281/13.

XX Regulating apoptosis in a cell, useful for treating cancer, comprises  
PT targeting an abnormally or alternatively spliced mRNA, an abnormally or  
PT alternatively structured mRNA, or a product of either.

XX Disclosure; Page 14; 35pp; English.

XX The invention describes a method of regulating apoptosis in a cell  
CC comprising targeting an abnormally or alternatively spliced mRNA, an  
CC abnormally or alternatively structured mRNA, or a product of either. Also  
CC described are: a nucleotide construct with a nucleotide sequence which is  
CC homologous to mRNA transcribed from an abnormally spliced gene; an agent  
CC selected from small molecule or protein; polypeptide; peptide; aptamer;

CC chemical; antibody; nucleic acid; polypeptide or nucleotide probe, which  
agent interacts with or binds with a protein expressed by an abnormally  
spliced mRNA for use as a medicament or for the manufacture of a  
medicament for the treatment of cancerous cell growth; a pharmaceutical  
composition comprising a nucleotide construct such as siRNA, anti-sense  
RNA, shRNA or miRNA; or the agent cited above, and a pharmaceutical  
diluent or carrier; a DNA or RNA expression vector comprising an  
expression cassette including the nucleotide sequence selected from: the  
nucleic acid sequence of the abnormally spliced gene element as given in  
the specification; a nucleic acid molecule which hybridizes to the  
nucleic acid sequence of (a); and a nucleic acid molecule which has a  
nucleic acid sequence which is degenerate because of the genetic code to  
the sequences in (a) and (b) and any sequence which is complementary to  
any of the above sequences, where the expression cassette is  
transcriptionally linked to a promoter sequence. The method is useful for  
regulating apoptosis in a cell or for treating cancer. The agent or  
nucleotide construct is useful as a medicament or for the manufacture of  
a medicament for the treatment of cancerous cell growth. In addition, the  
nucleotide construct is a means for silencing the expression of an  
abnormally spliced gene for use as a medicament for treating cancerous  
cell growth. The DNA or RNA expression vector is used as a delivery means  
for a molecule that is used in the targeting of an abnormally spliced  
mRNA or its product. This sequence represents a reverse transcriptase PCR  
primer used to isolate alternatively spliced Bcl-2 polynucleotides.

XX Sequence 26 BP; 6 A; 8 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 14; Length 26;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCATGG 21  
| | | | | | | | | | | | | | | | | | | | |  
Db 20 CCAGCGTGGCCCATCG 5

RESULT 33  
AAA15383

ID AAA15383 standard; DNA; 29 BP.

XX AC AAA15383;

XX 04-SEP-2000 (first entry)

XX PCR primer for a Neisseria pathogenic strain DNA sequence.

XX Pathogenic strain; Neisseria; vaccine; Neisseria infection; PCR primer;  
KW ss.

XX Neisseria meningitidis.

XX WO2000026375-A2.

XX 11-MAY-2000.

XX 28-OCT-1999; 99WO-FR002643.

XX 30-OCT-1998; 98FR-00013693.

XX (INMR ) PASTEUR MERIEUX SERUMS & VACCINS SA.  
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

XX Aujame L, Bouchardon A, Renauld-Mongenie G, Rokbi B, Nassif X;  
XX Tinsley C, Perrin A;

XX WPI; 2000-365622/31.

XX New polypeptide specific for pathogenic Neisseria useful in therapeutic  
or preventative vaccines and for diagnosis.

XX Example 1; Page 30; 187pp; French.

XX The present sequence represents a PCR primer that was used to amplify DNA

CC encoding a protein that is specific for pathogenic strains of *Neisseria*.  
CC The polynucleotides, polypeptides, or their antigenic fragments, are used  
CC in vaccines to treat or protect against *Neisseria* infections, are used  
CC particularly by *N. meningitidis*. The polynucleotide sequence is also used  
CC for recombinant production of the polypeptide and to produce attenuated  
CC *Neisseria* strains that overexpress it, or express it in a non-toxic  
CC mutant form  
XX  
SQ Sequence 29 BP; 5 A; 8 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 3; Length 29;  
Best Local Similarity 75.0%; Pred. No. 1e+04;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGGGG 24  
||| ||| ||| ||| ||| ||| |||  
DB 2 GGGATCCACCTGCTCATGGGTG 25

RESULT 34  
ADF28077/c  
ID ADF28077 standard; cDNA; 31 BP.  
XX  
AC ADF28077;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Caspase-resistant Bcl-2 5'-end terminal fragment.

XX Bcl-2; endothelial cell; mutant; vascularisation; human; antidiabetic;  
XX antiulcer; vulnery; cardiovascular; cell therapy; ss.  
XX  
XX Synthetic.

XX WO2003087337-A2.

XX 23-OCT-2003.

XX 14-APR-2003; 2003WO-US011371.

XX 12-APR-2002; 2002US-0371677P.

XX (UYUA ) UNIV YALE.

XX Bothwell ALM, Pober JS, Schechner JS;

XX WPI; 2003-833725/77.

XX New engineered human skin equivalent that becomes perfused in vivo after  
PT engraftment on an immunodeficient animal, useful for treating conditions  
PT involving impaired angiogenesis, e.g. diabetes, chronic leg ulcers or  
PT wounds.

XX Example 2; SEQ ID NO 3; 144pp; English.

XX The invention relates to an engineered human skin equivalent, where the  
CC skin equivalent becomes perfused in vivo after engraftment on an  
CC immunodeficient animal. The method involves implanting onto a skin  
CC surface wound of an animal a construct prepared by a method comprising:  
CC preparing a solution comprising collagen and fibronectin; suspending  
CC endothelial cells in the solution where the suspended endothelial cells  
CC comprise a nucleic acid encoding a caspase-resistant Bcl-2 polypeptide;  
CC adjusting the solution of step (b) to about pH 7.0-8.0; and warming the  
CC solution of step (c) to about 25-40 °C to form a three-dimensional  
CC gel. The method of endothelial cell transplantation promotes  
CC vascularisation of human skin equivalents in vivo. Administration can be  
CC orthotopic or subcutaneous. The engineered human skin equivalents and  
CC methods are useful in treating diseases or conditions involving impaired  
CC angiogenesis, such as diabetes, chronic leg ulcers, wounds,  
CC cardiovascular disease or burns. The present sequence represents a  
XX Caspase-resistant Bcl-2 5'-end terminal fragment

XX Sequence 31 BP; 7 A; 10 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 10; Length 31;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 8 AGCGTGGCCATGGGG 23  
||||| ||||| ||||| |||||  
DB 31 AGCGTGGCCATGGTG 16

RESULT 35  
ABA92890/c  
ID ABA92890 standard; DNA; 32 BP.

XX ABA92890;

XX 03-APR-2002 (first entry)

XX Human 5' end of Bcl-2 DNA SEQ ID NO:3.

XX Human; D34A caspase-resistant Bcl-2; Bcl-2; mutant; vasotropic;  
XX vascularisation; angiogenesis; tissue transplantation; grafting;  
XX organ transplantation; gene; ss.

XX Homo sapiens.

XX WO200193880-A1.

XX 13-DEC-2001.

XX 05-JUN-2001; 2001WO-US018034.

XX 05-JUN-2000; 2000US-0208931P.

XX 30-MAR-2001; 2001US-0279797P.

XX (UYUA ) UNIV YALE.

XX Bothwell ALM, Pober JS, Schechner JS, Zheng L;

XX WPI; 2002-130568/17.

XX New synthetic composition comprising collagen, fibronectin and cells,  
PT useful for forming cultured endothelial cells for tissue/organ  
PT transplantation or grafting onto recipients with impaired  
PT vascularization.

XX Example 2; Page 55; 99pp; English.

XX The present invention describes a synthetic composition, which comprises  
CC collagen, fibronectin and at least one cell. Also described are: (1) a  
CC construct prepared by a method (M1) comprising: (a) preparing a solution  
CC comprising collagen and fibronectin; (b) suspending endothelial cells in  
CC the solution of step (a), where the suspended endothelial cells comprise  
CC a nucleic acid encoding a caspase-resistant Bcl-2 polypeptide; and (c)  
CC polymerising the collagen within the solution of step (b) to form a three  
CC dimensional gel; (2) a method (M2) of animal implantation comprising  
CC implanting into an animal the construct produced by the method of (1);  
CC (3) a method (M3) for forming endothelial cells into tubes within a  
CC matrix; (4) a method (M4) of producing endothelial cell tubules in vivo;  
CC (5) a method (M5) of promoting vascularisation in a tissue or an organ,  
CC or in animal; (6) methods (M6) for identifying genes or gene products  
CC involved in the process of vascularisation; (7) a method (M7) of  
CC identifying an agent, which modulates vascularisation or vascular  
CC remodeling; and (8) the endothelial cell tubules produced by the method  
CC of (M4). The synthetic composition has vasotropic activity. The  
CC composition is useful in methods for forming cultured endothelial cells  
CC into tubes or forming cultured endothelial cells into tubes within a  
CC three-dimensional gel. This is particularly useful in the grafting of  
CC engineered skin onto recipients with impaired vascularisation or impaired  
CC angiogenesis, or in all aspects of tissue and organ transplantation and  
CC grafting. The present sequence represents the 5' end of human Bcl-2,  
XX which is used in an example from the present invention



SQ Sequence 32 BP; 7 A; 10 C; 9 G; 6 T; 0 U; 0 Other;  
 Query Match 60.0%; Score 14.4; DB 6; Length 32;  
 Best Local Similarity 93.8%; Pred. No. 1e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 AGCGTGGCCATGGGG 23  
 DB 32 AGCGTGGCCATGGTG 17  
 |||||  
 |||||

RESULT 36  
 ABK90294  
 ID ABK90294 standard; DNA; 34 BP.  
 XX AC ABK90294;  
 XX DT 21-OCT-2002 (first entry)  
 XX DE Bcl-2/CRE hybrid antisense oligonucleotide #1.  
 XX KW Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;  
 KW CAMP response element; bacterial infection; viral infection;  
 KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;  
 KW autoimmune disorder; parasitic infection; virucide; hyperplasia;  
 KW tumorigenesis; hepatitis B infection; human.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT modified\_base 1..34  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 XX PN WO200257480-A2.  
 XX PD 25-JUL-2002.  
 XX PF 22-JAN-2002; 2002WO-US001967.  
 XX PR 22-JAN-2001; 2001US-0263244P.  
 XX PA (GENT-) GENTA INC.  
 XX PI Klem RE;  
 XX DR WPI; 2002-590754/63.  
 XX PT Hybrid oligomer comprises a cyclic AMP response element sequence and a  
 PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for  
 PT preventing or treating cell-proliferative disorders e.g., cancer.  
 XX PS Disclosure; Page 25; 78pp; English.  
 XX CC The invention relates to a hybrid oligomer comprising a cyclic AMP  
 CC response element (CRE) sequence and a sequence that hybridizes to the bcl  
 CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of  
 CC cancer cells in vitro, which comprises contacting the cancer cells with a  
 CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;  
 CC (2) treating or preventing cancer in a human, which comprises  
 CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE  
 CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid  
 CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a  
 CC carrier. The pharmaceutical composition of the invention is useful for  
 CC preventing or treating cell-proliferative disorders e.g., cancer,  
 CC hyperplasia or tumorigenesis and also bacterial infection, viral  
 CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,  
 CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and  
 CC hepatitis B virus infection. The hybrid oligomers can also be used for  
 CC screening candidate transcription factors or other molecules e.g., gene  
 CC regulatory proteins or for diagnostic assays. The present sequence is a  
 CC Bcl-2/CRE hybrid antisense oligonucleotide  
 XX SQ Sequence 34 BP; 6 A; 12 C; 8 G; 8 T; 0 U; 0 Other;  
 Query Match 60.0%; Score 14.4; DB 6; Length 34;

Best Local Similarity 93.8%; Pred. No. 1e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCACGTCGCCCATGG 21  
 DB 13 CCACGTCGCCCATGG 28  
 |||||  
 |||||

RESULT 37  
 ABK90296  
 ID ABK90296 standard; DNA; 34 BP.  
 XX AC ABK90296;  
 XX DT 21-OCT-2002 (first entry)  
 XX DE Bcl-2-targeting antisense oligonucleotide BK1-PS.  
 XX KW Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;  
 KW CAMP response element; bacterial infection; viral infection;  
 KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;  
 KW autoimmune disorder; parasitic infection; virucide; hyperplasia;  
 KW tumorigenesis; hepatitis B infection; human.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT modified\_base 1..34  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 XX PN WO200257480-A2.  
 XX PD 25-JUL-2002.  
 XX PF 22-JAN-2002; 2002WO-US001967.  
 XX PR 22-JAN-2001; 2001US-0263244P.  
 XX PA (GENT-) GENTA INC.  
 XX PI Klem RE;  
 XX DR WPI; 2002-590754/63.  
 XX PT Hybrid oligomer comprises a cyclic AMP response element sequence and a  
 PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for  
 PT preventing or treating cell-proliferative disorders e.g., cancer.  
 XX PS Example 1; Page 58; 78pp; English.  
 XX CC The invention relates to a hybrid oligomer comprising a cyclic AMP  
 CC response element (CRE) sequence and a sequence that hybridizes to the bcl  
 CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of  
 CC cancer cells in vitro, which comprises contacting the cancer cells with a  
 CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;  
 CC (2) treating or preventing cancer in a human, which comprises  
 CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE  
 CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid  
 CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a  
 CC carrier. The pharmaceutical composition of the invention is useful for  
 CC preventing or treating cell-proliferative disorders e.g., cancer,  
 CC hyperplasia or tumorigenesis and also bacterial infection, viral  
 CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,  
 CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and  
 CC hepatitis B virus infection. The hybrid oligomers can also be used for  
 CC screening candidate transcription factors or other molecules e.g., gene  
 CC regulatory proteins or for diagnostic assays. The present sequence is a  
 CC Bcl-2 antisense oligonucleotide

SQ Sequence 34 BP; 6 A; 12 C; 8 G; 8 T; 0 U; 0 Other;  
Query Match 60.0%; Score 14.4; DB 6; Length 34;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 CCAGCGTGGCCCATGG 21  
DB 13 CCAGCGTGGCCCATGG 28  
RESULT 38  
ABK90352  
ID ABK90352 standard; DNA; 34 BP.  
AC ABK90352;  
XX 21-OCT-2002 (first entry)  
DE Bcl-2/CRE hybrid antisense oligonucleotide BK7-DE.  
XX Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;  
KW cAMP response element; bacterial infection; viral infection;  
KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;  
KW autoimmune disorder; parasitic infection; virucide; hyperplasia;  
KW tumorigenesis; hepatitis B infection; human.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200257480-A2.  
XX 25-JUL-2002.  
XX 22-JAN-2002; 2002WO-US001967.  
XX 22-JAN-2001; 2001US-0263244P.  
XX (GENT-) GENTA INC.  
XX Klem RE;  
XX WPI; 2002-590754/63.  
XX Hybrid oligomer comprises a cyclic AMP response element sequence and a  
PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for  
PT preventing or treating cell-proliferative disorders e.g., cancer.  
XX Example 1; Page 58; 78pp; English.  
XX The invention relates to a hybrid oligomer comprising a cyclic AMP  
CC response element (CRE) sequence and a sequence that hybridizes to the bcl  
CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of  
CC cancer cells in vitro, which comprises contacting the cancer cells with a  
CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;  
CC (2) treating or preventing cancer in a human, which comprises  
CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE  
CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid  
CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a  
CC carrier. The pharmaceutical composition of the invention is useful for  
CC preventing or treating cell-proliferative disorders e.g., cancer,  
CC hyperplasia or tumorigenesis and also bacterial infection, viral  
CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,  
CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and  
CC bcl-2 antisense oligomer are also useful for preventing or treating  
CC hepatitis B virus infection. The hybrid oligomers can also be used for  
CC screening candidate transcription factors or other molecules e.g., gene  
CC regulatory proteins or for diagnostic assays. The present sequence is a  
CC Bcl-2/CRE hybrid antisense oligonucleotide  
XX  
SQ Sequence 34 BP; 6 A; 12 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 6; Length 34;

Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 CCAGCGTGGCCCATGG 21  
DB 13 CCAGCGTGGCCCATGG 28  
RESULT 39  
ADF50458/C  
ID ADF50458 standard; DNA; 34 BP.  
XX ADF50458;  
XX 12-FEB-2004 (first entry)  
DE PCR primer used to amplify human GPCR G2A cDNA (SeqID 138).  
XX human; PCR; primer; ss; transformation; endocrine cell line;  
KW expression cloning system; bioactive peptide; GPCR ligand.  
XX Homo sapiens.  
OS WO2003087366-A1.  
PN 23-OCT-2003.  
XX 16-APR-2003; 2003WO-JP004840.  
XX 16-APR-2002; 2002JP-00113030.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;  
PI Nishi T, Obinata M;  
XX WPI; 2003-833737/77.  
XX Endocrine cell lines originated from mammalian hypothalamus and  
PT pancreatic islet, applicable in expression cloning systems of bioactive  
PT peptide precursor genes, and in screening G protein-coupled receptor  
PT ligands.  
XX Example 22; SEQ ID NO 138; 316pp; Japanese.  
XX This invention relates to a novel method for obtaining a DNA that encodes  
CC a peptide acting as agonist, antagonist or inverse agonist on a target  
CC receptor. Specifically, it comprises transformation of endocrine cell  
CC lines originating from mammalian hypothalamus and pancreatic islets,  
CC culturing the transformants and contacting with cells expressing the  
CC target receptor. The identification of those cells with a response  
CC reaction can be used for selecting a transformant cell line with the  
CC appropriate target activity that is expressing the novel transformed DNA.  
CC Accordingly, the present invention describes novel cell lines that are  
CC applicable in expression cloning systems of bioactive peptide precursor  
CC genes, and in screening GPCR ligands for use as drugs including agonists,  
CC antagonists and inverse agonists i.e. activators and inhibitors. Such  
CC cell lines can provide a highly sensitive and convenient GPCR ligand  
CC assay system. This oligonucleotide sequence is a PCR primer used to  
CC amplify human GPCR cDNA of the invention.  
XX Sequence 34 BP; 8 A; 14 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 10; Length 34;  
Best Local Similarity 75.0%; Pred. No. 1e+04;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 GGGGTCCAGCGTGGCCCATGGGG 24  
DB 27 GGGGTCTCTGGCGGCCCAATGTGG 4

RESULT 40

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ADK171713/c
ID ADK171713 standard; DNA; 41 BP.
AC ADK171713;
XX
XX 06-MAY-2004 (first entry)
XX
XX Cytochrome P450 gene polymorphism detecting oligo, SEQ ID No 27.
XX
XX detection; gene polymorphism; cytochrome P450; drug evaluation; safety;
XX drug screening; single nucleotide polymorphism; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX variation replace(21,T)
XX /*tag= a
XX /standard_name="single nucleotide polymorphism"
XX
XX WO2003102181-A1.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-JP006750.
XX
XX 30-MAY-2002; 2002JP-00158237.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX
XX WPI; 2004-043114/04.
XX
XX Detecting gene polymorphism particularly of cytochrome P450- encoded gene
XX with specific oligonucleotides, applicable obtaining gene information,
XX evaluation of drugs and screening drug candidates.
XX
XX Claim 1; SEQ ID NO 27; 144pp; Japanese.
XX
XX The invention relates to a novel method for detecting gene polymorphisms
XX of a gene that encodes cytochrome P450. The method involves using an
XX oligonucleotide and/or a primer selected from those having sequences with
XX at least 13 bases, including the base at position-21 in the base
XX sequences represented by the oligos of 40-41 base pairs, or their
XX complementary sequences, provided in the specification. The method is
XX applicable in obtaining gene information, evaluation of drugs including
XX safety and therapeutic efficacy, and screening drug candidates. This
XX polynucleotide sequence represents one of the 40-41 base pair long oligos
XX used in the gene polymorphism detection method of the invention.
XX
XX Sequence 41 BP; 12 A; 13 C; 11 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 14.4; DB 12; Length 41;
XX Best Local Similarity 93.8%; Pred. No. 1e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GGGGTCCAGCGTGGCG 16
XX ||| |||||
XX Db 35 GGGATCCAGCGTGGCG 20
XX
XX RESULT 41
XX AAL33952/c
XX ID AAL33952 standard; DNA; 50 BP.
XX
XX AC AAL33952;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #7160.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuoprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
XX

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KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX Homo sapiens.
XX
XX OS OS
XX WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
XX 28-DEC-1999; 99US-0173419P.
XX
XX 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX
XX WPI; 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX
XX Claim 1; Page 3440; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
XX protein coupled receptors and thioesterases. The present sequence is one
XX such oligonucleotide. The oligonucleotides and the peptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of the proteins listed above.
XX Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms
XX
XX Sequence 50 BP; 8 A; 24 C; 13 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 14.4; DB 4; Length 50;
XX Best Local Similarity 75.0%; Pred. No. 1e+04;
XX Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 GGGGTCCAGCGTGGCGATCGGGG 24
XX ||| |||||
XX Db 33 GGGGGCCAGCGTGGCGATCGGGG 10
XX
XX RESULT 42
XX AAC88236
XX ID AAC88236 standard; DNA; 19 BP.
XX
XX AC AAC88236;
XX
XX 02-MAR-2001 (first entry)
XX
XX Murine lineage-restricted precursor cell population PCR primer #14.
XX
XX Mouse; lineage restricted precursor cell; neuron-restricted precursor;
XX NRP; glial-restricted precursor; GRP; mouse neural tube; transplantation;
XX antibody; PCR primer; ss.
XX
XX Mus sp.

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XX WO200068359-A1.
PN
XX
XX 16-NOV-2000.
PD
XX
XX 05-MAY-2000; 2000WO-US012446.
PF
XX
XX 07-MAY-1999; 99US-0133159P.
XX
XX (UTAH ) UNIV UTAH RES FOUND.
PA
XX
XX Mujtaba T, Rao MS;
PI
XX
XX WPI; 2001-024863/03.
DR
XX
XX New pure populations of neuron- or glial-restricted precursor cells and
PT neuroepithelial stem cells from mouse neural tubes or embryonic stem
PT cells for developing new drugs or techniques that enhance survival of
PT transplanted cell.
XX
XX Example 8; Page 22; 37pp; English.
PS
XX
XX The present invention provides populations of lineage-restricted
XX precursor cells from mouse neural tube and mouse embryonic stem cells.
CC These populations are of neuron-restricted precursor cells (NRPs) and
CC glial-restricted precursor cells (GRPs). These cell populations are
CC useful in the development of new transplant techniques, for
CC transplantation in diseases where neuronal or glial degeneration has
CC occurred, in the identification of drugs which enhance the survival and
CC proliferation of transplanted cells, to identify genes specific to
CC selected stages of development, and in the generation of cell-specific
CC antibodies
XX
XX Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 59.2%; Score 14.2; DB 4; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GGTCCAGCGTGGCCATGG 21
DB 1 GGTCCAGCAATTGGCATGG 19
RESULT 43
ACI94928
ID ACI94928 standard; DNA; 25 BP.
XX
XX ACI94928;
AC
XX
XX 14-OCT-2003 (first entry)
DT
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 94919.
DE
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
OS
XX
XX US2003104410-A1.
PN
XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
PA
XX
XX Mittmann MP;
PI
XX
XX WPI; 2003-567953/53.
DR
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 94919; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridisation to a DNA library,
XX in analysis of genetic variation or in hybridisation of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridising at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridisation. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying biallelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in in situ hybridisation, in Southern, Northern or dot-
XX blot hybridisation to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX primer extensions or in screening cDNA or genomic libraries or subclones
XX for additional subclones containing segments of DNA that have been
XX isolated and previously sequenced. The sequence presented is one of the
XX nucleic acid probes incorporated in the microarray. Note: The sequence
XX data for this patent can also be obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html
SQ
Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 GTCCAGCGTGGCCATGG 22
DB 6 GTCCACTGTGCTCCATGG 24
RESULT 44
ACI94310
ID ACI94310 standard; DNA; 25 BP.
XX
XX ACI94310;
AC
XX
XX 14-OCT-2003 (first entry)
DT
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 94301.
DE
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
OS
XX
XX US2003104410-A1.
PN
XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
PA
XX
XX Mittmann MP;
PI
XX
XX WPI; 2003-567953/53.
DR
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in

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PT Southern, Northern or dot-blot hybridization to identify or detect the  
 XX sequence or specific mutations of any gene.  
 XX  
 PS Claim 1; SEQ ID NO 94301; 9pp; English.  
 XX  
 CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library.  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying biallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
 XX  
 XX Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 59.2%; Score 14.2; DB 9; Length 25;  
 Best Local Similarity 84.2%; Pred. No. 1.2e+04;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 4 GTCCAGCTGCGCCATGGG 22  
 Db 6 GTCCACTGTGCTCCATGGG 24  
 RESULT 45  
 ADK43158  
 ID ADK43158 standard; DNA; 31 BP.  
 XX  
 AC ADK43158;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human N-acetylglucosamine transferase NGalNAC-T1 PCR primer #3.  
 XX  
 KW oligosaccharide; N-acetylglucosamine; N-acetylglucosamine;  
 KW beta1-4 linkage; human; N-acetylglucosamine transferase; NGalNAC-T1; ss;  
 KW PCR; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004016790-A1.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 13-AUG-2003; 2003WO-JP010309.  
 XX  
 PR 14-AUG-2002; 2002JP-00236292.  
 XX  
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 FA (AMSH) AMERSHAM BIOSCIENCES KK.  
 XX  
 PI Narimatsu H, Gotoh M, Sato T;  
 XX  
 DR WPI; 2004-203801/19.  
 XX  
 XX New isolated protein having specified amino acid sequence for enzyme used  
 PT in producing oligosaccharides.  
 PT

XX Example 1; SEQ ID NO 16; 79pp; English.  
 PS  
 XX  
 CC The invention relates to an isolated N-acetylglucosamine transferase  
 CC protein. The protein is useful for enzyme used in producing  
 CC oligosaccharides. The inventive isolated protein has the activity of  
 CC transferring N-acetylglucosamine to N-acetylglucosamine via beta1-4  
 CC linkage. The present sequence represents human N-acetylglucosamine  
 CC transferase, NGalNAC-T1, PCR primer.  
 XX  
 SQ Sequence 31 BP; 4 A; 12 C; 10 G; 5 T; 0 U; 0 Other;  
 Query Match 59.2%; Score 14.2; DB 12; Length 31;  
 Best Local Similarity 84.2%; Pred. No. 1.2e+04;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 GGGGTCCAGCTGCGCCAT 19  
 Db 13 GGGGTCCAGCTGCGCCAT 31  
 RESULT 46  
 AAV05322/c  
 ID AAV05322 standard; DNA; 33 BP.  
 XX  
 AC AAV05322;  
 XX  
 DT 22-MAY-1998 (first entry)  
 XX  
 DE PCR primer 1 used in RT-PCR to amplify bcl-2 cDNA.  
 XX  
 KW bcl-2 gene; anti-apoptotic gene; prevention; cell death; treatment;  
 KW neurodegenerative disease; disease; Huntington's; Parkinson's;  
 KW Alzheimer's; retroviral vector; LNCX; LNCX; live packaging cell;  
 KW biocompatible capsule; release; viral vector; implant; gene therapy;  
 KW tumour; PCR primer; amplify; ss.  
 OS Synthetic.  
 OS Mammalia.  
 XX  
 FH Key Location/Qualifiers  
 FT RBS 10..16  
 FT /\*tag= a  
 FT /note= "Kozak sequence which enhances translation  
 FT efficiency of bcl-2"  
 XX  
 XX WO9744065-A2.  
 PN  
 XX  
 PD 27-NOV-1997.  
 XX  
 PF 20-MAY-1997; 97WO-US008463.  
 XX  
 PR 20-MAY-1996; 96US-00650726.  
 XX  
 XX (CYTO-) CYTOTHERAPEUTICS INC.  
 XX  
 XX Hamang JP, Aebischer P;  
 PI  
 XX WPI; 1998-018231/02.  
 DR  
 XX Capsule containing packaging cells that produce viral vectors for gene  
 PT therapy - used as replaceable implants in treatment of cancer,  
 PT atherosclerosis etc., providing localised, long-term vector delivery.  
 XX  
 XX Example 5; Page 33; 45pp; English.  
 PS  
 XX  
 CC PCR primers AAV05322-23 are used in a reverse transcription polymerase  
 CC PCR reaction (RT-PCR) to amplify bcl-2 cDNA from human, rat, or mouse  
 CC thymus total RNA. Bcl-2 genes are anti-apoptotic genes whose products  
 CC prevent unwanted death of certain cell populations, and are useful for  
 CC treating neurodegenerative diseases such as Huntington's, Parkinson's or  
 CC Alzheimer's disease. The PCR product was ligated into retroviral vectors  
 CC LNCX and LNCX, to produce retroviral vectors LNCX-bcl-2 and LNCX-bcl-2.



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XX AAV19660;
AC
XX 25-MAR-2003 (revised)
DT 12-JUN-1998 (first entry)
XX
XX Human bcl-2 antisense oligonucleotide 6.
DE
XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW cancer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US5734033-A.
PN
XX 31-MAR-1998.
PD
XX
XX 24-MAR-1994; 94US-00217082.
PF
XX
XX 22-DEC-1988; 88US-00288692.
PR
XX 21-FEB-1992; 92US-00840716.
PX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Reed J;
PI
XX
XX WPI; 1998-229881/20.
DR
XX
XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful for
PT treating cancers, e.g. lymphoma(s) and some leukaemia(s).
PT
XX
XX Claim 6; Col 14; 21pp; English.
PS
XX
XX This antisense oligonucleotide is complementary to the translation
CC initiation site of the human bcl-2 mRNA. The bcl-2 antisense
CC oligonucleotides are phosphorothioate derivatives and can straddle
CC strategic sites such as the translation initiation site, donor and
CC acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias. (Updated on 25-MAR-2003 to
CC correct PF field.)
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SQ
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XX Best Local Similarity 100.0%; Pred. No. 1.5e+04;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX ID AAV19659 standard; DNA; 17 BP.
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XX AAV19659;
AC
XX
XX 25-MAR-2003 (revised)
DT 12-JUN-1998 (first entry)
XX
XX Human bcl-2 antisense oligonucleotide 5.
DE
XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW cancer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX
XX

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PN US5734033-A.
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XX 31-MAR-1998.
PD
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XX 24-MAR-1994; 94US-00217082.
PF
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XX 22-DEC-1988; 88US-00288692.
PR
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PX
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XX
XX Reed J;
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XX
XX WPI; 1998-229881/20.
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XX
XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful for
PT treating cancers, e.g. lymphoma(s) and some leukaemia(s).
PT
XX
XX Claim 6; Col 14; 21pp; English.
PS
XX
XX This antisense oligonucleotide is complementary to the translation
CC initiation site of the human bcl-2 mRNA. The bcl-2 antisense
CC oligonucleotides are phosphorothioate derivatives and can straddle
CC strategic sites such as the translation initiation site, donor and
CC acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
SQ
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XX Query Match 58.3%; Score 14; DB 2; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+04;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Db 4 CCAGCGTGGCCAT 17
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XX Search completed: February 15, 2006, 18:07:05
XX Job time : 189.893 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:07:43 ; Search time 1596.3 Seconds  
(without alignments)  
703.434 Million cell updates/sec

Title: US-09-669-187A-81

Perfect score: 24  
Sequence: 1 ggggtccagcgtgcgcattggggg 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 100%  
Listing first 300 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_hc:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_est7:\*
- 9: gb\_ges1:\*
- 10: gb\_ges2:\*
- 11: gb\_ges3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 8        | 13.6  | 56.7        | 50     | 1  | AU102746    |
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| C 33 | 12.6 | 52.5 | 28 | 9  | AZ829200 |
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227 11.2 46.7 23 9 A2461315 A2461315 1M0267F09  
228 11.2 46.7 25 1 A1682835 A1682835 wc66h10.x  
229 11.2 46.7 26 6 CD746276 CD746276 S6\_E09\_S6  
230 11.2 46.7 30 10 BX662165 BX662165 Arabidops  
231 11.2 46.7 31 1 AI459772 AI459772 ao93c06.x  
232 11.2 46.7 32 2 BF529719 BF529719 602043970  
233 11.2 46.7 32 2 BG819845 BG819845 602781913  
234 11.2 46.7 33 1 AV834163 AV834163 Arabidops  
235 11.2 46.7 34 9 A2492829 A2492829 1M0327J11  
236 11.2 46.7 35 9 A2767704 A2767704 1M0327J11  
237 11.2 46.7 35 10 CZ551699 CZ551699 CB1 4902  
238 11.2 46.7 37 1 A1683527 A1683527 tx67e09.x  
239 11.2 46.7 38 9 A2513025 A2513025 1M0358P20  
240 11.2 46.7 38 9 A1002051 A1002051 ov19h03.s  
241 11.2 46.7 40 9 BH629306 BH629306 1007070B0

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242 11 45.8 43 9 A2473927
243 11 45.8 44 8 H92936
244 11 45.8 44 10 CL520163
245 11 45.8 45 7 CN757501
246 11 45.8 45 7 CN757501
247 11 45.8 45 9 A0025518
248 11 45.8 46 1 A2802142
249 11 45.8 46 1 AA630952
250 11 45.8 46 1 AA828900
251 11 45.8 47 1 AJ728273
252 11 45.8 47 3 BM046104
253 11 45.8 47 3 BM047185
254 11 45.8 47 6 CD530897
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257 11 45.8 47 10 CL213837
258 11 45.8 49 5 C20871
259 11 45.8 49 9 A2812913
260 11 45.8 50 1 AU103440
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263 11 45.8 50 1 AU106643
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265 11 45.8 50 1 AU107016
266 10.8 45.0 19 9 A232931
267 10.8 45.0 25 1 AA909237
268 10.8 45.0 25 10 CZ474839
269 10.8 45.0 28 1 A1287864
270 10.8 45.0 28 1 A1357706
271 10.8 45.0 29 10 CG718745
272 10.8 45.0 31 1 AA868659
273 10.8 45.0 31 1 A1262512
274 10.8 45.0 33 10 AB082692
275 10.8 45.0 33 11 TA82C04P
276 10.8 45.0 35 9 A2784718
277 10.8 45.0 35 10 AL938116
278 10.8 45.0 36 7 CV064406
279 10.8 45.0 36 8 DN652373
280 10.8 45.0 38 1 AU256510
281 10.8 45.0 38 2 BG292849
282 10.8 45.0 38 10 AJ599761
283 10.8 45.0 38 10 AL760976
284 10.8 45.0 38 10 AL940456
285 10.8 45.0 40 1 AA878864
286 10.8 45.0 40 2 BE296536
287 10.8 45.0 41 1 AA680963
288 10.8 45.0 41 1 AA509356
289 10.8 45.0 41 9 BH639962
290 10.8 45.0 42 9 BH626517
291 10.8 45.0 43 1 A1423979
292 10.8 45.0 43 2 BG866682
293 10.8 45.0 44 5 BX520428
294 10.8 45.0 44 8 N47451
295 10.8 45.0 44 10 CZ194596
296 10.8 45.0 44 11 TA131E01P
297 10.8 45.0 45 9 BH810609
298 10.8 45.0 46 1 AA847140
299 10.8 45.0 46 1 AA867748
300 10.8 45.0 46 1 A1793579
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## ALIGNMENTS

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RESULT 1
AUI07435 AUI07435 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone linear EST 28-JAN-2004
LOCUS AUI07435 50 bp mRNA
DEFINITION AUI07435 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AUI07435.1 GI:13556956
VERSION AUI07435.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
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Best Local Similarity 78.3%; Pred. No. 7.3e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 GGGTCGACGCGCGCCATGGGG 24
||| ||||| ||| ||||| ||
Db 5 GGGCCACGCGCTCGCATGGCGG 27
||| ||||| ||| ||||| ||

RESULT 2
AUI07436 AUI07436 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone linear EST 28-JAN-2004
LOCUS AUI07436 50 bp mRNA
DEFINITION AUI07436 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AUI07436
VERSION AUI07436.1 GI:13556957
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="ADSE00456"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      62.5%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 7.3e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGGTCACGCGTCGCCATGGGG 24
    ||| ||||| || ||||| ||
Db 5 GGGCCACGCGTCGCCATGGCG 27

RESULT 3
AJ796516
LOCUS      AJ796516 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
DEFINITION 018_3_11_d04, mRNA sequence.
ACCESSION  AJ796516
VERSION     AJ796516.1 GI:51111844
KEYWORDS   Antirrhinum majus (snapdragon)
SOURCE     Antirrhinum majus
ORGANISM   Antirrhinum majus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiales; Plantaginales; Antirrhineae;
            Antirrhinum.
REFERENCE  1 (bases 1 to 49)
            Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H.,
            Saedler, H. and Zachgo, S.
            Characterization of Antirrhinum Petal Development and
            Identification of Target Genes of the Class B MADS Box Gene
            DEFICIENS
JOURNAL   Plant Cell 16 (12), 3197-3215 (2004)
PUBMED   15539471
COMMENT   Contact: Schwarz-Sommer Z
            Molekulare Pflanzen-genetik
            MPI fuer Zuechtungs-forschung
            Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES             source
            1..49
            /organism="Antirrhinum majus"
            /mol_type="mRNA"
            /db_xref="taxon:4151"
            /clone="018_3_11_d04"
            /tissue_type="whole plant"
            /clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match      61.7%; Score 14.8; DB 1; Length 49;
Best Local Similarity 88.9%; Pred. No. 8.9e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TCCAGCGTCGCCATGGG 22
    ||| ||||| ||||| ||
Db 26 TCCAGCGTCGCCAAGG 43

RESULT 4
AA878878/c
LOCUS      AA878878/c
DEFINITION of88h03.s1 NCI CGAP L15 Homo sapiens cDNA clone IMAGE.1437461.3,
            similar to WP:FS9E12.9 Cell1534 ; contains PTR5.t3 MSRI repetitive
            element ;, mRNA sequence.
ACCESSION  AA878878
VERSION    AA878878.1 GI:2987843
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

/db_xref="taxon:9606"
/clone="ADSE00456"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      60.0%; Score 14.4; DB 1; Length 46;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTCGCCATGGGG 24
    ||| ||| || ||||| |||||
Db 45 GGGGCCCTCCATCGCCAGGGGG 22

RESULT 5
CF661152/c
LOCUS      CF661152
DEFINITION CcLM09a34a07f1 Carp muscle library 1 Cyprinus carpio cDNA clone
            34a07_5', mRNA sequence.
ACCESSION  CF661152
VERSION     CF661152.2 GI:50743359
KEYWORDS   EST.
SOURCE     Cyprinus carpio (common carp)
ORGANISM   Cyprinus carpio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE  1 (bases 1 to 47)
            Gracey, A.Y., Fraser, E.J., Li, W., Fang, Y., Taylor, R.R., Rogers, J.,
            Brass, A. and Cossins, A.R.
            Coping with cold: An integrative, multitissue analysis of the
            transcriptome of a poikilothermic vertebrate
            Proc. Natl. Acad. Sci. U.S.A. 101 (48), 16970-16975 (2004)
JOURNAL   15550548
PUBMED
COMMENT   On Oct 7, 2003 this sequence version replaced gi:37558281.
            Contact: Andrew R. Cossins
            Laboratory for Environmental Gene Regulation
            University of Liverpool
            School of Biological Sciences, The Biosciences Building, Crown
            Street, Liverpool, United Kingdom, L69 7ZB
            Tel: +44(0)151-795-4510
            Fax: +44(0)151-795-4431
            Email: cossins@liv.ac.uk
            Vector has been trimmed from this EST.
            Plate: 34 row: a column: 07
            Seq primer: TripleX 5' LD (5'-CTCGGAGCGCCGCGCATGTGTGGT-3')
            High quality sequence stop: 47
            POLYA=No.
FEATURES             Location/Qualifiers
            1..47
            /organism="Cyprinus carpio"
            /mol_type="mRNA"

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REFERENCE 1 (bases 1 to 46)
AUTHORS  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL  Tumor Gene Index
COMMENT  Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaps-x@mail.nih.gov
            unknown library type
            Trace considered overall poor quality
            Insert Length: 315 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
            Location/Qualifiers
            1..46
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1437461"
            /tissue_type="hepatic adenoma"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP L15"
            /note="Organ: Liver; Vector: pCMV-SPORT4; Site 1: SalI;
            Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 0.8 kb."

ORIGIN
Query Match      60.0%; Score 14.4; DB 1; Length 46;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTCGCCATGGGG 24
    ||| ||| || ||||| |||||
Db 45 GGGGCCCTCCATCGCCAGGGGG 22

RESULT 5
CF661152/c
LOCUS      CF661152
DEFINITION CcLM09a34a07f1 Carp muscle library 1 Cyprinus carpio cDNA clone
            34a07_5', mRNA sequence.
ACCESSION  CF661152
VERSION     CF661152.2 GI:50743359
KEYWORDS   EST.
SOURCE     Cyprinus carpio (common carp)
ORGANISM   Cyprinus carpio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE  1 (bases 1 to 47)
            Gracey, A.Y., Fraser, E.J., Li, W., Fang, Y., Taylor, R.R., Rogers, J.,
            Brass, A. and Cossins, A.R.
            Coping with cold: An integrative, multitissue analysis of the
            transcriptome of a poikilothermic vertebrate
            Proc. Natl. Acad. Sci. U.S.A. 101 (48), 16970-16975 (2004)
JOURNAL   15550548
PUBMED
COMMENT   On Oct 7, 2003 this sequence version replaced gi:37558281.
            Contact: Andrew R. Cossins
            Laboratory for Environmental Gene Regulation
            University of Liverpool
            School of Biological Sciences, The Biosciences Building, Crown
            Street, Liverpool, United Kingdom, L69 7ZB
            Tel: +44(0)151-795-4510
            Fax: +44(0)151-795-4431
            Email: cossins@liv.ac.uk
            Vector has been trimmed from this EST.
            Plate: 34 row: a column: 07
            Seq primer: TripleX 5' LD (5'-CTCGGAGCGCCGCGCATGTGTGGT-3')
            High quality sequence stop: 47
            POLYA=No.
FEATURES             Location/Qualifiers
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            /organism="Cyprinus carpio"
            /mol_type="mRNA"

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/db_xref="taxon:7962"
/clone="34a07"
/sex="Male & female"
/tissue type="Muscle"
/dev stage="Adult"
/lab host="E.coli Electromax DH10B"
/clone_lib="Carp muscle library 1"
/notes="Vector: pTriplex2; Site 1: sf11 GCCATTAGCGCC;
Site 2: sf11 GCCCGCTCGGCC; Serially subcloned cDNA
library prepared from muscle of warm, cold and hypoxia
challenged animals"

ORIGIN
Query Match          59.2%; Score 14.2; DB 6; Length 47;
Best Local Similarity 84.2%; Pred. No. 1.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  4  GTCCAGCTGCGCCATGGG 22
Db   47 GTCCAGAGAGTGCATGGG 29

RESULT 6
AA993146/c
LOCUS
DEFINITION
ot77a10.81 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone
IMAGE:1622778 3' similar to SW:FBRL_HUMAN P22087 FIBRILLARIN ;
mRNA sequence.
ACCESSION
AA993146
VERSION
AA993146.1 GI:3179691
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 49)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: ccgaps-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1622778"
/dev stage="8-9 weeks"
/lab host="DH10B"
/clone_lib="Soares total fetus Nb2HF8 9w"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAATGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match          59.2%; Score 14.2; DB 1; Length 49;
Best Local Similarity 84.2%; Pred. No. 1.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  4  GTCCAGCTGCGCCATGGG 22
Db   47 GTCCAGAGAGTGCATGGG 29

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Qy  6  CCAGCGTGGCCATGGGG 24
Db   33 CCTTCTGCGCCATGGGG 15

RESULT 7
AI098584/c
LOCUS
DEFINITION
ue29h07.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1481821 3' similar to SW:A2HS MOUSE P29699
ALPHA-2-HS-GLYCOPROTEIN PRECURSOR ; mRNA sequence.
ACCESSION
AI098584
VERSION
AI098584.1 GI:3448109
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 49)
REFERENCE
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
JOURNAL
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
MGI:930177
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
1. 49
/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:1481821"
/sex="female"
/dev stage="adult"
/lab host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/notes="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAGCTCGG and 3' end
primer CGACCTGCAGCTCGACACA."

ORIGIN
Query Match          56.7%; Score 13.6; DB 1; Length 49;
Best Local Similarity 80.0%; Pred. No. 2.9e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  3  GGTCACGCTGCGCCATGGG 22
Db   33 CCTTCTGCGCCATGGGG 15

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2219127"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_OV23"
/notes="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"

ORIGIN
Query Match          55.8%; Score 13.4; DB 1; Length 40;
Best Local Similarity 73.9%; Pred. No. 3.5e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 GGGTCCAGCGTGGCCATGGGG 24
      ||||| ||| ||| |||||
Db   35 GGGTCCCGCGGCGCGCGGGGG 13

RESULT 11
AA863355
LOCUS
DEFINITION
oh04e09.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1456840 3'
similar to SW:FRP_HUMAN P02814 PROLINE-RICH PEPTIDE P-B.; mRNA
sequence.
AA863355
VERSION
AA863355.1 GI:2955834
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 606 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1456840"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid3"
/notes="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. mRNA
source: 2 pooled kidneys. Library went through one round

of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldo. "

ORIGIN
Query Match          55.8%; Score 13.4; DB 1; Length 43;
Best Local Similarity 73.9%; Pred. No. 3.5e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 GGGGTCCAGCGTGGCCATGGGG 23
      ||||| ||||| ||| |||||
Db   17 GGGGGCCAGCGGTCCCGAGGGGG 39

RESULT 12
AA2434579
LOCUS
DEFINITION
1M0221110F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0221110 F, genomic survey sequence.
AA2434579
ACCESSION
AA2434579.1 GI:10558592
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 33)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0221 row: I column: 10
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 33.
FEATURES
Location/Qualifiers
1..33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0221110"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

```

adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
Query Match 54.2%; Score 13; DB 9; Length 33;  
Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 GGGGTCCAGCGTGGCCATGG 21  
Db 7 GGGGTCAAGCGTGGGTGGTG 27

RESULT 13  
BI548958  
LOCUS  
DEFINITION  
603189912F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5260442 5',  
mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 38)  
NTH-MGC http://mgc.nci.nih.gov/.  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM11656 Row: g Column: 03  
High quality sequence stop: 38.

FEATURES  
Location/Qualifiers  
1..38  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5260442"  
/tissue\_type="hippocampus"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_95"  
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 54.2%; Score 13; DB 3; Length 38;  
Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 4 GTCCAGCGTGGCCATGGGG 24  
Db 11 GTCAGCGGGGGCCAGGGGG 31

RESULT 14  
AU104320  
LOCUS  
DEFINITION  
AU104320 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HEP06849, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AU104320.1 GI:13553841  
EST.  
Homo sapiens (human)  
Homo sapiens

REFERENCE  
AUTHORS  
1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL  
PUBMED  
COMMENT  
11375929  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
Sugano, S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).

FEATURES  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HEP06849"  
/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN  
Query Match 54.2%; Score 13; DB 1; Length 50;  
Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCATGG 21  
Db 10 GGTGTCATCGTGGGCATGG 30

RESULT 15  
AU105443  
LOCUS  
DEFINITION  
AU105443 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
KAT00863, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AU105443.1 GI:13554964  
EST.  
Homo sapiens (human)  
Homo sapiens

REFERENCE  
AUTHORS  
1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL  
PUBMED  
COMMENT  
11375929  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

FEATURES  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="KAT00863"  
/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN  
Query Match 54.2%; Score 13; DB 1; Length 50;  
Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCATGG 21  
Db 10 GGTGTCATCGTGGGCATGG 30

RESULT 15  
AU105443  
LOCUS  
DEFINITION  
AU105443 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
KAT00863, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AU105443.1 GI:13554964  
EST.  
Homo sapiens (human)  
Homo sapiens

REFERENCE  
AUTHORS  
1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL  
PUBMED  
COMMENT  
11375929  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

FEATURES  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="KAT00863"  
/clone\_lib="Sugano Homo sapiens cDNA library"



Email: yszuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
 source Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="KAT00863"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;  
 Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GTCCAGCGTGGCCCATGGGG 24  
 ||||| ||||| ||||| |||||  
 Db 26 GCCCAGCGCCGCCCATGGGTG 46

## RESULT 16

AU107884  
 LOCUS AU107884 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 DEFINITION CAS03672, mRNA sequence.  
 ACCESSION AU107884  
 VERSION AU107884.1 GI:13557406  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 50)  
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 PUBMED 11375929  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yszuki@ims.u-tokyo.ac.jp  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

## REFERENCE

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 PUBMED 11375929  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yszuki@ims.u-tokyo.ac.jp  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

FEATURES  
 source Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CAS03672"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;  
 Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCCATGG 21  
 ||||| ||||| ||||| |||||  
 Db 18 GCGAGCGCGCGCCCATGG 38

## RESULT 17

AU107885  
 LOCUS AU107885 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 DEFINITION HSI05714, mRNA sequence.  
 ACCESSION AU107885  
 VERSION AU107885.1 GI:13557407  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 50)  
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 PUBMED 11375929  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yszuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

## FEATURES

## source

1. 50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HS105735"  
/clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;  
Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCATGG 21

Db 20 GGGAGCGCGGAGGCCATGG 40

## RESULT 19

R85071/c

## LOCUS

DEFINITION Y042d10.r1 Soares adult brain N2b4HB55V Homo sapiens cDNA clone IMAGE:180595 5', similar to gb:J05096\_rna1 SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN (HUMAN);, mRNA sequence.

## ACCESSION

R85071

## VERSION

R85071.1 GI:943477

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 50)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, K., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 2244

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 2244 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

1. 50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3827242"

/db\_xref="taxon:9606"

/clone="IMAGE:180595"

/sex="Male"

/dev\_stage="55-year old"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares adult brain N2b4HB55V"

/note="Organ: brain; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTCAATCTCAAGTGGAGCGCGCGCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

## ORIGIN

Query Match 54.2%; Score 13; DB 8; Length 50;  
Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGGCCATGGGG 23

Db 34 GGTCCAGCGTGGCGTCGGGG 14

## RESULT 20

BF384787

## LOCUS

DEFINITION 602046279F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:4195795 5', mRNA sequence.

## ACCESSION

BF384787

## VERSION

BF384787.1 GI:11366092

## KEYWORDS

EST.

## SOURCE

Mus musculus

## ORGANISM

Mus musculus (house mouse)

## REFERENCE

1 (bases 1 to 34)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: csapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LIAM9531 row: n column: 20

High quality sequence stop: 34.

Location/Qualifiers

1. 34

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="FVB/N"

/db\_xref="taxon:10090"

/clones="IMAGE:4195795"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI CGAP Li9"

/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.9 kb. Constructed by Life

Technologies. Note: this is a NCI CGAP Library."

## ORIGIN

Query Match 53.3%; Score 12.8; DB 2; Length 34;  
Best Local Similarity 70.8%; Pred. No. 6.2e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

QY 1 GGGGTCACGCGGCCCATGGGG 24
    ||||| ||||| ||||| |||||
Db 8 GGGGCCAGCTGGGGCCACTCGG 31

RESULT 21
AI755616
LOCUS EtsEtes38h12.y1 Eimeria S5-2 Sporozoite stage Eimeria tenella cDNA
DEFINITION 5' similar to TR:Q28583 Q28583 KAP5.4 KERATIN PROTEIN. ; mRNA
sequence.
ACCESSION AI755616
VERSION AI755616.1 GI:5149339
KEYWORDS Eimeria tenella
SOURCE Eimeria tenella
ORGANISM Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
Eimeria.
REFERENCE 1 (bases 1 to 37)
AUTHORS Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,
Mallin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B.,
Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D.,
Harvey,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T.,
Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and
Sibley,D.
TITLE WashU-Merck Eimeria tenella project
JOURNAL Unpublished (1999)
COMMENT Contact: David Sibley, Ph.D.
WashU-Merck Eimeria tenella project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Contact David Sibley (toxest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
FEATURES
    source
    1..37
    /organism="Eimeria tenella"
    /mol_type="mRNA"
    /strain="LS18"
    /db_xref="taxon:5802"
    /dev_stage="Sporozoite"
    /lab_host="SOLR E. coli"
    /clone_lib="Eimeria S5-2 Sporozoite stage"
    /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Sporozoites were obtained from in vitro sporulated
and excysted oocysts of E. tenella grown in chickens.
cDNA was synthesized from poly mRNA using an oligo-dT
primer containing a XhoI site. Following second strand
synthesis, EcoRI adapters were ligated to the cDNA and
products were size-selected on Sephacryl S500. cDNAs were
digested with EcoRI/XhoI and cloned into lambda Zap II
(Stratagene). Clones were converted to phagemids by mass
excision using EXassist helper phage and SOLR cells
(Stratagene). Insert sizes range from 1.2-2.9 kb."

ORIGIN
    Query Match 53.3%; Score 12.8; DB 1; Length 37;
    Best Local Similarity 70.8%; Pred. No. 6.2e+05;
    Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGTCACGCGGCCCATGGGG 24
    ||||| ||||| ||||| |||||
Db 5 GGGGCCAGGGGCCACCGGGGG 28

RESULT 22
BI597957
LOCUS 603249661F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301590 5',
DEFINITION mRNA sequence.
ACCESSION BI597957
VERSION BI597957.1 GI:15490896
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 38)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L2AM11763 row: 1 column: 15
High quality sequence stop: 38.
FEATURES
    source
    1..38
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:5301590"
    /tissue_type="hypothalamus"
    /lab_host="DH10B"
    /clone_lib="NIH_MGC_96"
    /note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gtccag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to 200. This is a
primary library enriched for full-length clones and
constructed using the cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN
    Query Match 53.3%; Score 12.8; DB 3; Length 38;
    Best Local Similarity 70.8%; Pred. No. 6.2e+05;
    Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGTCACGCGGCCCATGGGG 24
    ||||| ||||| ||||| |||||
Db 6 GAGGCCCTGGCGGCCCATGAGG 29

RESULT 23
AJ683869/c
LOCUS AJ683869 CSEORAN04 Sus scrofa cDNA clone C0001803_F11, mRNA
DEFINITION sequence.
ACCESSION AJ683869
VERSION AJ683869.1 GI:49416459
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 39)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and

```



ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 [gll4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 44;  
Best Local Similarity 70.8%; Pred. No. 6.2e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGCATGGGG 24  
db 12 GGGCGGGCGGGGCCATCGGG 35

|                  |        |              |                |   |                          |
|------------------|--------|--------------|----------------|---|--------------------------|
| <b>RESULT 27</b> |        |              |                |   |                          |
| AZS10921         |        |              |                |   |                          |
| LOCUS            |        |              |                |   |                          |
| DEFINITION       |        |              |                |   |                          |
| AZS10921         | linear | DNA          | 48 bp          | GSS 05-OCT-2000                             |                          |
| IM0355P08R       | Mouse  | 10kb plasmid | UUGC1M library | Mus musculus genomic clone UUGC1M0355P08 R. | genomic survey sequence. |

```

VERSION  AZ510921.1  GI:10692237
KEYWORDS GSS.

```

**Mus musculus**  
ORGANISM

REFERENCE  
AUTHORS

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

**COMMENT**      **Contact: Robert B. Weiss**

Survivability of Ocean  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112. USA

**Tel: 801 585 5606**

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Plate: 0355 row: P column: 08

Class: plasmid ends

High quality sequence stop: 48.

## FEATURES

source 1. .48

```
/mol_type="genomic DNA"
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/db\_xref="taxon:10090"

```
/sex="Male"
```

```
/clone_lib="Mouse 10kb plasmid UUGC1M library"
```

musculus C57BL/6J (male) was obtained from the Jackson

(<http://www.jax.org/resources/documents/dnares/>). The DNA

0.005 inch orifice at constant velocity. The sheared DNA

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gi|4732114|gb|AF129072.1|], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 48;  
Best Local Similarity 70.8%; Pred. No. 6.2e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCATGGGG 24  
23 GTGTCTCTGGTGGCCCTCTGGG 46

## RESULT 28

AA903627 49 bp mRNA linear EST 09-JUN-1998  
LOCUS  
DEFINITION OK59902.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1518290 3' similar to SW:ICLN HUMAN P54105 CHLORIDE CONDUCTANCE REGULATORY PROTEIN ICLN ;, mRNA sequence.

ACCESSION AA903627 GI:3038750  
VERSION  
KEYWORDS  
SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)

## JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.  
cDNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 555 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

## FEATURES

source

1..49  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1518290"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_GC4"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 53.3%; Score 12.8; DB 1; Length 49;  
Best Local Similarity 70.8%; Pred. No. 6.2e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCATGGGG 24  
2 GGGCCCTCTCGTGGGCCAGGGG 25

## RESULT 29

AU106561 50 bp mRNA linear EST 28-JAN-2004  
LOCUS  
DEFINITION AU106561 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAT03341, mRNA sequence.

ACCESSION AU106561  
VERSION  
KEYWORDS  
SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

11375929

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: [ysuzuki@ims.u-tokyo.ac.jp](mailto:ysuzuki@ims.u-tokyo.ac.jp)

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.

Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="KAT03341"  
/clone\_lib="Sugano Homo sapiens cDNA library"

## FEATURES

source

1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="KAT03341"  
/clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 53.3%; Score 12.8; DB 1; Length 50;  
Best Local Similarity 87.5%; Pred. No. 6.2e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGGCC 17  
35 GGGTCCGGCTGGCC 50

## RESULT 30

BB616279 50 bp mRNA linear EST 26-OCT-2001  
LOCUS  
DEFINITION BB616279 RIKEN full-length enriched, adult male testis Mus musculus cDNA clone 4931436G19 5', mRNA sequence.

ACCESSION BB616279

VERSION BB616279.1 GI:16456400

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 50)

REFERENCE

AUTHORS

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,

Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, T., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gscc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing Pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome.* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

## FEATURES

```

Location/Qualifiers
1. 50
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4931436G19"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="SOLR"

```

/lab\_n08t="SOLR"  
/clone\_lib="RIKEN full-length enriched, adult male testis"  
/notes="Site 1: XhoI; Site 2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGACGAGAGAAGATCCACAGACTCTTTTTCCTTTTTTNN 3', cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
primer adapter of sequence [5'  
GAGACGAGAGAAGCGGCCGCAATAATTCGAGTTAAATTAATCCCCCCC  
3'. cDNA was cloned into the XhoI and BamHI sites." "

## ORIGIN

Query Match 53.3%; Score 12.8; DB 2; Length 50;  
Best Local Similarity 70.8%; Pred. No. 6.2e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels

|            |   |                          |    |
|------------|---|--------------------------|----|
| QY         | 1   | GGGGTCCAGCGTCGCCCATGGGGG | 24 |
| Db         | 16  | CGCGCCGTCGGGAGCCATGGCGG  | 39 |
| RESULT 31  |   |                          |    |
| AZ982659/c |   |                          |    |
| LOCUS      | AZ982659 Mouse 10kb plasmid UUGC2M library Mus musculus genomic   |                          |    |
| DEFINITION | clone UUGC2M0263J03 R, genomic survey sequence.   |                          |    |
| ACCESSION  | AZ982659  |                          |    |
| VERSION    | AZ982659.1  |                          |    |
| KEYWORDS   | GI:13853886   |                          |    |
| SOURCE     | GSS.  |                          |    |
| ORGANISM   | Mus musculus (house mouse)  |                          |    |
| REFERENCE  | Mus musculus  |                          |    |
| AUTHORS    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.   |                          |    |
| TITLE      | 1 (bases 1 to 50)   |                          |    |
| JOURNAL    | Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.   |                          |    |
| COMMENT    | Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts<br>Unpublished (2000)<br>Contact: Robert B. Weiss<br>University of Utah Genome Center<br>University of Utah<br>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA<br>Tel: 801 585 5606<br>Fax: 801 585 7177<br>Email: rdunn@genetics.utah.edu<br>Insert Length: 10000 Std Error: 0.00<br>Plate: 0263 row: J column: 03<br>Seq primer: CACACAGGAACAGCTATGACC<br>Class: plasmid ends<br>High quality sequence stop: 50.<br>Location/Qualifiers |                          |    |
| FEATURES   |   |                          |    |

FEATURES  
source

```

location/Quadriceps
1.50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0263703"
/sex="Female"
/lab_host="E. coli strain"
/clone_lib="Moose 10kb p"
/note="Vector: PWD42nv;
musculus C57BL/6J (female)
Laboratory Mouse DNA Res."

```

laboratory mouse DNA resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1|, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 50;  
Best Local Similarity 70.8%; Pred. No. 6.2e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels

```

Qy 1 GGGTCCAGCGTGCCTCATGGGG 24
    |||||
Db 32 GGGTCCAGCGTTCGAGAGGGGG 9

RESULT 32
CL521622/c
LOCUS
DEFINITION
  SAL3H08 Planking Sequence Tag of Oryza sativa T-DNA insertion lines
  Oryza sativa (japonica cultivar-group) genomic, genomic survey
  sequence.
ACCESSION
  CL521622
VERSION
  CL521622.1 GI:46148422
KEYWORDS
  GSS.
SOURCE
  Oryza sativa (japonica cultivar-group)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 50)
  Sallaud,C., Gay,C., Larmande,P., Bes,M., Piffanelli,P., Piegou,B.,
  Droc,G., Regad,F., Bourgeois,E., Meynard,D., Perin,C.,
  Chesquiere,A., Delseeny,M., Glaszmann,J.C. and Guiderdoni,E.
  High throughput T-DNA insertion mutagenesis in rice: A first step
  towards in silico reverse genetics
  Plant J. (2004) In press
  Contact: Guiderdoni
  UMR PIA Biotrop program
  CIRAD
  TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
  Tel: 33467615629
  Fax: 33467615605
  Email: emmanuel.guiderdoni@cirad.fr
  Class: TDNA tagged.
FEATURES
    source
      1..50
      Location/Qualifiers
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="genomic DNA"
        /cultivar="Nipponbare"
        /db_xref="taxon:39947"
        /clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA
        insertion lines"
        /note="PCR was performed on DNA of primary transformants
        of Oryza sativa plants. The DNA fragment(s) resulting of
        PCR were directly sequenced from the left border to
        determine the genomic sequence flanking the insertion.
        T-DNA derived sequences were removed. Information to order
        the corresponding mutant line and a link to a database
        providing a graphical display is available from June 2004
        at http://genoplante-info.infobiogen.fr/oryzatagline/.
        This sequence has been generated in the framework of the
        French plant genomics program Genoplante
        (http://www.genoplante.org and
        http://genoplante-info.infobiogen.fr)."
ORIGIN
  Query Match 53.3%; Score 12.8; DB 10; Length 50;
  Best Local Similarity 70.8%; Pred. NO. 6.2e+05;
  Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGCCTCATGGGG 24
    |||||
Db 46 GGGCTGAGCGCGCTCCATAGGAG 23

RESULT 33
AZ829200/c
LOCUS
DEFINITION
  2M0106N1LR Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0106N11 R, genomic survey sequence.
ACCESSION
  AZ829200
VERSION
  AZ829200.1 GI:12999108

```

```

KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 28)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0106 row: N column: 11
  Seq primer: CACACGAGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 28.
FEATURES
    source
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      Location/Qualifiers
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC2M0106N11"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."
ORIGIN
  Query Match 52.5%; Score 12.6; DB 9; Length 28;
  Best Local Similarity 78.9%; Pred. No. 7.5e+05;
  Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGCCTCATGG 21
    |||||
Db 21 GGTCTCCGTGGCCATCG 3

RESULT 34
AK216071
LOCUS
DEFINITION
  Mus musculus cDNA, clone:Y2G0137B14, strand:plus,
  reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000040729, based
  on BLAT search.

```



ACCESSION AK216071.1 GI:56040248  
 VERSION HTc; ASSETS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE  
 ORGANISM  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
 Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S., Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M., Hayashizaki, Y., and Carninci, P. (2004) Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas Nat. Methods 1, 233-239 (2004)

REFERENCE 2  
 Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N., Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M., Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watahiki, A., and Hayashizaki, Y. Direct Submission Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT Alternative Splicing Libraries (ASLs) are prepared by: Preparing of single-stranded DNA using a RNA template from full length cDNA of libraries, hybridizing of single-stranded DNAs, removing of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligation of Y-shaped primers to isolated DNA hybrids with loop structures, PCR amplification of ligation products and their cloning into pFLCI vector. (Reference).

FEATURES  
 source  
 1..45  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="Y260137B14"  
 /cell\_lines="mixture of B16-F10Y and melan-c"  
 /cell\_type="mixture of melanoma cell and melanocyte cell"  
 /clone\_lib="Alternative Splicing Library L3"  
 /note="strand, plus, reference:ENSEMBL:Mouse-Transcript-ENS:ENSMUST0000040729, based on BLAT search"

ORIGIN  
 Query Match 52.5%; Score 12.6; DB 4; Length 45;  
 Best Local Similarity 78.9%; Pred. No. 7.5e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGTCCAGCGTGGCCATGG 21  
 ||||| ||| |||||  
 Db 29 GGTCTCAGTGGCCATGG 39  
 ||||| ||| |||||

RESULT 35  
 CC183529/c  
 LOCUS XE347 BayGenomics Gene Trap Library pGTILxf Mus musculus cDNA, mRNA  
 DEFINITION

ACCESSION CC183529.1 GI:30427429  
 VERSION GSS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE  
 ORGANISM  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 45)

REFERENCE 1

AUTHORS BayGenomics.  
 TITLE http://baygenomics.ucsf.edu/  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: BayGenomics  
 Bay Area Functional Genomics Consortium (BayGenomics)  
 Email: info@baygenomics.ucsf.edu  
 Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from  
 http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL\_LINE&KEY=XE347  
 Class: Gene Trap.  
 Location/Qualifiers  
 1..45  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Ola"  
 /db\_xref="taxon:10090"  
 /sex="Male"  
 /cell\_type="Embryonic stem cell"  
 /clone\_lib="BayGenomics Gene Trap Library pGTILxf"  
 /note="Vector: pGTILxf"

ORIGIN  
 Query Match 52.5%; Score 12.6; DB 9; Length 45;  
 Best Local Similarity 78.9%; Pred. No. 7.5e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGTCCAGCGTGGCCATGG 21  
 ||||| ||| |||||  
 Db 29 GGTCCCGGCTGGCCATGG 11  
 ||||| ||| |||||

RESULT 36  
 CG728115/c  
 LOCUS 1119098B04.2EL\_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.  
 DEFINITION  
 ACCESSION CG728115.1 GI:37768518  
 VERSION GSS.  
 KEYWORDS Zea mays  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 45)

REFERENCE 1  
 Walbot, V.  
 Maize genomic sequences found using engineered RescueMu transposon  
 Unpublished (2001)  
 TITLE Contact: Walbot V  
 JOURNAL Department of Biological Sciences  
 COMMENT Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.  
 Plate: 1119098 row: 39  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1..45  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /culturivar="mixed background W23/A188/B73/K55"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="1119 - RescueMu Grid AA"  
 /note="Organ: leaf; Vector: RescueMu (engineered from

FEATURES  
 source  
 1..45  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /culturivar="mixed background W23/A188/B73/K55"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="1119 - RescueMu Grid AA"  
 /note="Organ: leaf; Vector: RescueMu (engineered from



**SOURCE**  
**ORGANISM** Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 49)  
**REFERENCE**  
**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Life technologies catalog #: 11547-015  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
 Insert Length: 1030 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
**FEATURES**  
 source  
 1..49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2133436"  
 /tissue\_type="lymphoma, follicular mixed small and large cell"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP Lym12"  
 /note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

**ORIGIN**  
 Query Match 52.5%; Score 12.6; DB 1; Length 49;  
 Best Local Similarity 78.9%; Pred. No. 7.5e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 GGGGTCCAGCGTGGCCAT 19  
 ||||| |||||  
 Db 9 GGGGCCCGCGCGCCAT 27

**RESULT 40**  
**AA594397**  
**LOCUS** n193g10.s1 NCI CGAP Col0 Homo sapiens cDNA clone IMAGE:1058274 3'  
**DEFINITION** similar to gb:J03905 GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30  
**PRECUSOR** (HUMAN); mRNA sequence.  
**AA594397**  
**VERSION** AA594397.1 GI:2409747  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 49)  
**REFERENCE**  
**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
 Insert Length: 1930 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.  
**FEATURES**  
 source  
 1..49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1058274"  
 /tissue\_type="colon tumor RER+"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Col0"  
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Donaldo (N-Soares4)."

**ORIGIN**  
 Query Match 52.5%; Score 12.6; DB 1; Length 49;  
 Best Local Similarity 78.9%; Pred. No. 7.5e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 4 GTCCAGCGTGGCCATGGG 22  
 ||||| |||||  
 Db 24 GTCCAGCATTCACATGGG 42

**RESULT 41**  
**CZ295110**  
**LOCUS** P070E01 GGTC Gene Trap Library GV18C05 Mus musculus cDNA clone  
**DEFINITION** P070E01, mRNA sequence.  
**ACCESSION** CZ295110  
**VERSION** CZ295110.1 GI:61682860  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 49)  
**REFERENCE**  
**AUTHORS** Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schmutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.  
**TITLE** A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
**PUBMED** 12904583  
**COMMENT** Contact: GGTC  
 German Genetrap Consortium (GGTC)  
 Email: info@genetrap.de  
 FlipRAGCoC2 gene trap. Sequence tag generated by 5' RACE.  
 Additional sequence information can be found at:  
 'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=P070E01'. ES cell line harboring insertion mutation of target gene is available at:  
 'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm'  
 1' Inhouse Sequence Identifier: 25645  
 Class: Gene Trap.  
 Location/Qualifiers  
 1..49  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Sv"  
 /db\_xref="taxon:10090"

```

/clone="P070E01"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells [C57BL/6J x 129S6/SvEvTac] F1"
/clone_lib="GTC Gene Trap Library GV18C05"
/note="Vector: FlpROSAceoC+2"

ORIGIN
Query Match          52.5%; Score 12.6; DB 10; Length 49;
Best Local Similarity 78.9%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCATGGGG 24
| |||| |||| |||| ||||
Db 8 CAAGCGCGCCACGGGG 26

RESULT 42
CR900779/c
LOCUS CR900779 49 bp DNA linear GSS 23-NOV-2004
DEFINITION Sus scrofa BES, genomic survey sequence.
ACCESSION CR900779
VERSION CR900779.1 GI:56225276
KEYWORDS GSS; Bac-end sequence BES; Genome Survey Sequence.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 49)
AUTHORS Rogel-Gallard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
Chardon,P.
TITLE Construction of a swine BAC library: application to the
characterization and mapping of porcine type C endoviral elements
JOURNAL Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
PUBMED 10449899
REFERENCE 2 (bases 1 to 49)
AUTHORS Chardon,P., Iannuccelli,N., Roig,A., Dossat,C., Demars,J.,
Rogel-Gallard,C., Roy,A., Schibler,L. and Milan,D.
TITLE A physical map of the swine genome
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 49)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secre@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
FEATURES
source
Location/Qualifiers
1..49
/organism="Sus scrofa"
/mol_type="genomic DNA"
/strain="Large White"
/db_xref="taxon:9823"
/clone="bi0280E04"
/sex="male"
/cell_type="fibroblast"
/clone_lib="SBAB"
/note="Genoscope sequence ID : IH0AAA28BF12FM1"

ORIGIN
Query Match          52.5%; Score 12.6; DB 11; Length 49;
Best Local Similarity 78.9%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGGCCATGGGG 23
| |||| |||| |||| ||||
Db 49 TCCAGTGTGCCCAACGGG 31

RESULT 43
CB221472
LOCUS 1Du013A09 Bos taurus Duodenum #1 library Bos taurus cDNA, mRNA
DEFINITION
```

```

sequence.
ACCESSION CB221472
VERSION CB221472.1 GI:28291986
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 50)
AUTHORS Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Senses,C.W.,
Gordon,P.M.K. and Moore,S.S.
TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
Insert Length: 50 Std Error: 0.00
POLYA-No.

FEATURES
source
Location/Qualifiers
1..50
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Simple columnar epithelial"
/dev_stage="Young adult"
/lab_host="Xl1-BlueMRF'strain"
/clone_lib="Bos taurus Duodenum #1 library"
/note="Organ: Intestine/duodenum; Vector: Uni-ZAPXR;
Site_1: EcoRI; Site_2: Xho I"

ORIGIN
Query Match          52.5%; Score 12.6; DB 6; Length 50;
Best Local Similarity 78.9%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGGCCATGG 21
| || |||| |||| ||||
Db 2 GGGCCGCGTGTGCGGTGG 20

RESULT 44
AZ619403
LOCUS AZ619403 23 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0451E09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0451E09 R, genomic survey sequence.
ACCESSION AZ619403
VERSION AZ619403.1 GI:11741593
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
```

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0451 row: E column: 09  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 23.  
 Location/Qualifiers  
 1. .23

#### FEATURES

source  
 1. .23  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0451E09"  
 /sex="Male"  
 /lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

#### ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 23;  
 Best Local Similarity 72.7%; Pred. No. 9.1e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTCAGGTCGCGCATGGGG 24  
 ||||| ||||| |||||  
 Db 1 GGTCAGGTCGCGCATGGGG 22

#### RESULT 45

Ai619702/c  
 LOCUS  
 DEFINITION  
 ty52a05.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2282672 3',  
 similar to TR:000599 O00599 CON1.; contains element MSR1 repetitive  
 element ; mRNA sequence.

Accession Ai619702.1 GI:4628828

Version EST.  
 Keywords Homo sapiens (human)

Source  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

Reference 1 (bases 1 to 37)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Authors National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

Journal Unpublished (1997)

Comment Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Insert Length: 2109 Std Error: 0.00  
 Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

#### FEATURES

source  
 1. .37  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2282672"  
 /tissue types="moderately-differentiated endometrial  
 adenocarcinoma, 3 pooled tumors"  
 /lab\_hosts="DH10B"  
 /clone\_lib="NCI CGAP Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.85 kb. Life Technologies catalog #:  
 11539-012"

#### ORIGIN

Query Match 51.7%; Score 12.4; DB 1; Length 37;  
 Best Local Similarity 72.7%; Pred. No. 9.1e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGTCCAGGTCGCGCATGGG 22  
 ||||| ||||| |||||  
 Db 22 GGGCCCCCGGGCGCCCTGGG 1

#### RESULT 46

AZ434030  
 LOCUS  
 DEFINITION  
 IM0220B14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0220B14 F, genomic survey sequence.

Accession AZ434030

Version AZ434030.1 GI:10558043

Keywords GSS.

Source Mus musculus (house mouse)

Organism Mus musculus

Reference  
 AUTHORS  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.

1 (bases 1 to 45)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

Journal Unpublished (2000)

Comment Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0220 row: B column: 14

Seq primer: CGTGTAAACAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 45.

Location/Qualifiers

1. .45

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

```

/db_xref="taxon:10090"
/clone="UUGC1M0220B14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GII4732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

## ORIGIN

```

Query Match      51.7%; Score 12.4; DB 9; Length 45;
Best Local Similarity 72.7%; Pred. No. 9.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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```

QY 1 GGGGTCCAGCGTGGCCATGGG 22
    ||||| ||||| ||||| |||||
Db 20 GAGTCTCTGGTGTGCTAGGGG 41

```

## RESULT 47

```

CL210842/c
LOCUS      46 bp mRNA linear GSS 22-MAR-2005
DEFINITION W126F07 GGTC Gene Trap Library GV03C04 Mus musculus cDNA clone
            W126F07, mRNA sequence.
VERSION    CL210842
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

```

REFERENCE   1 (bases 1 to 46)
AUTHORS    Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,
            Arnold,H.H., Schnuggen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
TITLE       A large-scale, gene-driven mutagenesis approach for the functional
            analysis of the mouse genome
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
PUBMED     12904583
COMMENT     On Mar 22, 2005 this sequence version replaced gi:40727743.
            Contact: GGTC
            German Genetrap Consortium (GGTC)
            Email: info@genetrap.de
            pribetago gene trap. Sequence tag generated by 5'RACE. Additional
            sequence information can be found at:
            'http://genetrap.gsf.de/project/web/new/database/result_clone.html?
            clone_id=W126F07', gsf cell line harboring insertion mutation of
            target gene is available at:
            'http://genetrap.gsf.de/project/web/new/order_clones/howtoorder.htm
            1', Inhouse Sequence Identifier: 08571
            Class: Gene Trap.

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## FEATURES

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source
1..46
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"

```

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/clone="W126F07"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells 129S2 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV03C04"
/notes="Vector: pTlbetago"

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## ORIGIN

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Query Match      51.7%; Score 12.4; DB 10; Length 46;
Best Local Similarity 72.7%; Pred. No. 9.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 1 GGGGTCCAGCGTGGCCATGGG 22
    ||||| ||||| ||||| |||||
Db 36 GGGGTCCCGTGGCCACGGG 15

```

## RESULT 48

```

BZ585242
LOCUS      47 bp DNA linear GSS 17-DEC-2002
DEFINITION BZ585242 3590.1_30.1_H08.2EL.x.1 3590 - RescueMu Grid M Zea mays genomic,
            genomic survey sequence.

```

```

ACCESSION   BZ585242
VERSION     BZ585242.1
KEYWORDS    GSS.
SOURCE      Zea mays
ORGANISM    Zea mays

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.

```

```

REFERENCE   1 (bases 1 to 47)
AUTHORS    Walbot,V.
TITLE       Maize genomic sequences found using engineered RescueMu transposon
JOURNAL     Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu

```

```

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3590.1_30.1 column: 14
Class: transposon-tagged.
FEATURES
source
1..47
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3590 - RescueMu Grid M"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid M was grown at University of Arizona in
2001. DNA was extracted from leaf punches, double digested
using BamHI and BglII, and ligated to form circular
plasmids. DH10B cells were transformed and then screened
on LB plates with ampicillin."

```

## FEATURES

```

source
1..47
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3590 - RescueMu Grid M"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid M was grown at University of Arizona in
2001. DNA was extracted from leaf punches, double digested
using BamHI and BglII, and ligated to form circular
plasmids. DH10B cells were transformed and then screened
on LB plates with ampicillin."

```

## ORIGIN

```

Query Match      51.7%; Score 12.4; DB 9; Length 47;
Best Local Similarity 72.7%; Pred. No. 9.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 2 GGGTCCAGCGTGGCCATGGGG 23
  | | | | | | | | | | | | | |
Db 16 GCGGCCAGCGGGCGCCATGGCG 37

RESULT 49
BWS90752
LOCUS BWS90752 48 bp mRNA linear EST 01-SEP-2004
DEFINITION BWS90752 Yutaka Satou unpublished cDNA library (csef2) Ciona
ACCESSION BWS90752
VERSION BWS90752.1 GI:51841552
KEYWORDS EST.
SOURCE Ciona savignyi
ORGANISM Ciona savignyi
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 48)
Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona savignyi (Satou, Shin-i, Kohara, Satoh)
Unpublished (2004)
Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
FEATURES
    source
        1..48
            /organism="Ciona savignyi"
            /mol_type="mRNA"
            /db_xref="taxon:51511"
            /clone="csef029n10"
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            /clone_lib="Yutaka Satou unpublished cDNA library (csef2)"

ORIGIN
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Best Local Similarity 66.7%; Pred. No. 9.2e+05;
Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCATGGGG 24
  | | | | | | | | | | | | | |
Db 6 GGGCTGCAGNATCGGCACGNGGG 29

RESULT 50
AA906151/c
LOCUS AA906151 49 bp mRNA linear EST 09-JUN-1998
DEFINITION AA906151 Soares NPL T GBC S1 Homo sapiens cDNA clone
IMAGE:1504849 3', similar to TR:P94909 P94909 HYPOTHETICAL 58.7 KD
PROTEIN :, mRNA sequence.
ACCESSION AA906151
VERSION AA906151.1 GI:3041274
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 49)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1605 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham

FEATURES
    source
        1..49
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1504849"
            /lab_host="DH10B"
            /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
            a modified polylinker; Site 1: Not I; Site 2: Eco RI;
            Equal amounts of plasmid DNA from three normalized
            libraries (fetal lung NBHL19W, testis NHT, and B-cell
            NCI CGAP GCBI) were mixed, and ss circles were made in
            vitro. Following HAP purification, this DNA was used as
            tracer in a subtractive hybridization reaction. The driver
            was PCR-amplified cDNAs from pools of 5,000 clones made
            from the same 3 libraries. The pools consisted of
            I.M.A.G.E. clones 257480-302087, 682632-687239,
            726408-728711, and 729096-731399. Subtraction by Bento
            Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 51.7%; Score 12.4; DB 1; Length 49;
Best Local Similarity 72.7%; Pred. No. 9.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGGCCATGGGG 24
  | | | | | | | | | | | | | |
Db 24 GATCCCGGTGGCGTGGCGGG 3

Search completed: February 15, 2006, 21:10:23
Job time : 1612.3 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:56:18 ; Search time 53.9504 Seconds  
(without alignments)  
790.754 Million cell updates/sec

Title: US-09-669-187A-81

Perfect score: 24

Sequence: 1 ggggtccagcgtgcgcattggggg 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/1-COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5-COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A-COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B-COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H-COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PCTRUS-COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP-COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE-COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description           |
|------------|-------|-------------|--------|----|-----------------------|
| 1          | 16.2  | 67.5        | 25     | 3  | US-08-617-874-1       |
| 2          | 16    | 66.7        | 33     | 3  | US-09-249-585A-11     |
| 3          | 15.8  | 65.8        | 33     | 3  | US-08-650-726-1       |
| 4          | 15.2  | 63.3        | 25     | 3  | US-09-396-196G-107962 |
| 5          | 15.2  | 63.3        | 35     | 3  | US-09-875-453B-69     |
| 6          | 15    | 62.5        | 27     | 2  | US-08-410-804-13      |
| 7          | 15    | 62.5        | 27     | 2  | US-08-607-269-8       |
| 8          | 15    | 62.5        | 27     | 2  | US-08-259-514-13      |
| 9          | 15    | 62.5        | 27     | 2  | US-08-858-311-13      |
| 10         | 15    | 62.5        | 27     | 6  | PCT-US95-04600-8      |
| 11         | 14.6  | 60.8        | 47     | 3  | US-09-258-689-5       |
| 12         | 14.6  | 60.8        | 47     | 3  | US-09-866-073A-5      |
| 13         | 14.4  | 60.0        | 29     | 3  | US-09-830-433A-127    |
| 14         | 14.2  | 59.2        | 19     | 3  | US-09-109-858-14      |
| 15         | 14    | 58.3        | 17     | 2  | US-08-217-082A-9      |
| 16         | 14    | 58.3        | 17     | 2  | US-08-217-082A-10     |
| 17         | 14    | 58.3        | 18     | 2  | US-08-217-082A-17     |
| 18         | 14    | 58.3        | 18     | 2  | US-08-465-485A-17     |
| 19         | 14    | 58.3        | 18     | 2  | US-08-465-485A-24     |
| 20         | 14    | 58.3        | 18     | 3  | US-09-080-285-17      |
| 21         | 14    | 58.3        | 18     | 3  | US-09-080-285-24      |
| 22         | 14    | 58.3        | 18     | 3  | US-09-249-730-218     |
| 23         | 14    | 58.3        | 18     | 3  | US-09-118-220-1       |
| 24         | 14    | 58.3        | 18     | 3  | US-08-738-652-55      |

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|------|---|-----------------------|--------------------|
| 18   | 3 | US-09-030-701-27      | Sequence 27, Appl  |
| 18   | 3 | US-09-286-098-59      | Sequence 59, Appl  |
| 18   | 3 | US-09-286-098-104     | Sequence 104, Appl |
| 18   | 3 | US-08-960-774-45      | Sequence 45, Appl  |
| 18   | 3 | US-08-078-954-14      | Sequence 14, Appl  |
| 18   | 3 | US-03-325-193A-51     | Sequence 51, Appl  |
| 18   | 3 | US-09-724-426-17      | Sequence 17, Appl  |
| 18   | 3 | US-09-724-426-24      | Sequence 24, Appl  |
| 18   | 3 | US-09-191-170-53      | Sequence 53, Appl  |
| 18   | 3 | US-09-136-080E-45     | Sequence 45, Appl  |
| 18   | 3 | US-09-690-921-2       | Sequence 2, Appl   |
| 18   | 3 | US-09-301-829A-2      | Sequence 2, Appl   |
| 18   | 3 | US-09-249-247-218     | Sequence 218, Appl |
| 18   | 3 | US-09-337-619-45      | Sequence 45, Appl  |
| 18   | 3 | US-09-835-370-21      | Sequence 21, Appl  |
| 18   | 3 | US-09-634-320-7       | Sequence 7, Appl   |
| 18   | 3 | US-09-654-373-14      | Sequence 14, Appl  |
| 18   | 3 | US-09-724-425-17      | Sequence 17, Appl  |
| 18   | 3 | US-09-724-425-24      | Sequence 24, Appl  |
| 18   | 3 | US-09-895-480A-14     | Sequence 14, Appl  |
| 18   | 3 | US-10-002-884A-6      | Sequence 6, Appl   |
| 18   | 3 | US-09-108-673A-34     | Sequence 34, Appl  |
| 18   | 3 | US-09-835-371-21      | Sequence 21, Appl  |
| 18   | 3 | US-09-954-987B-115    | Sequence 115, Appl |
| 18   | 3 | US-09-672-126B-110    | Sequence 110, Appl |
| 19   | 3 | US-09-634-320-8       | Sequence 8, Appl   |
| 19   | 3 | US-09-634-320-9       | Sequence 9, Appl   |
| 19   | 3 | US-09-632-748-7       | Sequence 7, Appl   |
| 19   | 3 | US-09-082-649B-60     | Sequence 60, Appl  |
| 20   | 3 | US-09-985-101-60      | Sequence 60, Appl  |
| 23   | 3 | US-09-634-320-1       | Sequence 1, Appl   |
| 23   | 3 | US-09-634-320-2       | Sequence 2, Appl   |
| 25   | 3 | US-09-396-196G-16637  | Sequence 16637, A  |
| 30   | 3 | US-09-349-884-12      | Sequence 12, Appl  |
| 35   | 2 | US-08-217-082A-2      | Sequence 2, Appl   |
| 35   | 2 | US-08-465-485A-2      | Sequence 2, Appl   |
| 35   | 3 | US-09-080-285-2       | Sequence 2, Appl   |
| 35   | 3 | US-09-724-426-2       | Sequence 2, Appl   |
| 35   | 3 | US-09-724-425-2       | Sequence 2, Appl   |
| 40   | 2 | US-08-301-722A-6      | Sequence 6, Appl   |
| 50   | 3 | US-10-131-827-4669    | Sequence 4669, Ap  |
| 25   | 3 | US-09-396-196G-55452  | Sequence 55452, A  |
| 30   | 3 | US-09-720-655B-4      | Sequence 4, Appl   |
| 45   | 3 | US-08-979-608A-40     | Sequence 40, Appl  |
| 45   | 3 | US-09-517-849-40      | Sequence 40, Appl  |
| 45   | 3 | US-09-616-289-40      | Sequence 40, Appl  |
| 45   | 3 | US-09-976-740-40      | Sequence 40, Appl  |
| 45   | 3 | US-09-971-773-40      | Sequence 40, Appl  |
| 47   | 3 | US-09-422-978-3636    | Sequence 3636, Ap  |
| 21   | 2 | US-08-461-030C-3      | Sequence 3, Appl   |
| 21   | 6 | PCT-US95-07135-3      | Sequence 3, Appl   |
| 27   | 3 | US-09-877-243A-21     | Sequence 21, Appl  |
| 27   | 3 | US-09-877-243A-22     | Sequence 22, Appl  |
| 27   | 3 | US-09-877-705A-21     | Sequence 21, Appl  |
| 27   | 3 | US-09-877-705A-22     | Sequence 22, Appl  |
| 27   | 3 | US-09-877-738C-21     | Sequence 21, Appl  |
| 27   | 3 | US-09-877-738C-22     | Sequence 22, Appl  |
| 33   | 3 | US-09-816-697-4       | Sequence 4, Appl   |
| 38   | 2 | US-08-671-947-30      | Sequence 30, Appl  |
| 38   | 2 | US-08-671-947-31      | Sequence 31, Appl  |
| 43   | 2 | US-08-467-568-4       | Sequence 4, Appl   |
| 43   | 2 | US-08-467-568-8       | Sequence 8, Appl   |
| 43   | 2 | US-09-030-582-4       | Sequence 4, Appl   |
| 43   | 2 | US-09-030-582-8       | Sequence 8, Appl   |
| 25   | 3 | US-09-396-196G-109443 | Sequence 109443,   |
| 25   | 3 | US-09-396-196G-109444 | Sequence 109444,   |
| 25   | 3 | US-09-396-196G-109445 | Sequence 109445,   |
| 29   | 3 | US-09-195-666A-22     | Sequence 22, Appl  |
| 29   | 3 | US-09-635-705-22      | Sequence 22, Appl  |
| 29   | 3 | US-09-634-858A-22     | Sequence 22, Appl  |
| 29   | 3 | US-08-869-927C-22     | Sequence 22, Appl  |
| 20   | 2 | US-08-217-082A-1      | Sequence 1, Appl   |
| 20   | 2 | US-08-217-082A-7      | Sequence 7, Appl   |
| 13   |   |                       |                    |
| 54.2 |   |                       |                    |

|       |      |      |    |      |                       |                    |                       |                    |                    |       |      |      |    |   |                      |                   |
|-------|------|------|----|------|-----------------------|--------------------|-----------------------|--------------------|--------------------|-------|------|------|----|---|----------------------|-------------------|
| c 98  | 13   | 54.2 | 13 | 54.2 | 20                    | 2                  | US-08-465-485A-1      | Sequence 1, Appli  | Sequence 1, Appli  | c 171 | 12.4 | 51.7 | 21 | 3 | US-09-657-472-2332   | Sequence 2332, Ap |
| c 99  | 13   | 54.2 | 13 | 54.2 | 20                    | 2                  | US-08-465-485A-7      | Sequence 7, Appli  | Sequence 7, Appli  | c 172 | 12.4 | 51.7 | 23 | 3 | US-09-756-283A-12    | Sequence 12, Appl |
| c 100 | 13   | 54.2 | 13 | 54.2 | 20                    | 2                  | US-09-080-285-1       | Sequence 1, Appli  | Sequence 1, Appli  | c 173 | 12.4 | 51.7 | 24 | 2 | US-08-281-082A-18    | Sequence 18, Appl |
| c 101 | 13   | 54.2 | 13 | 54.2 | 20                    | 3                  | US-09-080-285-7       | Sequence 7, Appli  | Sequence 7, Appli  | c 174 | 12.4 | 51.7 | 25 | 3 | US-09-396-196G-41595 | Sequence 41595, A |
| c 102 | 13   | 54.2 | 13 | 54.2 | 20                    | 3                  | US-09-379-718-1       | Sequence 1, Appli  | Sequence 1, Appli  | c 175 | 12.4 | 51.7 | 25 | 3 | US-09-396-196G-61432 | Sequence 61432, A |
| c 103 | 13   | 54.2 | 13 | 54.2 | 20                    | 3                  | US-09-379-718-2       | Sequence 2, Appli  | Sequence 2, Appli  | c 176 | 12.4 | 51.7 | 25 | 3 | US-09-396-196G-61443 | Sequence 61443, A |
| c 104 | 13   | 54.2 | 13 | 54.2 | 20                    | 3                  | US-09-724-426-1       | Sequence 1, Appli  | Sequence 1, Appli  | c 177 | 12.4 | 51.7 | 25 | 3 | US-09-396-196G-61444 | Sequence 61444, A |
| c 105 | 13   | 54.2 | 13 | 54.2 | 20                    | 3                  | US-09-724-426-7       | Sequence 7, Appli  | Sequence 7, Appli  | c 178 | 12.4 | 51.7 | 27 | 3 | US-09-612-852A-9     | Sequence 9, Appli |
| c 106 | 13   | 54.2 | 13 | 54.2 | 20                    | 3                  | US-09-724-425-1       | Sequence 1, Appli  | Sequence 1, Appli  | c 179 | 12.4 | 51.7 | 30 | 2 | US-07-988-194A-45    | Sequence 45, Appl |
| c 107 | 13   | 54.2 | 13 | 54.2 | 20                    | 3                  | US-09-724-425-7       | Sequence 7, Appli  | Sequence 7, Appli  | c 180 | 12.4 | 51.7 | 30 | 2 | US-07-860-925-15     | Sequence 15, Appl |
| c 108 | 13   | 54.2 | 13 | 54.2 | 25                    | 3                  | US-09-396-196G-26931  | Sequence 26931, A  | Sequence 26931, A  | c 181 | 12.4 | 51.7 | 30 | 2 | US-08-334-215-15     | Sequence 15, Appl |
| c 109 | 13   | 54.2 | 13 | 54.2 | 35                    | 3                  | US-09-396-196G-101993 | Sequence 101993,   | Sequence 101993,   | c 182 | 12.4 | 51.7 | 30 | 3 | US-08-479-737-47     | Sequence 47, Appl |
| c 110 | 13   | 54.2 | 13 | 54.2 | 35                    | 3                  | US-09-215-252-41      | Sequence 41, Appl  | Sequence 41, Appl  | c 183 | 12.4 | 51.7 | 30 | 3 | US-08-475-442A-47    | Sequence 47, Appl |
| c 111 | 13   | 54.2 | 13 | 54.2 | 35                    | 3                  | US-09-043-930B-6      | Sequence 6, Appli  | Sequence 6, Appli  | c 184 | 12.4 | 51.7 | 32 | 3 | US-09-128-354-7      | Sequence 7, Appli |
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| c 118 | 12.8 | 53.3 | 24 | 2    | US-08-281-082A-17     | Sequence 17, Appl  | Sequence 17, Appl     | Sequence 17, Appl  | Sequence 17, Appl  | c 191 | 12.2 | 50.8 | 17 | 3 | US-09-476-387-571    | Sequence 571, App |
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| c 125 | 12.8 | 53.3 | 29 | 3    | US-08-869-327C-19     | Sequence 19, Appl  | Sequence 19, Appl     | Sequence 19, Appl  | Sequence 19, Appl  | c 198 | 12.2 | 50.8 | 22 | 2 | US-08-607-269-6      | Sequence 6, Appli |
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## ALIGNMENTS

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RESULT 1
US-08-617-874-1
; Sequence 1, Application US/08617874
; Patent No. 633850
; GENERAL INFORMATION:
; APPLICANT: Jevnikar, Anthony M.
; APPLICANT: Ma, Shengwu
; APPLICANT: Sciller, Calvin R.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING
; TITLE OF INVENTION: IMMUNE RESPONSES IN MAMMALS
; NUMBER OF SEQUENCES: 10
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: George Mason Building, 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/617,874
; FILING DATE: 21-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 024916-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
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; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA - primer"
US-08-617-874-1
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Db 2 GGATCCGGCGCGCCCATGG 22
RESULT 2
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; Sequence 11, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentn version 3.0
; SEQ ID NO 11
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; ORGANISM: artificial sequence
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; OTHER INFORMATION: oligonucleotide used for RT-PCR amplification of Bcl2
US-09-249-585A-11
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Db 27 CCAGCGTGGCGCCATGG 12
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RESULT 3
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; Sequence 1, Application US/08650726
; Patent No. 6027721
; GENERAL INFORMATION:
; APPLICANT: Hamming, Joseph P
; APPLICANT: Aebischer, Patrick
; TITLE OF INVENTION: DEVICE AND METHOD FOR ENCAPSULATED GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Ave. of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,726
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Eirifi, Ivor R
; REGISTRATION NUMBER: 39,529
; REFERENCE/DOCKET NUMBER: CFI-35
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 596 9000
; TELEFAX: 212 596 9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
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US-08-650-726-1

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RESULT 4
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; Sequence 107962, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
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US-09-396-196G-107962

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGGCCCATGGG 22
| | | | | | | | | | | | | | |
Db 1 GTTCCAGCCTTGGCCCATGGG 20

RESULT 5
US-09-875-453B-69/c
; Sequence 69, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-875-453B-69

Query Match 63.3%; Score 15.2; DB 3; Length 35;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGTCCAGCGTGGCCCATGG 21
| | | | | | | | | | | | | | |
Db 28 GGTCCAGCGCGAGCCATGG 9

RESULT 6
US-08-410-804-13/c
; Sequence 13, Application US/08410804
; Patent No. 5632994
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cathryn Campbell
; STREET: 4370 La Jolla Village Drive. Ste 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,804
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,514
; FILING DATE: 14-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-410-804-13

Query Match 62.5%; Score 15; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCCATG 20
DB 21 CCAGCGTGGCCATG 7

RESULT 7
US-08-607-269-8/c
; Sequence 8, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226,876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs

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```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-607-269-8

Query Match 62.5%; Score 15; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCCATG 20
DB 21 CCAGCGTGGCCATG 7

RESULT 8
US-08-259-514-13/c
; Sequence 13, Application US/08259514
; Patent No. 5747245
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cathryn Campbell
; STREET: 4370 La Jolla Village Drive, Ste 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9954
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-259-514-13

Query Match 62.5%; Score 15; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCCATG 20
DB 21 CCAGCGTGGCCATG 7

RESULT 9
US-08-858-311-13/c
; Sequence 13, Application US/08858311
; Patent No. 5876939
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 22

```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Cathryn Campbell  
;; STREET: 4370 La Jolla Village Drive, Ste 700  
;; CITY: San Diego  
;; STATE: California  
;; COUNTRY: United States  
;; ZIP: 92122  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/858,311  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/410,804  
;; FILING DATE: 27-MAR-1995  
;; APPLICATION NUMBER: US 08/259,514  
;; FILING DATE: 14-JUN-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LJ 1389  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cdna  
US-08-858-311-13

Query Match 62.5%; Score 15; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCACGGTGGCCCATG 20  
Db 21 CCACGGTGGCCCATG 7

RESULT 10  
PCT-US95-04600-8/c  
; Sequence 8, Application PC/TUS9504600  
; GENERAL INFORMATION:  
; APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION  
; TITLE OF INVENTION: Interaction of Proteins Involved in  
; TITLE OF INVENTION: a Cell Death Pathway  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04600  
; FILING DATE: 12-APR-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Imbra, Richard J.  
; REGISTRATION NUMBER: 37,643

;; REFERENCE/DOCKET NUMBER: FP-LJ 1361  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
PCT-US95-04600-8

Query Match 62.5%; Score 15; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCACGGTGGCCCATG 20  
Db 21 CCACGGTGGCCCATG 7

RESULT 11  
US-09-258-689-5  
; Sequence 5, Application US/09258689  
; Patent No. 6451527  
; GENERAL INFORMATION:  
; APPLICANT: Larocca, David  
; APPLICANT: Baird, Andrew  
; APPLICANT: Kassner, Paul  
; TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR  
; TITLE OF INVENTION: SELECTING INTERNALIZING LIGANDS FOR GENE DELIVERY  
; FILE REFERENCE: 760100.430C3  
; CURRENT APPLICATION NUMBER: US/09/258,689  
; CURRENT FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-09-258-689-5

Query Match 60.8%; Score 14.6; DB 3; Length 47;  
Best Local Similarity 81.0%; Pred. No. 3.2e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCCATGG 21  
Db 10 GGGTTCGGCGTGGCGCATGG 30

RESULT 12  
US-09-866-073A-5  
; Sequence 5, Application US/09866073A  
; Patent No. 6723512  
; GENERAL INFORMATION:  
; APPLICANT: Larocca, David  
; APPLICANT: Baird, Andrew  
; APPLICANT: Kassner, Paul  
; TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR  
; TITLE OF INVENTION: DETECTING AND IDENTIFYING PROTEIN-PROTEIN  
; TITLE OF INVENTION: INTERACTIONS THAT FACILITATE INTERNALIZATION  
; TITLE OF INVENTION: AND TRANSGENE EXPRESSION AND CELLS OR TISSUE  
; TITLE OF INVENTION: COMPETENT FOR THE SAME AND METHODS FOR EVOLVING  
; TITLE OF INVENTION: GENE DELIVERY VECTORS  
; FILE REFERENCE: 760100.430C4  
; CURRENT APPLICATION NUMBER: US/09/866,073A  
; CURRENT FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5

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; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-866-073A-5

Query Match          60.8%; Score 14.6; DB 3; Length 47;
Best Local Similarity 81.0%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGCGCCATGG 21
    |||||
Db 10 GGGTCCAGCGTGCGCCATGG 30
    |||||

RESULT 13
US-09-830-433A-127
; Sequence 127, Application US/09830433A
; Patent No. 6835384
; GENERAL INFORMATION:
; APPLICANT: AUJAME et al.
; TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic
; FILE REFERENCE: P07180US00/BAS
; CURRENT APPLICATION NUMBER: US/09/830,433A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: FR 98 13 693
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-830-433A-127

Query Match          60.0%; Score 14.4; DB 3; Length 29;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGCGCCATGGGG 24
    |||||
Db 2 GGGATCCAACTGCTTCATGGTG 25
    |||||

RESULT 14
US-09-109-858-14
; Sequence 14, Application US/09109858
; Patent No. 6787353
; GENERAL INFORMATION:
; APPLICANT: Rao, Mahendra S.
; APPLICANT: Kalyani, Anjali J.
; TITLE OF INVENTION: Lineage-Restricted Neuronal Precursors
; FILE REFERENCE: T5530.CIP
; CURRENT APPLICATION NUMBER: US/09/109,858
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 08/909,435
; EARLIER FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: WordPerfect 8.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-109-858-14

Query Match          59.2%; Score 14.2; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-866-073A-5

Query Match          60.8%; Score 14.6; DB 3; Length 47;
Best Local Similarity 81.0%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGCGCCATGG 21
    |||||
Db 10 GGGTCCAGCGTGCGCCATGG 30
    |||||

RESULT 15
US-08-217-082A-9
; Sequence 9, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: Synthetic DNA
; ANTI-SENSE: YES
US-08-217-082A-9

Query Match          58.3%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGCGCCAT 19
    |||||
Db 4 CCAGCGTGCGCCAT 17
    |||||

RESULT 16
US-08-217-082A-10
; Sequence 10, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; NUMBER OF SEQUENCES: 17
```

;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
;/ ADDRESSEE: P.C.  
;/ STREET: 224 Airport Parkway  
;/ CITY: San Jose  
;/ STATE: California  
;/ COUNTRY: U.S.A.  
;/ ZIP: 95110  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/217,082A  
;/ FILING DATE: 24-MAR-1994  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/840,716  
;/ FILING DATE: 21-FEB-1992  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/288,692  
;/ FILING DATE: 22-DEC-1988  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Fortney, Andrew D.  
;/ REGISTRATION NUMBER: 34,600  
;/ REFERENCE/DOCKET NUMBER: 3335-067-55 FWC  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (408) 436-2070  
;/ INFORMATION FOR SEQ ID NO: 10:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 17 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: other nucleic acid  
;/ DESCRIPTION: Synthetic DNA  
;/ ANTI-SENSE: YES  
;/ US-08-217-082A-10

Query Match 58.3%; Score 14; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CCAGCGTGGCCCAT 19  
Db 1 CCAGCGTGGCCCAT 14

RESULT 17  
US-08-217-082A-17  
;/ Sequence 17, Application US/08217082A  
;/ Patent No. 5734033  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Reed, John  
;/ TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE  
;/ GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE  
;/ NUMBER OF SEQUENCES: 17  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
;/ ADDRESSEE: P.C.  
;/ STREET: 224 Airport Parkway  
;/ CITY: San Jose  
;/ STATE: California  
;/ COUNTRY: U.S.A.  
;/ ZIP: 95110  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:

;/ APPLICATION NUMBER: US/08/217,082A  
;/ FILING DATE: 24-MAR-1994  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/840,716  
;/ FILING DATE: 21-FEB-1992  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/288,692  
;/ FILING DATE: 22-DEC-1988  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Fortney, Andrew D.  
;/ REGISTRATION NUMBER: 34,600  
;/ REFERENCE/DOCKET NUMBER: 3335-067-55 FWC  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (408) 436-2070  
;/ TELEFAX: (408) 436-2075  
;/ INFORMATION FOR SEQ ID NO: 17:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 18 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: other nucleic acid  
;/ DESCRIPTION: Synthetic DNA  
;/ US-08-217-082A-17  
  
Query Match 58.3%; Score 14; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CCAGCGTGGCCCAT 19  
Db 5 CCAGCGTGGCCCAT 18

RESULT 18  
US-08-465-485A-17  
;/ Sequence 17, Application US/08465485A  
;/ Patent No. 5831066  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Reed, John  
;/ TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
;/ NUMBER OF SEQUENCES: 29  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
;/ ADDRESSEE: P.C.  
;/ STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
;/ CITY: Arlington  
;/ STATE: Virginia  
;/ COUNTRY: U.S.A.  
;/ ZIP: 22202  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/465,485A  
;/ FILING DATE: 05-JUN-1995  
;/ CLASSIFICATION: 514  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/124,256  
;/ FILING DATE: 20-SEP-1993  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/840,716  
;/ FILING DATE: 21-FEB-1992  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/288,692  
;/ FILING DATE: 22-DEC-1988  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Fortney, Andrew D.  
;/ REGISTRATION NUMBER: 34,600  
;/ REFERENCE/DOCKET NUMBER: 3335-070-55 CONT



TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (408) 436-2070  
 TELEFAX: (408) 436-2075  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-465-485A-17

Query Match 58.3%; Score 14; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
 Db 5 CCAGCGTGGCCAT 18

RESULT 19  
 US-08-465-485A-24  
 Sequence 24, Application US/08465485A  
 Patent No. 5831066  
 GENERAL INFORMATION:  
 APPLICANT: Reed, John  
 TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESSEE: P.C.  
 STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/465,485A  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/124,256  
 FILING DATE: 20-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/840,716  
 FILING DATE: 21-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/288,692  
 FILING DATE: 22-DEC-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fortney, Andrew D.  
 REGISTRATION NUMBER: 34,600  
 REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (408) 436-2070  
 TELEFAX: (408) 436-2075  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Other nucleic acid;  
 DESCRIPTION: Synthetic DNA  
 ANTI-SENSE: YES  
 FEATURE:  
 NAME/KEY: Modified\_base  
 LOCATION: 16..17

OTHER INFORMATION: Last two internucleoside linkages are  
 OTHER INFORMATION: phosphorothioates  
 US-08-465-485A-24

Query Match 58.3%; Score 14; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
 Db 5 CCAGCGTGGCCAT 18

RESULT 20  
 US-09-080-285-17  
 Sequence 17, Application US/09080285  
 Patent No. 6040181  
 GENERAL INFORMATION:  
 APPLICANT: Reed, John  
 TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESSEE: P.C.  
 STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/080,285  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/465,485  
 FILING DATE: 05-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/124,256  
 FILING DATE: 20-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/840,716  
 FILING DATE: 21-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/288,692  
 FILING DATE: 22-DEC-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fortney, Andrew D.  
 REGISTRATION NUMBER: 34,600  
 REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (408) 436-2070  
 TELEFAX: (408) 436-2075  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-080-285-17

Query Match 58.3%; Score 14; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
 Db 5 CCAGCGTGGCCAT 18

RESULT 21  
US-09-080-285-24  
; Sequence 24, Application US/09080285  
; Patent No. 6040181  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John  
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/080,285  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/465,485  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/124,256  
; FILING DATE: 20-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/840,716  
; FILING DATE: 21-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/288,692  
; FILING DATE: 22-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fortney, Andrew D.  
; REGISTRATION NUMBER: 34,600  
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (408) 435-2070  
; TELEFAX: (408) 436-2075  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid;  
; DESCRIPTION: Synthetic DNA  
; ANTI-SENSE: YES  
; FEATURE:  
; NAME/KEY: Modified\_base  
; LOCATION: 16..17  
; OTHER INFORMATION: Last two internucleoside linkages are  
; OTHER INFORMATION: phosphorothioates  
US-09-080-285-24

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 22  
US-09-249-730-218  
; Sequence 218, Application US/09249730

; Patent No. 6121000  
; GENERAL INFORMATION:  
; APPLICANT: WRIGHT, Jim A.  
; APPLICANT: YOUNG, Alping H.  
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and  
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase  
; FILE REFERENCE: 032396-040  
; CURRENT APPLICATION NUMBER: US/09/249,730  
; CURRENT FILING DATE: 1999-02-11  
; NUMBER OF SEQ ID NOS: 220  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 218  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-249-730-218

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 23  
US-09-118-220-1  
; Sequence 1, Application US/09118220  
; Patent No. 6140051  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Lauren R.  
; APPLICANT: Xu, Cheng  
; TITLE OF INVENTION: FLUORESCENT DIBENZAZOLE DERIVATIVES  
; TITLE OF INVENTION: AND METHODS RELATED THERETO  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive, 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/118,220  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bartfeld, Neil S  
; REGISTRATION NUMBER: 39,901  
; REFERENCE/DOCKET NUMBER: GENTA.050A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-09-118-220-1

Query Match 58.3%; Score 14; DB 3; Length 18;

```
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18

RESULT 24
US-08-738-652-55
; Sequence 55, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-55

Query Match 58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18

RESULT 25
US-09-030-701-27
; Sequence 27, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-27

Query Match 58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18

RESULT 26
US-09-286-098-59
; Sequence 59, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; Immune System Using Immunotherapeutic Oligonucleotides and
; Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-59

Query Match 58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18

RESULT 27
US-09-286-098-104
; Sequence 104, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; Immune System Using Immunotherapeutic Oligonucleotides and
; Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-104

Query Match 58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18

RESULT 28
US-08-960-774-45
; Sequence 45, Application US/08960774
```

Patent No. 6239116  
; GENERAL INFORMATION:  
; APPLICANT: Krieg et al.,  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/960,774  
; FILING DATE: 30-October-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652  
; FILING DATE: October 30, 1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 08918/012001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-960-774-45

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCGCCAT 19  
|||||  
DB 5 CCAGCGTGGCGCCAT 18

RESULT 29  
US-09-078-954-14  
; Sequence 14, Application US/09078954  
; Patent No. 6287591  
; GENERAL INFORMATION:  
; APPLICANT: SEMPLE, Sean C.  
; APPLICANT: Klimuk, Sandra K.  
; APPLICANT: Harasym, Troy  
; APPLICANT: Hope, Michael J.  
; APPLICANT: Ansell, Steven M.  
; APPLICANT: Cullis, Pieter  
; APPLICANT: Scherrer, Peter  
; APPLICANT: Geisler, Timothy  
; APPLICANT: Zon, Gerald  
; APPLICANT: Debever, Dan  
; TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic Agents in  
; TITLE OF INVENTION: Lipid Vesicles  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oppedahl & Larson  
; STREET: PO Box 5270  
; CITY: Frisco  
; STATE: CO

COUNTRY: USA  
; ZIP: 80443-5270  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/078,954  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/856,374  
; FILING DATE: 14-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marina T. Larson  
; REGISTRATION NUMBER: 32,038  
; REFERENCE/DOCKET NUMBER: INEX.P-003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (970) 668-2050  
; TELEFAX: (970) 668-2082  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: no  
; ANTI-SENSE: yes  
US-09-078-954-14

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCGCCAT 19  
|||||  
DB 5 CCAGCGTGGCGCCAT 18

RESULT 30  
US-09-325-193A-51  
; Sequence 51, Application US/09325193A  
; Patent No. 6406705  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Krieg, Arthur M.  
; TITLE OF INVENTION: Use of Nucleic Acids Containing  
; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant  
; FILE REFERENCE: C1039/7025/HCL  
; CURRENT APPLICATION NUMBER: US/09/325,193A  
; CURRENT FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: US 09/154,614  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: PCT/US98/04703  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: US 60/040,376  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 51  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-325-193A-51

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 31

US-09-724-426-17  
; Sequence 17, Application US/09724426

; Patent No. 6414134

; GENERAL INFORMATION:

; APPLICANT: Reed, John

; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression

; FILE REFERENCE: 10412-024

; CURRENT APPLICATION NUMBER: US/09/724,426

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 17

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-426-17

Query Match 58.3%; Score 14; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 32

US-09-724-426-24

; Sequence 24, Application US/09724426

; Patent No. 6414134

; GENERAL INFORMATION:

; APPLICANT: Reed, John

; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression

; FILE REFERENCE: 10412-024

; CURRENT APPLICATION NUMBER: US/09/724,426

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 24

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-426-24

Query Match 58.3%; Score 14; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 33

US-09-191-170-53

; Sequence 53, Application US/09191170

; Patent No. 6429199

; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.

; APPLICANT: Hartmann, Gunther

; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules

; TITLE OF INVENTION: for Activating Dendritic Cells

; FILE REFERENCE: C1039/7017

; CURRENT APPLICATION NUMBER: US/09/191,170

; CURRENT FILING DATE: 1998-11-13

; EARLIER APPLICATION NUMBER: US 08/960,774  
; EARLIER FILING DATE: 1997-10-30  
; EARLIER APPLICATION NUMBER: US 08/738,652  
; EARLIER FILING DATE: 1996-10-30  
; EARLIER APPLICATION NUMBER: US 08/386,063  
; EARLIER FILING DATE: 1995-02-07  
; EARLIER APPLICATION NUMBER: US 08/276,358  
; EARLIER FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 53  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide

US-09-191-170-53

Query Match 58.3%; Score 14; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 34

US-09-136-080E-45

; Sequence 45, Application US/09136080E

; Patent No. 6518017

; GENERAL INFORMATION:

; APPLICANT: Riley, Timothy A.

; APPLICANT: Brown, Bob D.

; APPLICANT: Arnold, Lyle J.

; TITLE OF INVENTION: COMBINATORIAL ANTISENSE LIBRARY

; FILE REFERENCE: OASBIO.003A

; CURRENT APPLICATION NUMBER: US/09/136,080E

; CURRENT FILING DATE: 1998-08-18

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 45

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic oligonucleotide

US-09-136-080E-45

Query Match 58.3%; Score 14; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 35

US-09-690-921-2

; Sequence 2, Application US/09690921

; Patent No. 6544518

; GENERAL INFORMATION:

; APPLICANT: Friede, Martin

; APPLICANT: Gerard, Catherine

; APPLICANT: Hermand, Philippe

; TITLE OF INVENTION: Vaccines

; FILE REFERENCE: B45181-1

; CURRENT APPLICATION NUMBER: US/09/690,921

; CURRENT FILING DATE: 2000-10-18

; PRIOR APPLICATION NUMBER: PCT/EP00/02920

; PRIOR FILING DATE: 2000-04-04

; PRIOR APPLICATION NUMBER: 09/301,829

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; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
; US-09-690-921-2

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 36
US-09-301-829A-2
; Sequence 2, Application US/09301829A
; Patent No. 6558670
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Hermand, Philippe
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: B45181
; CURRENT APPLICATION NUMBER: US/09/301,829A
; CURRENT FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: GB9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunostimulatory oligonucleotide sequence comprising
; OTHER INFORMATION: one or more CpG motifs
US-09-301-829A-2

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 37
US-09-249-247-218
; Sequence 218, Application US/09249247
; Patent No. 6593305
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; FILE REFERENCE: 032396-023
; CURRENT APPLICATION NUMBER: US/09/249,247
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: US 60/023,040
; EARLIER FILING DATE: 1996-08-02
; EARLIER APPLICATION NUMBER: US 60/039,959
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: US 08/904,901
; EARLIER FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
;

; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
; US-09-690-921-2

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 38
US-09-337-619-45
; Sequence 45, Application US/09337619
; Patent No. 6653292
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; FILE REFERENCE: C1039/7021/HCL
; CURRENT APPLICATION NUMBER: US/09/337,619
; CURRENT FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-337-619-45

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 39
US-09-835-370-21
; Sequence 21, Application US/09835370
; Patent No. 6777544
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: WILL, DAVID W
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
; FILE REFERENCE: 02481.1742 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/835,370
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; SEQ ID NO 218
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
; US-09-249-247-218

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 38
US-09-337-619-45
; Sequence 45, Application US/09337619
; Patent No. 6653292
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; FILE REFERENCE: C1039/7021/HCL
; CURRENT APPLICATION NUMBER: US/09/337,619
; CURRENT FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-337-619-45

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 39
US-09-835-370-21
; Sequence 21, Application US/09835370
; Patent No. 6777544
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: WILL, DAVID W
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
; FILE REFERENCE: 02481.1742 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/835,370
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: nucleotide  
; OTHER INFORMATION: base sequence of PNA derivatives that bind to  
; OTHER INFORMATION: viral and cellular targets  
US-09-835-370-21

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
|||||  
Db 5 CCAGCGTGGCCAT 18

## RESULT 40

US-09-634-320-7/c  
; Sequence 7, Application US/09634320  
; Patent No. 6822086  
; GENERAL INFORMATION:  
; APPLICANT: Papisov, Mikhail, I.  
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF  
; FILE REFERENCE: 0838.1003-001  
; CURRENT APPLICATION NUMBER: US/09/634,320  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: US 60/147,919  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-634-320-7

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
|||||  
Db 14 CCAGCGTGGCCAT 1

## RESULT 41

US-09-654-373-14  
; Sequence 14, Application US/09654373  
; Patent No. 6835395  
; GENERAL INFORMATION:

; APPLICANT: SEMPLE, Sean C.  
; Klimuk, Sandra K.  
; Harasym, Troy O.  
; Dos Santos, Nancy  
; Ansell, Steven M.  
; Cullis, Pieter R.  
; Hope, Michael J.  
; Scherrer, Peter  
; McIntosh, Deidre  
; Wong, Kim F.  
; TITLE OF INVENTION: Small Multilamellar Oligodeoxynucleotide-Containing Lipid Vesicles and Method of Making Same

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: Oppedahl & Larson LLP  
STREET: PO Box 5068  
CITY: Dillon  
STATE: CO  
COUNTRY: USA  
ZIP: 80435-5068  
COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/654,373  
; FILING DATE: 01-Sep-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/152,179  
; FILING DATE: SEPTEMBER 2, 1999  
; APPLICATION NUMBER: 09/078,954  
; FILING DATE: MAY 14, 1998  
; APPLICATION NUMBER: 08/856,374  
; FILING DATE: MAY 14, 1997  
; ATTORNEY/AGENT INFORMATION:

; NAME: Marina T. Larson  
; REGISTRATION NUMBER: 32,038  
; REFERENCE/DOCKET NUMBER: INEX.P-007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (970) 468-6600  
; TELEFAX: (970) 468-0104  
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: no  
; ANTI-SENSE: Yes  
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-654-373-14

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
|||||  
Db 5 CCAGCGTGGCCAT 18

## RESULT 42

US-09-724-425-17  
; Sequence 17, Application US/09724425  
; Patent No. 6841541  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION  
; FILE REFERENCE: 04040/1200990-US7  
; CURRENT APPLICATION NUMBER: US/09/724,425  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/375,514  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: US 09/080,285  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: US 08/465,485  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: US 08/124,256  
; PRIOR FILING DATE: 1993-09-20  
; PRIOR APPLICATION NUMBER: US 07/840,716  
; PRIOR FILING DATE: 1992-02-21  
; PRIOR APPLICATION NUMBER: US 07/288,692  
; PRIOR FILING DATE: 1988-12-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-425-17





;; TITLE OF INVENTION: Oligonucleotides Via the Alimentary Canal  
;; NUMBER OF SEQUENCES: 132  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6887906ris LLP  
;; STREET: One Liberty Place, 46th Floor  
;; CITY: Philadelphia  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19103  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
;; COMPUTER: IBM PS/2  
;; OPERATING SYSTEM: PC-DOS  
;; SOFTWARE: WORDPERFECT 6.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/108,673A  
;; FILING DATE: July 1, 1998  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/886,829  
;; FILING DATE: 01-JUL-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Paul K. Legaard  
;; REGISTRATION NUMBER: 38,534  
;; REFERENCE/DOCKET NUMBER: ISIS-3105  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 568-3100  
;; TELEFAX: (215) 568 3439  
;; INFORMATION FOR SEQ ID NO: 34:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 base pairs  
;; TYPE: Nucleic Acid  
;; STRANDEDNESS: Single  
;; TOPOLOGY: Linear  
;; ANTI-SENSE: Yes  
;; FEATURE:  
;; OTHER INFORMATION: Antisense to bcl-2 mRNA; a.k.a. "BCL-2"  
;; PUBLICATION INFORMATION:  
;; DOCUMENT NUMBER: WO 95/08350 (SEQ ID NO:17)  
;; FILING DATE: 20-SEP-1994  
;; PUBLICATION DATE: 30-MAR-1995  
;; US-09-108-673A-34

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCAT 18

RESULT 47  
US-09-835-371-21  
; Sequence 21, Application US/09835371  
; Patent No. 6905820  
; GENERAL INFORMATION:  
; APPLICANT: UHLMANN, Eugen  
; APPLICANT: BREIPOHL, Gerhard  
; APPLICANT: WILL, David W  
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND  
; TITLE OF INVENTION: PROCESSES FOR PREPARING THEM  
; FILE REFERENCE: 02481.1743 SEQUENCE LISTING  
; CURRENT APPLICATION NUMBER: US/09/835,371  
; CURRENT FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: base sequence

;; OTHER INFORMATION: of PNA targeting CMV  
US-09-835-371-21

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCAT 18

RESULT 48  
US-09-954-987B-115  
; Sequence 115, Application US/09954987B  
; Patent No. 6943240  
; GENERAL INFORMATION:  
; APPLICANT: Stefan Bauer  
; APPLICANT: Grayson B. Lipford  
; APPLICANT: Hermann Wagner  
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF  
; TITLE OF INVENTION: CPG-BASED IMMUNO-AGONIST/ANTAGONIST  
; FILE REFERENCE: C1041/7016 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/954,987B  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: US 60/233,035  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: US 60/263,657  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: US 60/291,726  
; PRIOR FILING DATE: 2001-05-17  
; PRIOR APPLICATION NUMBER: US 60/300,210  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 230  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 115  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
; US-09-954-987B-115

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCAT 18

RESULT 49  
US-09-672-126B-110  
; Sequence 110, Application US/09672126B  
; Patent No. 6949520  
; GENERAL INFORMATION:  
; APPLICANT: Hartmann, Gunther  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Krieg, Arthur  
; TITLE OF INVENTION: Methods Related to Immunostimulatory  
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon  
; FILE REFERENCE: C1039/7044  
; CURRENT APPLICATION NUMBER: US/09/672,126B  
; CURRENT FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/156,147  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 110  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-672-126B-110
  Query Match      58.3%; Score 14; DB 3; Length 18;
  Best Local Similarity 100.0%; Pred. No. 5.8e+03;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGC GCCAT 19
      |||||
Db      5 CCAGCGTGC GCCAT 18

RESULT 50
US-09-634-320-8
; Sequence 8, Application US/09634320
; Patent No. 6822086
; GENERAL INFORMATION:
; APPLICANT: Papisov, Mikhail, I.
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 0838.1003-001
; CURRENT APPLICATION NUMBER: US/09/634.320
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 2000-08-09
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; OTHER INFORMATION: c indicates an RNA base
US-09-634-320-8
  Query Match      58.3%; Score 14; DB 3; Length 19;
  Best Local Similarity 100.0%; Pred. No. 5.8e+03;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGC GCCAT 19
      |||||
Db      5 CCAGCGTGC GCCAT 18

Search completed: February 15, 2006, 21:14:18
Job time : 57.9504 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 01:43:22 ; Search time 348.298 Seconds  
(without alignments)  
569.815 Million cell updates/sec

Title: US-09-669-187A-81

Perfect score: 24

Sequence: 1 ggggtccagctgcgcattggggg 24

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 300 summaries

Database : Published Applications NA Main:

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- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 24    | 100.0       | 24     | 3  | US-09-888-326-440    |
| 2          | 24    | 100.0       | 24     | 3  | US-09-776-479-81     |
| 3          | 24    | 100.0       | 24     | 3  | US-09-776-479-81     |
| 4          | 24    | 100.0       | 24     | 5  | US-10-112-653-75     |
| 5          | 24    | 100.0       | 24     | 5  | US-10-017-995-81     |
| 6          | 24    | 100.0       | 24     | 6  | US-10-314-578-81     |
| 7          | 24    | 100.0       | 24     | 8  | US-10-831-778-81     |
| 8          | 16.2  | 67.5        | 25     | 5  | US-10-005-073-1      |
| 9          | 15.4  | 64.2        | 25     | 7  | US-10-713-956-368311 |
| 10         | 15.2  | 63.3        | 25     | 9  | US-10-809-189-107962 |
| 11         | 15.2  | 63.3        | 25     | 9  | US-10-956-157-200607 |
| 12         | 15.2  | 63.3        | 25     | 10 | US-11-036-317-240612 |
| 13         | 15.2  | 63.3        | 25     | 10 | US-11-036-317-827644 |
| 14         | 15.2  | 63.3        | 35     | 3  | US-09-875-453-69     |
| 15         | 15    | 62.5        | 16     | 3  | US-09-888-326-533    |
| 16         | 15    | 62.5        | 16     | 3  | US-09-776-479-90     |
| 17         | 15    | 62.5        | 16     | 3  | US-09-776-479-90     |
| 18         | 15    | 62.5        | 16     | 5  | US-10-112-653-84     |
| 19         | 15    | 62.5        | 16     | 5  | US-10-017-995-90     |
| 20         | 15    | 62.5        | 16     | 6  | US-10-314-578-90     |
| 21         | 15    | 62.5        | 16     | 8  | US-10-831-778-90     |
| 22         | 15    | 62.5        | 25     | 5  | US-10-098-263B-96172 |
| 23         | 15    | 62.5        | 29     | 3  | US-09-817-387-12     |
|            |       |             |        |    | Sequence 440, App    |
|            |       |             |        |    | Sequence 81, Appl    |
|            |       |             |        |    | Sequence 81, Appl    |
|            |       |             |        |    | Sequence 75, Appl    |
|            |       |             |        |    | Sequence 81, Appl    |
|            |       |             |        |    | Sequence 81, Appl    |
|            |       |             |        |    | Sequence 81, Appl    |
|            |       |             |        |    | Sequence 1, Appl     |
|            |       |             |        |    | Sequence 368311,     |
|            |       |             |        |    | Sequence 107962,     |
|            |       |             |        |    | Sequence 200607,     |
|            |       |             |        |    | Sequence 240612,     |
|            |       |             |        |    | Sequence 827644,     |
|            |       |             |        |    | Sequence 69, Appl    |
|            |       |             |        |    | Sequence 533, App    |
|            |       |             |        |    | Sequence 90, Appl    |
|            |       |             |        |    | Sequence 84, Appl    |
|            |       |             |        |    | Sequence 90, Appl    |
|            |       |             |        |    | Sequence 90, Appl    |
|            |       |             |        |    | Sequence 90, Appl    |
|            |       |             |        |    | Sequence 90, Appl    |
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|            |       |             |        |    | Sequence 96172, A    |
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| c 41 | 14.4 | 60.0 | 25 | 10 | US-11-036-317-531172 | Sequence 531172,  |
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| 43   | 14.4 | 60.0 | 25 | 10 | US-11-036-317-937038 | Sequence 937038,  |
| 44   | 14.4 | 60.0 | 25 | 10 | US-11-036-317-942273 | Sequence 942273,  |
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| c 46 | 14.4 | 60.0 | 32 | 7  | US-10-287-321-3      | Sequence 3, Appl  |
| 47   | 14.4 | 60.0 | 34 | 6  | US-10-053-645A-33    | Sequence 33, Appl |
| 48   | 14.4 | 60.0 | 34 | 6  | US-10-053-645A-35    | Sequence 35, Appl |
| 49   | 14.4 | 60.0 | 34 | 6  | US-10-053-645A-41    | Sequence 41, Appl |
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| 64   | 14   | 58.3 | 16 | 10 | US-11-021-729-51     | Sequence 51, Appl |
| 65   | 14   | 58.3 | 16 | 10 | US-11-021-729-52     | Sequence 52, Appl |
| 66   | 14   | 58.3 | 17 | 10 | US-11-021-729-41     | Sequence 41, Appl |
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| c 72 | 14   | 58.3 | 18 | 3  | US-09-965-116A-7     | Sequence 7, Appl  |
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| 75   | 14   | 58.3 | 18 | 3  | US-09-965-116A-99    | Sequence 99, Appl |
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| 79   | 14   | 58.3 | 18 | 3  | US-09-920-313-51     | Sequence 51, Appl |
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| 102 | 14 | 58.3 | 18 | 5 | US-10-017-995-91  | Sequence 91, Appl | 175 | 14 | 58.3 | 18 | 8  | US-10-831-775-51   | Sequence 51, Appl  |
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| 112 | 14 | 58.3 | 18 | 6 | US-10-187-264A-45 | Sequence 45, Appl | 185 | 14 | 58.3 | 18 | 9  | US-10-961-458-17   | Sequence 24, Appl  |
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| 117 | 14 | 58.3 | 18 | 6 | US-10-053-645A-24 | Sequence 24, Appl | 190 | 14 | 58.3 | 18 | 9  | US-10-972-301-51   | Sequence 51, Appl  |
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| 130 | 14 | 58.3 | 18 | 6 | US-10-437-275-24  | Sequence 24, Appl | 203 | 14 | 58.3 | 18 | 10 | US-11-021-729-1    | Sequence 1, Appl   |
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| 157 | 14 | 58.3 | 18 | 8 | US-10-694-075-98  | Sequence 98, Appl | 230 | 14 | 58.3 | 28 | 3  | Sequence 356907, S | Sequence 356907, S |
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| 167 | 14 | 58.3 | 18 | 8 | US-10-858-658-21  | Sequence 21, Appl | 240 | 14 | 58.3 | 32 | 8  | Sequence 78, Appl  | Sequence 78, Appl  |
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; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
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RESULT 4
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; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
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; NUMBER OF SEQ ID NOS: 1040
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RESULT 5
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; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-16
; PRIOR APPLICATION NUMBER: US 60/255,534
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; NUMBER OF SEQ ID NOS: 1093
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RESULT 6
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; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-81

Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCATGGGG 24
Db 1 GGGTCCAGCGTGGCCATGGGG 24

RESULT 7
US-10-831-778-81
; Sequence 81, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence

```

US-10-831-778-81

Query Match 100.0%; Score 24; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Gaps 0;  
Matches 24; Conservative 0; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGCCTATGGGG 24  
Db 1 GGGTCCAGCGTGCCTATGGGG 24

RESULT 8

US-10-005-073-1  
; Sequence 1, Application US/10005073  
; Publication No. US20020090371A1  
; GENERAL INFORMATION:  
; APPLICANT: Jevnikar, Anthony M.  
; Ma, Shengwu  
; Stiller, Calvin R.  
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING  
; IMMUNE RESPONSES IN MAMMALS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.  
; STREET: George Mason Building, 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314-3187

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/005,073  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/617,874  
; FILING DATE: 21-MAY-1996

ATTORNEY/AGENT INFORMATION:  
; NAME: Rea, Teresa Stanek  
; REGISTRATION NUMBER: 30,427  
; REFERENCE/DOCKET NUMBER: 024916-002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA - primer"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-005-073-1  
Query Match 67.5%; Score 16.2; DB 5; Length 25;  
Best Local Similarity 85.7%; Pred. No. 3.4e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCCTATGGG 22  
Db 2 GGATCCGGCGCGCCATGGG 22

RESULT 9

US-10-719-956-36811/c  
; Sequence 36811, Application US/10719956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 368311  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-368311

Query Match 64.2%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 7.4e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 GGTCCAGCGTGCCTATGG 19  
Db 18 GTTCCAGCGTGCCTATGG 2

RESULT 10

US-10-809-189-107962  
; Sequence 107962, Application US/10809189  
; Publication No. US20050048531A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/10/809,189  
; CURRENT FILING DATE: 2004-03-25  
; PRIOR APPLICATION NUMBER: US/09/396,196  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 107962  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-10-809-189-107962

Query Match 63.3%; Score 15.2; DB 9; Length 25;  
Best Local Similarity 85.0%; Pred. No. 9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 3 GGTCCAGCGTGCCTATGGG 22  
Db 1 GTTCCAGCGTGCCTATGGG 20

RESULT 11

US-10-956-157-200607/c  
; Sequence 200607, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 200607

; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-200607

Query Match 63.3%; Score 15.2; DB 9; Length 25;  
Best Local Similarity 85.0%; Pred. No. 9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCGCCATGG 21  
|||||  
Db 20 GGGTCCAGCATTTGCCCATGG 1

## RESULT 12

US-11-036-317-240612/c  
; Sequence 240612, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 240612  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-240612

Query Match 63.3%; Score 15.2; DB 10; Length 25;  
Best Local Similarity 85.0%; Pred. No. 9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCGCCATGG 21  
|||||  
Db 20 GGGTCCGCGTGCGCACTGG 1

## RESULT 13

US-11-036-317-827644/c  
; Sequence 827644, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 827644  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-827644

Query Match 63.3%; Score 15.2; DB 10; Length 25;  
Best Local Similarity 85.0%; Pred. No. 9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCGCCATGG 21  
|||||  
Db 23 GGGGCGCTCGTTCGCCATGG 4

## RESULT 14

US-09-875-453-69/c  
; Sequence 69, Application US/09875453  
; Publication No. US20030027320A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jungsuuh P.  
; APPLICANT: Starr, Douglas B.  
; APPLICANT: Tam, Albert W.  
; APPLICANT: Laurance, Megan E.  
; APPLICANT: Michelotti, Emil F.  
; APPLICANT: Velligan, Mark D.  
; APPLICANT: Latour, Derek R.  
; APPLICANT: Thomas, Rita L.  
; APPLICANT: Kongpachith, Ana  
; APPLICANT: Sheppard, Liana T.  
; APPLICANT: Lam, Moon Young  
; APPLICANT: Bruice, Thomas W.  
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION  
; FILE REFERENCE: 4600-0135.30  
; CURRENT APPLICATION NUMBER: US/09/875,453  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/209,549  
; PRIOR FILING DATE: 2000-06-06  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-09-875-453-69

Query Match 63.3%; Score 15.2; DB 3; Length 35;  
Best Local Similarity 85.0%; Pred. No. 8.3e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCGCCATGG 21  
|||||  
Db 28 GGGTCCAGCGGAGCCATGG 9

## RESULT 15

US-09-888-326-533  
; Sequence 533, Application US/09888326  
; Publication No. US20030026801A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Hartmann, Gunther  
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
; TITLE OF INVENTION: Cell Lysis and Treating Cancer  
; FILE REFERENCE: C1039/7052 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/888,326  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/213,346  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 848  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 533  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone  
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends  
US-09-888-326-533

Query Match 62.5%; Score 15; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;



Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
Db 1 TCCAGCGTGC GCCAT 15

## RESULT 16

US-09-776-479-90  
; Sequence 90, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 90  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-90

Query Match 62.5%; Score 15; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
Db 1 TCCAGCGTGC GCCAT 15

## RESULT 17

US-09-776-479-90  
; Sequence 90, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 90  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-90

Query Match 62.5%; Score 15; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
Db 1 TCCAGCGTGC GCCAT 15

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 18  
US-10-112-653-84  
; Sequence 84, Application US/10112653  
; Publication No. US20030050268A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Daniel J.  
; APPLICANT: Beig, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR  
; FILE REFERENCE: C01039/70060(AWS)  
; CURRENT APPLICATION NUMBER: US/10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 84  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-112-653-84

Query Match 62.5%; Score 15; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
Db 1 TCCAGCGTGC GCCAT 15

## RESULT 19

US-10-017-995-90  
; Sequence 90, Application US/10017995  
; Publication No. US20030055014A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
; FILE REFERENCE: C1037/7025 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/017,995  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,534  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 90  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-90

Query Match 62.5%; Score 15; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
Db 1 TCCAGCGTGC GCCAT 15

## RESULT 20

US-10-314-578-90  
; Sequence 90, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Daniel J.  
; APPLICANT: Schetter, Christian

; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
; FILE REFERENCE: C1039/7035 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/314,578  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/156,113  
; PRIOR FILING DATE: 1999-09-25  
; PRIOR APPLICATION NUMBER: US 60/156,135  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 60/227,436  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 1145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 90  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-90

Query Match 62.5%; Score 15; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGGCCCAT 19  
| | | | | | | | | | | | | | | | | |  
Db 1 TCCAGCGTGGCCCAT 15

## RESULT 21

US-10-831-778-90  
; Sequence 90, Application US/10831778  
; Publication No. US20040235774A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/831,778  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 90  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-90

Query Match 62.5%; Score 15; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGGCCCAT 19  
| | | | | | | | | | | | | | | | | |  
Db 1 TCCAGCGTGGCCCAT 15

## RESULT 22

US-10-098-263B-96172/c  
; Sequence 96172, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittleman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 96172  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-96172

Query Match 62.5%; Score 15; DB 5; Length 25;  
Best Local Similarity 78.3%; Pred. No. 1.1e+04;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGGG 23  
| | | | | | | | | | | | | | | | | |  
Db 24 GGAGTCCACAGTCCGCCACGGGG 2

## RESULT 23

US-09-817-387-12  
; Sequence 12, Application US/09817387  
; Patent No. US20010039263A1  
; GENERAL INFORMATION:  
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin  
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof  
; FILE REFERENCE: 101195-24  
; CURRENT APPLICATION NUMBER: US/09/817,387  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: DE 197 20 151.2  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:  
; OTHER INFORMATION: oligonucleotide  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotides, linkages between positions 1  
; OTHER INFORMATION: to 18 are phosphorothioates, linkages between  
; OTHER INFORMATION: positions 18 to 26 are phosphodiester  
; OTHER INFORMATION: positions 19 to 29 carry 2'-OCH3 modified ribosyl  
; OTHER INFORMATION: residues  
; OTHER INFORMATION: linkages between positions 26 to 29 are  
; OTHER INFORMATION: phosphorothioates  
US-09-817-387-12

Query Match 62.5%; Score 15; DB 3; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCATG 20  
| | | | | | | | | | | | | | | | | |  
Db 5 CCAGCGTGGCCCATG 19

## RESULT 24

US-10-719-900-91312  
; Sequence 91312, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 91312
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-91312

Query Match      61.7%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 CAGCGTGCCTCCATGGGG 24
      ||||| ||||| ||||| |||||
Db      7 CAGCGTGCCTCCATGGCG 24

RESULT 25
US-10-098-263B-35445
; Sequence 35445, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 35445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-35445

Query Match      60.8%; Score 14.6; DB 5; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GTCCAGCGTGCCTCCATGGGG 24
      ||||| ||||| ||||| |||||
Db      1 GTCCACTGTGCTCCATGGGT 21

RESULT 26
US-10-098-263B-55179
; Sequence 55179, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 55179
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-55179

Query Match      60.8%; Score 14.6; DB 5; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GTCCAGCGTGCCTCCATGGGG 24
      ||||| ||||| ||||| |||||
Db      4 GTCCACTGTGCTCCATGGTG 24
```

```
RESULT 27
US-10-098-263B-87293
; Sequence 87293, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87293
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87293

Query Match      60.8%; Score 14.6; DB 5; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GTCCAGCGTGCCTCCATGGGG 24
      ||||| ||||| ||||| |||||
Db      3 GTCCACTGTGCTCCATGGGT 23

RESULT 28
US-10-098-263B-87909
; Sequence 87909, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87909

Query Match      60.8%; Score 14.6; DB 5; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GTCCAGCGTGCCTCCATGGGG 24
      ||||| ||||| ||||| |||||
Db      3 GTCCACTGTGCTCCATGGGT 23

RESULT 29
US-10-719-900-765784
; Sequence 765784, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 765784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-765784

Query Match      60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
   |||||
Db 4 GTGGACCAGATGGCCATGG 24

RESULT 30
US-10-719-900-765785
; Sequence 765785, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 765785
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-765785

Query Match      60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
   |||||
Db 4 GTGGACCAGATGGCCATGG 24

RESULT 31
US-11-036-317-773179/c
; Sequence 773179, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 773179
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-773179

Query Match      60.8%; Score 14.6; DB 10; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
   |||||
Db 22 GGGCTCCAGCATAGCCATGG 2

; SEQ ID NO 765784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-765784

Query Match      60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
   |||||
Db 4 GTGGACCAGATGGCCATGG 24

RESULT 32
US-09-866-073-5
; Sequence 5, Application US/09866073
; Patent No. US20020068272A1
; GENERAL INFORMATION:
; APPLICANT: Larocca, David
; APPLICANT: Baird, Andrew
; APPLICANT: Kassner, Paul
; TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR
; TITLE OF INVENTION: DETECTING AND IDENTIFYING PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT FACILITATE INTERNALIZATION
; TITLE OF INVENTION: AND TRANSGENE EXPRESSION AND CELLS OR TISSUE
; TITLE OF INVENTION: COMPETENT FOR THE SAME AND METHODS FOR EVOLVING
; TITLE OF INVENTION: GENE DELIVERY VECTORS
; FILE REFERENCE: 760100.430C4
; CURRENT APPLICATION NUMBER: US/09/866,073
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-866-073-5

Query Match      60.8%; Score 14.6; DB 3; Length 47;
Best Local Similarity 81.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
   |||||
Db 10 GGGTTCGCCGTGGCCATGG 30

RESULT 33
US-10-151-204-5
; Sequence 5, Application US/10151204
; Publication No. US20030148263A1
; GENERAL INFORMATION:
; APPLICANT: Larocca, David
; APPLICANT: Kassner, Paul
; APPLICANT: Baird, Andrew
; APPLICANT: Burg, Michael
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USING
; TITLE OF INVENTION: GENETIC PACKAGE DISPLAY
; FILE REFERENCE: 760100.430C5
; CURRENT APPLICATION NUMBER: US/10/151,204
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-151-204-5

Query Match      60.8%; Score 14.6; DB 6; Length 47;
Best Local Similarity 81.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
   |||||
Db 10 GGGTTCGCCGTGGCCATGG 30

RESULT 34
US-10-735-592-52
; Sequence 52, Application US/10735592
```

```
0; Gaps 0;
```

0; Gaps 0;

Gaps 0;

Mouse

Gaps 0;

Gaps 0:

```

RESULT 39
US-11-036-317-304181
; Sequence 304181, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 304181
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-304181

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGC GCC 17
| | | | | | | | | | | | | | |
Db 4 GCGTCCAGCGTGC GCC 19

RESULT 40
US-11-036-317-313397
; Sequence 313397, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 313397
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-313397

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGC GCC 17
| | | | | | | | | | | | | | |
Db 4 GCGTCCAGCGTGC GCC 19

RESULT 41
US-11-036-317-531172/c
; Sequence 531172, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 531172
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-531172

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGC GCC 17
| | | | | | | | | | | | | | |
Db 1 GCGTCCAGCGTGC GCC 16

RESULT 42
US-11-036-317-874107
; Sequence 874107, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 874107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-874107

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGC GCC 16
| | | | | | | | | | | | | | |
Db 23 GCGTCCAGCGTGC GCC 8

RESULT 43
US-11-036-317-937038
; Sequence 937038, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 937038
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-937038

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGC GCC 17
| | | | | | | | | | | | | | |
Db 2 GCGTCCAGCGTGC GCC 17

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Db      4 GCGTCCAGCGTGGGCC 19
|||||
RESULT 44
US-11-036-317-942273
; Sequence 942273, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 942273
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-942273
Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGGTCCAGCGTGGGCC 17
|||||
Db      1 GCGTCCAGCGTGGGCC 16
|||||

RESULT 45
US-10-909-436-127
; Sequence 127, Application US/10909436
; Publication No. US20050032103A1
; GENERAL INFORMATION:
; APPLICANT: AUJAME et al.
; TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic
; TITLE OF INVENTION: strains of the Neisseria genus
; FILE REFERENCE: P07180500/BAS
; CURRENT APPLICATION NUMBER: US/10/909,436
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: FR 98 13 693
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-909-436-127
Query Match      60.0%; Score 14.4; DB 8; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.9e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 GGGGTCCAGCGTGGCCATGGGG 24
|||||
Db      2 GGGATCCACCTGCTTCATGGGTG 25
|||||

RESULT 46
US-10-297-321-3/c
; Sequence 3, Application US/10297321
; Publication No. US20040072342A1
; GENERAL INFORMATION:
; APPLICANT: Bothwell, Alfred L. M.
; TITLE OF INVENTION: Pober, Jordan S.

```

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; APPLICANT: Schechner, Jeffrey S.
; APPLICANT: Zheng, Lian
; TITLE OF INVENTION: Production and Use of Microvessels in a
; TITLE OF INVENTION: Fibronectin-containing Gel
; FILE REFERENCE: 44574-5074-WO
; CURRENT APPLICATION NUMBER: US/10/297,321
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US 60/208,931
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/279,797
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5' end of
; OTHER INFORMATION: Bcl-2 cDNA
US-10-297-321-3
Query Match      60.0%; Score 14.4; DB 7; Length 32;
Best Local Similarity 93.8%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 AGCGTGGCCATGGGG 23
|||||
Db      32 AGCGTGGCCATGGTG 17
|||||

RESULT 47
US-10-053-645A-33
; Sequence 33, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
; APPLICANT: Robert E. Klem
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
; FILE REFERENCE: 10412-022-999
; CURRENT APPLICATION NUMBER: US/10/053,645A
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,244
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
; OTHER INFORMATION: Oligonucleotide
US-10-053-645A-33
Query Match      60.0%; Score 14.4; DB 6; Length 34;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCATGG 21
|||||
Db      13 CCAGCGTGGCCATTG 28
|||||

RESULT 48
US-10-053-645A-35
; Sequence 35, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
; APPLICANT: Robert E. Klem
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2

```

```
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
; FILE REFERENCE: 10412-022-999
; CURRENT APPLICATION NUMBER: US/10/053,645A
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,244
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
; OTHER INFORMATION: Oligonucleotide
US-10-053-645A-35

Query Match          60.0%; Score 14.4; DB 6; Length 34;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCATTG 21
Db      13 CCAGCGTGGCCATTG 28

RESULT 49
US-10-053-645A-41
; Sequence 41, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
; APPLICANT: Robert E. Klem
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
; FILE REFERENCE: 10412-022-999
; CURRENT APPLICATION NUMBER: US/10/053,645A
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,244
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
; OTHER INFORMATION: Oligonucleotide
US-10-053-645A-41

Query Match          60.0%; Score 14.4; DB 6; Length 34;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCATTG 21
Db      13 CCAGCGTGGCCATTG 28

RESULT 50
US-10-911-374-14
; Sequence 14, Application US/10911374
; Publication No. US20050003531A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Mahendra S
; APPLICANT: Mayer-Proschel, Margot
; APPLICANT: Kalyani, Anjali J
; TITLE OF INVENTION: Lineage-Restricted Neuronal Precursors
; FILE REFERENCE: T5530.CIP
; CURRENT APPLICATION NUMBER: US/10/911,374
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US/09/109,858
```

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 08/909,435
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-911-374-14

Query Match          59.2%; Score 14.2; DB 8; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.6e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GGTCCAGCGTGGCCATTG 21
Db      1 GGTCCAGCATTTGCCATTG 19

Search completed: February 16, 2006, 02:34:08
Job time : 352.298 secs
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 02:03:53 ; Search time 223.736 Seconds  
(without alignments)  
98.157 Million cell updates/sec

Title: US-09-669-187a-81

Perfect score: 24

Sequence: 1 ggggtccagctgcgcattggggg 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 11812030

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications NA New.\*

1: /cgn2\_6/ptodata/2/pubpna/US08 NEW PUB.seq.\*

2: /cgn2\_6/ptodata/2/pubpna/US06 NEW PUB.seq.\*

3: /cgn2\_6/ptodata/2/pubpna/US07 NEW PUB.seq.\*

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5: /cgn2\_6/ptodata/2/pubpna/US09 NEW PUB.seq.\*

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12: /cgn2\_6/ptodata/2/pubpna/US60 NEW PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description            |
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| 3          | 16    | 66.7        | 25     | 7  | US-10-310-914A-402269  |
| 4          | 16    | 66.7        | 30     | 11 | US-11-201-322-2        |
| 5          | 15.8  | 65.8        | 22     | 7  | US-10-310-914A-1185838 |
| 6          | 15.8  | 65.8        | 25     | 11 | US-11-121-849-235244   |
| 7          | 15.2  | 63.3        | 24     | 7  | US-10-310-914A-34498   |
| 8          | 15    | 62.5        | 16     | 11 | US-11-127-654-84       |
| 9          | 15    | 62.5        | 23     | 7  | US-10-310-914A-94891   |
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| 11         | 15    | 62.5        | 25     | 11 | US-11-121-849-46868    |
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| 13         | 14.6  | 60.8        | 21     | 7  | US-10-310-914A-45418   |
| 14         | 14.6  | 60.8        | 21     | 7  | US-10-310-914A-402274  |
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| 16         | 14.6  | 60.8        | 26     | 7  | US-10-310-914A-895311  |
| 17         | 14.4  | 60.0        | 21     | 7  | US-10-310-914A-650086  |
| 18         | 14.2  | 59.2        | 24     | 7  | US-10-310-914A-721320  |
| 19         | 14    | 58.3        | 18     | 6  | US-10-994-213-7        |
| 20         | 14    | 58.3        | 18     | 7  | US-10-918-638-24       |
| 21         | 14    | 58.3        | 18     | 7  | US-10-658-947-14       |

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| 18 | 7  | US-10-469-561-6        | 58.3 | 14 | 22 |
| 18 | 7  | US-10-619-279-45       | 58.3 | 14 | 23 |
| 18 | 7  | US-10-435-656-55       | 58.3 | 14 | 24 |
| 18 | 11 | US-11-127-654-1        | 58.3 | 14 | 25 |
| 18 | 11 | US-11-127-654-85       | 58.3 | 14 | 26 |
| 18 | 11 | US-11-081-140-6        | 58.3 | 14 | 27 |
| 18 | 11 | US-11-134-918-55       | 58.3 | 14 | 28 |
| 18 | 11 | US-11-031-460-55       | 58.3 | 14 | 29 |
| 18 | 11 | US-11-067-587-55       | 58.3 | 14 | 30 |
| 18 | 11 | US-11-099-683-131      | 58.3 | 14 | 31 |
| 18 | 11 | US-11-099-683-132      | 58.3 | 14 | 32 |
| 18 | 11 | US-10-994-213-8        | 58.3 | 14 | 33 |
| 19 | 6  | US-10-994-213-9        | 58.3 | 14 | 34 |
| 19 | 6  | US-10-994-213-9        | 58.3 | 14 | 35 |
| 20 | 11 | US-11-127-654-81       | 58.3 | 14 | 36 |
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| 22 | 6  | US-10-994-213-1        | 58.3 | 14 | 38 |
| 23 | 6  | US-10-994-213-2        | 58.3 | 14 | 39 |
| 23 | 7  | US-10-310-914A-903934  | 58.3 | 14 | 40 |
| 25 | 7  | US-10-310-914A-989919  | 58.3 | 14 | 41 |
| 25 | 11 | US-11-121-849-46867    | 58.3 | 14 | 42 |
| 25 | 11 | US-11-121-849-46870    | 58.3 | 14 | 43 |
| 26 | 7  | US-10-310-914A-1042200 | 58.3 | 14 | 44 |
| 32 | 7  | US-10-939-294A-19743   | 58.3 | 14 | 45 |
| 32 | 7  | US-10-310-914A-906465  | 58.3 | 14 | 46 |
| 32 | 7  | US-10-310-914A-775551  | 58.3 | 14 | 47 |
| 32 | 7  | US-10-310-914A-321695  | 58.3 | 14 | 48 |
| 32 | 7  | US-11-121-849-330122   | 58.3 | 14 | 49 |
| 45 | 11 | US-11-131-212-40       | 58.3 | 14 | 50 |
| 45 | 11 | US-10-310-914A-223305  | 58.3 | 14 | 51 |
| 45 | 11 | US-10-310-914A-463905  | 58.3 | 14 | 52 |
| 45 | 11 | US-10-310-914A-525207  | 58.3 | 14 | 53 |
| 45 | 11 | US-10-310-914A-730516  | 58.3 | 14 | 54 |
| 45 | 11 | US-10-310-914A-730698  | 58.3 | 14 | 55 |
| 45 | 11 | US-11-121-849-6783     | 58.3 | 14 | 56 |
| 45 | 11 | US-11-121-849-46865    | 58.3 | 14 | 57 |
| 45 | 11 | US-11-121-849-46866    | 58.3 | 14 | 58 |
| 45 | 11 | US-11-121-849-113926   | 58.3 | 14 | 59 |
| 45 | 11 | US-11-121-849-453841   | 58.3 | 14 | 60 |
| 45 | 11 | US-11-136-527-351013   | 58.3 | 14 | 61 |
| 45 | 11 | US-10-310-914A-329739  | 58.3 | 14 | 62 |
| 45 | 11 | US-10-310-914A-1168346 | 58.3 | 14 | 63 |
| 45 | 11 | US-10-310-914A-736160  | 58.3 | 14 | 64 |
| 45 | 11 | US-11-084-055B-39      | 58.3 | 14 | 65 |
| 45 | 11 | US-10-310-914A-546291  | 58.3 | 14 | 66 |
| 45 | 11 | US-10-310-914A-737406  | 58.3 | 14 | 67 |
| 45 | 11 | US-10-310-914A-494493  | 58.3 | 14 | 68 |
| 45 | 11 | US-10-310-914A-539891  | 58.3 | 14 | 69 |
| 45 | 11 | US-10-310-914A-555994  | 58.3 | 14 | 70 |
| 45 | 11 | US-10-310-914A-823540  | 58.3 | 14 | 71 |
| 45 | 11 | US-10-310-914A-859672  | 58.3 | 14 | 72 |
| 45 | 11 | US-10-310-914A-941262  | 58.3 | 14 | 73 |
| 45 | 11 | US-10-310-914A-989930  | 58.3 | 14 | 74 |
| 45 | 11 | US-10-310-914A-1049085 | 58.3 | 14 | 75 |
| 45 | 11 | US-10-310-914A-1049917 | 58.3 | 14 | 76 |
| 45 | 11 | US-10-310-914A-1326697 | 58.3 | 14 | 77 |
| 45 | 11 | US-10-310-914A-696427  | 58.3 | 14 | 78 |
| 45 | 11 | US-10-310-914A-737407  | 58.3 | 14 | 79 |
| 45 | 11 | US-10-310-914A-534446  | 58.3 | 14 | 80 |
| 45 | 11 | US-11-121-849-123315   | 58.3 | 14 | 81 |
| 45 | 11 | US-11-136-527-358202   | 58.3 | 14 | 82 |
| 45 | 11 | US-10-310-914A-494533  | 58.3 | 14 | 83 |
| 45 | 11 | US-10-310-914A-341462  | 58.3 | 14 | 84 |
| 45 | 11 | US-10-310-914A-895309  | 58.3 | 14 | 85 |
| 45 | 11 | US-10-310-914A-434517  | 58.3 | 14 | 86 |
| 45 | 11 | US-10-310-914A-423448  | 58.3 | 14 | 87 |
| 45 | 11 | US-10-310-914A-1287444 | 58.3 | 14 | 88 |
| 45 | 11 | US-10-310-914A-63526   | 58.3 | 14 | 89 |
| 45 | 11 | US-10-310-914A-982302  | 58.3 | 14 | 90 |
| 45 | 11 | US-10-310-914A-98172   | 58.3 | 14 | 91 |
| 45 | 11 | US-10-310-914A-344433  | 58.3 | 14 | 92 |
| 45 | 11 | US-10-310-914A-633399  | 58.3 | 14 | 93 |
| 45 | 11 | US-10-310-914A-633407  | 58.3 | 14 | 94 |

|                   |                   |                   |                   |                    |                   |                   |                   |                   |                    |                   |                   |                   |                 |                   |                   |                 |                 |                   |                   |                  |                   |                 |                 |                 |                 |                   |                 |                 |                 |                 |                 |                 |                   |                   |                 |                 |                 |                 |                  |                 |                   |                 |                 |                 |                 |                 |                 |                 |                 |                 |                  |                  |                  |                 |                 |                 |                 |                 |                 |                 |                 |                 |                 |                  |                   |                 |                   |                 |                 |                 |
|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|-----------------|-----------------|-------------------|-------------------|------------------|-------------------|-----------------|-----------------|-----------------|-----------------|-------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-------------------|-------------------|-----------------|-----------------|-----------------|-----------------|------------------|-----------------|-------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|------------------|------------------|------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|------------------|-------------------|-----------------|-------------------|-----------------|-----------------|-----------------|
| Sequence 6, Appli | Sequence 45, Appl | Sequence 55, Appl | Sequence 1, Appli | Sequence 85, Appli | Sequence 6, Appli | Sequence 55, Appl | Sequence 55, Appl | Sequence 11, Appl | Sequence 132, Appl | Sequence 8, Appli | Sequence 9, Appli | Sequence 81, Appl | Sequence 100840 | Sequence 1, Appli | Sequence 2, Appli | Sequence 903934 | Sequence 989919 | Sequence 46867, A | Sequence 46870, A | Sequence 1042200 | Sequence 19743, A | Sequence 908465 | Sequence 775551 | Sequence 321695 | Sequence 330122 | Sequence 40, Appl | Sequence 223305 | Sequence 463905 | Sequence 525207 | Sequence 730516 | Sequence 730698 | Sequence 525225 | Sequence 6783, Ap | Sequence 46865, A | Sequence 113926 | Sequence 453841 | Sequence 351013 | Sequence 329739 | Sequence 1168346 | Sequence 736160 | Sequence 39, Appl | Sequence 546291 | Sequence 737406 | Sequence 494493 | Sequence 539891 | Sequence 555994 | Sequence 823540 | Sequence 859672 | Sequence 941262 | Sequence 989930 | Sequence 1049085 | Sequence 1049917 | Sequence 1326697 | Sequence 696427 | Sequence 737407 | Sequence 534446 | Sequence 123315 | Sequence 358202 | Sequence 494533 | Sequence 341462 | Sequence 895309 | Sequence 434517 | Sequence 423448 | Sequence 1287444 | Sequence 63526, A | Sequence 982302 | Sequence 98172, A | Sequence 344433 | Sequence 633399 | Sequence 633407 |
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|       |      |      |    |    |                        |                   |       |      |      |    |    |                        |                   |
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| c 96  | 13.2 | 55.0 | 25 | 7  | US-10-310-914A-952672  | Sequence 952672,  | c 169 | 12.8 | 53.3 | 25 | 7  | US-10-310-914A-124102  | Sequence 124102,  |
| 97    | 13.2 | 55.0 | 25 | 11 | US-11-121-849-46863    | Sequence 46863, A | c 170 | 12.8 | 53.3 | 25 | 7  | US-10-310-914A-654008  | Sequence 654008,  |
| c 98  | 13.2 | 55.0 | 25 | 11 | US-11-121-849-46864    | Sequence 46864, A | c 171 | 12.8 | 53.3 | 25 | 7  | US-10-310-914A-880056  | Sequence 880056,  |
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| c 100 | 13.2 | 55.0 | 25 | 11 | US-11-121-849-218741   | Sequence 218741,  | c 173 | 12.8 | 53.3 | 25 | 7  | US-10-310-914A-1108583 | Sequence 1108583, |
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| c 102 | 13.2 | 55.0 | 25 | 11 | US-11-121-849-530933   | Sequence 530933,  | c 175 | 12.8 | 53.3 | 25 | 11 | US-11-121-849-115647   | Sequence 115647,  |
| c 103 | 13.2 | 55.0 | 25 | 11 | US-11-121-849-610833   | Sequence 610833,  | c 176 | 12.8 | 53.3 | 25 | 11 | US-11-121-849-119305   | Sequence 119305,  |
| c 104 | 13.2 | 55.0 | 25 | 11 | US-11-136-527-322812   | Sequence 322812,  | c 177 | 12.8 | 53.3 | 25 | 11 | US-11-121-849-152114   | Sequence 152114,  |
| c 105 | 13.2 | 55.0 | 25 | 11 | US-11-136-527-322827   | Sequence 322827,  | c 178 | 12.8 | 53.3 | 25 | 11 | US-11-121-849-277491   | Sequence 277491,  |
| c 106 | 13.2 | 55.0 | 32 | 7  | US-10-939-294A-17085   | Sequence 17085, A | c 179 | 12.8 | 53.3 | 25 | 11 | US-11-121-849-477615   | Sequence 477615,  |
| c 107 | 13.2 | 55.0 | 32 | 7  | US-10-939-294A-19184   | Sequence 19184, A | c 180 | 12.8 | 53.3 | 25 | 11 | US-11-121-849-495760   | Sequence 495760,  |
| c 108 | 13.2 | 55.0 | 32 | 7  | US-10-939-294A-19322   | Sequence 19322, A | c 181 | 12.8 | 53.3 | 25 | 11 | US-11-121-849-531561   | Sequence 531561,  |
| c 109 | 13.2 | 55.0 | 32 | 7  | US-10-939-294A-19614   | Sequence 19614, A | c 182 | 12.8 | 53.3 | 25 | 11 | US-11-121-849-561885   | Sequence 561885,  |
| c 110 | 13   | 54.2 | 18 | 7  | US-10-310-914A-1145446 | Sequence 1145446, | c 183 | 12.8 | 53.3 | 25 | 11 | US-11-121-849-662630   | Sequence 662630,  |
| c 111 | 13   | 54.2 | 21 | 7  | US-10-310-914A-650092  | Sequence 650092,  | c 184 | 12.8 | 53.3 | 25 | 11 | US-11-136-527-202901   | Sequence 202901,  |
| c 112 | 13   | 54.2 | 21 | 7  | US-10-310-914A-999814  | Sequence 999814,  | c 185 | 12.8 | 53.3 | 25 | 11 | US-11-136-527-213830   | Sequence 213830,  |
| c 113 | 13   | 54.2 | 21 | 7  | US-10-310-914A-1326696 | Sequence 1326696, | c 186 | 12.8 | 53.3 | 25 | 11 | US-10-310-914A-456437  | Sequence 456437,  |
| c 114 | 13   | 54.2 | 21 | 7  | US-10-310-914A-1349496 | Sequence 1349496, | c 187 | 12.8 | 53.3 | 26 | 7  | US-10-310-914A-584159  | Sequence 584159,  |
| c 115 | 13   | 54.2 | 21 | 7  | US-10-310-914A-1353255 | Sequence 1353255, | c 188 | 12.8 | 53.3 | 27 | 7  | US-10-310-914A-16826   | Sequence 16826, A |
| c 116 | 13   | 54.2 | 22 | 7  | US-10-310-914A-247384  | Sequence 247384,  | c 189 | 12.8 | 53.3 | 32 | 7  | US-10-939-294A-19144   | Sequence 19144, A |
| c 117 | 13   | 54.2 | 22 | 7  | US-10-310-914A-419193  | Sequence 419193,  | c 190 | 12.8 | 53.3 | 32 | 7  | US-10-310-914A-143463  | Sequence 143463,  |
| c 118 | 13   | 54.2 | 22 | 7  | US-10-310-914A-43799   | Sequence 443799,  | c 191 | 12.6 | 52.5 | 19 | 7  | US-10-310-914A-329734  | Sequence 329734,  |
| c 119 | 13   | 54.2 | 22 | 7  | US-10-310-914A-919447  | Sequence 919447,  | c 192 | 12.6 | 52.5 | 19 | 7  | US-10-310-914A-45398   | Sequence 45398, A |
| c 120 | 13   | 54.2 | 23 | 7  | US-10-310-914A-192445  | Sequence 192445,  | c 193 | 12.6 | 52.5 | 20 | 7  | US-10-310-914A-362430  | Sequence 362430,  |
| c 121 | 13   | 54.2 | 23 | 7  | US-10-310-914A-373241  | Sequence 373241,  | c 194 | 12.6 | 52.5 | 20 | 7  | US-10-310-914A-949114  | Sequence 949114,  |
| c 122 | 13   | 54.2 | 23 | 7  | US-10-310-914A-779267  | Sequence 779267,  | c 195 | 12.6 | 52.5 | 20 | 7  | US-10-310-914A-996597  | Sequence 996597,  |
| c 123 | 13   | 54.2 | 23 | 7  | US-10-310-914A-779288  | Sequence 779288,  | c 196 | 12.6 | 52.5 | 20 | 7  | US-10-310-914A-965917  | Sequence 965917,  |
| c 124 | 13   | 54.2 | 23 | 7  | US-10-310-914A-854057  | Sequence 854057,  | c 197 | 12.6 | 52.5 | 21 | 7  | US-10-310-914A-313024  | Sequence 313024,  |
| c 125 | 13   | 54.2 | 24 | 7  | US-10-310-914A-543153  | Sequence 543153,  | c 198 | 12.6 | 52.5 | 21 | 11 | US-11-099-683-106      | Sequence 106, App |
| c 126 | 13   | 54.2 | 25 | 7  | US-10-310-914A-1120422 | Sequence 1120422, | c 199 | 12.6 | 52.5 | 22 | 7  | US-10-310-914A-227730  | Sequence 227730,  |
| c 127 | 13   | 54.2 | 25 | 7  | US-10-310-914A-1145447 | Sequence 1145447, | c 200 | 12.6 | 52.5 | 22 | 7  | US-10-310-914A-313230  | Sequence 313230,  |
| c 128 | 13   | 54.2 | 25 | 11 | US-11-121-849-46871    | Sequence 46871, A | c 201 | 12.6 | 52.5 | 22 | 7  | US-10-310-914A-338152  | Sequence 338152,  |
| c 129 | 13   | 54.2 | 25 | 11 | US-11-121-849-58477    | Sequence 58477, A | c 202 | 12.6 | 52.5 | 22 | 7  | US-10-310-914A-53929   | Sequence 53929,   |
| c 130 | 13   | 54.2 | 25 | 11 | US-11-121-849-111933   | Sequence 111933,  | c 203 | 12.6 | 52.5 | 22 | 7  | US-10-310-914A-53929   | Sequence 53929,   |
| c 131 | 13   | 54.2 | 25 | 11 | US-11-121-849-151665   | Sequence 151665,  | c 204 | 12.6 | 52.5 | 22 | 7  | US-10-310-914A-1059406 | Sequence 1059406, |
| c 132 | 13   | 54.2 | 25 | 11 | US-11-121-849-274533   | Sequence 274533,  | c 205 | 12.6 | 52.5 | 22 | 7  | US-10-310-914A-1353243 | Sequence 1353243, |
| c 133 | 13   | 54.2 | 25 | 11 | US-11-121-849-429863   | Sequence 429863,  | c 206 | 12.6 | 52.5 | 23 | 7  | US-10-310-914A-63757   | Sequence 63757, A |
| c 134 | 13   | 54.2 | 25 | 11 | US-11-136-527-272460   | Sequence 272460,  | c 207 | 12.6 | 52.5 | 23 | 7  | US-10-310-914A-81055   | Sequence 81055, A |
| c 135 | 13   | 54.2 | 26 | 7  | US-10-310-914A-252968  | Sequence 252968,  | c 208 | 12.6 | 52.5 | 23 | 7  | US-10-310-914A-81072   | Sequence 81072, A |
| c 136 | 13   | 54.2 | 26 | 7  | US-10-310-914A-1145495 | Sequence 1145495, | c 209 | 12.6 | 52.5 | 23 | 7  | US-10-310-914A-313223  | Sequence 313223,  |
| c 137 | 13   | 54.2 | 26 | 7  | US-10-939-294A-15978   | Sequence 15978, A | c 210 | 12.6 | 52.5 | 23 | 7  | US-10-310-914A-313245  | Sequence 313245,  |
| c 138 | 13   | 54.2 | 32 | 7  | US-10-939-294A-17843   | Sequence 17843, A | c 211 | 12.6 | 52.5 | 23 | 7  | US-10-310-914A-525260  | Sequence 525260,  |
| c 139 | 12.8 | 53.3 | 18 | 7  | US-10-310-914A-357751  | Sequence 357751,  | c 212 | 12.6 | 52.5 | 23 | 7  | US-10-310-914A-751283  | Sequence 751283,  |
| c 140 | 12.8 | 53.3 | 18 | 7  | US-10-310-914A-185928  | Sequence 185928,  | c 213 | 12.6 | 52.5 | 23 | 7  | US-10-310-914A-771167  | Sequence 771167,  |
| c 141 | 12.8 | 53.3 | 19 | 7  | US-10-310-914A-1223834 | Sequence 1223834, | c 214 | 12.6 | 52.5 | 23 | 7  | US-10-310-914A-919581  | Sequence 919581,  |
| c 142 | 12.8 | 53.3 | 19 | 9  | US-11-101-244-211677   | Sequence 211677,  | c 215 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-30115   | Sequence 30115, A |
| c 143 | 12.8 | 53.3 | 19 | 9  | US-11-101-244-211779   | Sequence 211779,  | c 216 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-313025  | Sequence 313025,  |
| c 144 | 12.8 | 53.3 | 19 | 9  | US-11-101-244-211877   | Sequence 211877,  | c 217 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-313231  | Sequence 313231,  |
| c 145 | 12.8 | 53.3 | 19 | 9  | US-11-101-244-175465   | Sequence 175465,  | c 218 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-313246  | Sequence 313246,  |
| c 146 | 12.8 | 53.3 | 19 | 10 | US-11-083-784-211677   | Sequence 211677,  | c 219 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-313284  | Sequence 313284,  |
| c 147 | 12.8 | 53.3 | 19 | 10 | US-11-083-784-211779   | Sequence 211779,  | c 220 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-362492  | Sequence 362492,  |
| c 148 | 12.8 | 53.3 | 19 | 10 | US-11-083-784-211877   | Sequence 211877,  | c 221 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-362500  | Sequence 362500,  |
| c 149 | 12.8 | 53.3 | 20 | 7  | US-11-083-784-1175465  | Sequence 1175465, | c 222 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-412606  | Sequence 412606,  |
| c 150 | 12.8 | 53.3 | 20 | 7  | US-10-310-914A-157160  | Sequence 157160,  | c 223 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-525261  | Sequence 525261,  |
| c 151 | 12.8 | 53.3 | 20 | 7  | US-10-310-914A-283526  | Sequence 283526,  | c 224 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-528504  | Sequence 528504,  |
| c 152 | 12.8 | 53.3 | 21 | 7  | US-10-310-914A-157161  | Sequence 157161,  | c 225 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-528562  | Sequence 528562,  |
| c 153 | 12.8 | 53.3 | 21 | 7  | US-10-310-914A-1117009 | Sequence 1117009, | c 226 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-528571  | Sequence 528571,  |
| c 154 | 12.8 | 53.3 | 22 | 7  | US-10-310-914A-283540  | Sequence 283540,  | c 227 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-865117  | Sequence 865117,  |
| c 155 | 12.8 | 53.3 | 22 | 7  | US-10-310-914A-283541  | Sequence 283541,  | c 228 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-865135  | Sequence 865135,  |
| c 156 | 12.8 | 53.3 | 22 | 7  | US-10-310-914A-309014  | Sequence 309014,  | c 229 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-865245  | Sequence 865245,  |
| c 157 | 12.8 | 53.3 | 22 | 7  | US-10-310-914A-654221  | Sequence 654221,  | c 230 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-865255  | Sequence 865255,  |
| c 158 | 12.8 | 53.3 | 23 | 7  | US-10-310-914A-157162  | Sequence 157162,  | c 231 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-865278  | Sequence 865278,  |
| c 159 | 12.8 | 53.3 | 23 | 7  | US-10-310-914A-1151691 | Sequence 1151691, | c 232 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-919569  | Sequence 919569,  |
| c 160 | 12.8 | 53.3 | 23 | 7  | US-10-310-914A-1223835 | Sequence 1223835, | c 233 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-919580  | Sequence 919580,  |
| c 161 | 12.8 | 53.3 | 24 | 7  | US-10-310-914A-29969   | Sequence 29969, A | c 234 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-919629  | Sequence 919629,  |
| c 162 | 12.8 | 53.3 | 24 | 7  | US-10-310-914A-33594   | Sequence 33594, A | c 235 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-1059297 | Sequence 1059297, |
| c 163 | 12.8 | 53.3 | 24 | 7  | US-10-310-914A-81056   | Sequence 81056, A | c 236 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-1059426 | Sequence 1059426, |
| c 164 | 12.8 | 53.3 | 24 | 7  | US-10-310-914A-206783  | Sequence 206783,  | c 237 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-1059466 | Sequence 1059466, |
| c 165 | 12.8 | 53.3 | 24 | 7  | US-10-310-914A-456389  | Sequence 456389,  | c 238 | 12.6 | 52.5 | 24 | 7  | US-10-310-914A-1138903 | Sequence 1138903, |
| c 166 | 12.8 | 53.3 | 24 | 7  | US-10-310-914A-1144958 | Sequence 1144958, | c 239 | 12.6 | 52.5 | 24 | 7  |                        |                   |
| c 167 | 12.8 | 53.3 | 24 | 7  | US-10-310-914A-1204871 | Sequence 1204871, | c 240 | 12.6 | 52.5 | 24 | 7  |                        |                   |



```

; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-402269

Query Match      66.7%; Score 16; DB 7; Length 25;
Best Local Similarity 70.8%; Pred. No. 5.4e+02;
Matches 17; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGTCAGCGTGGCCATGGGG 24
    |||||
Db 2 GGGGCCAGCGUCCACCUUGGUG 25

RESULT 4
US-11-201-322-2/c
; Sequence 2, Application US/11201322
; Publication No. US20050272129A1
; GENERAL INFORMATION:
; APPLICANT: Sharon, Amir
; APPLICANT: Goldstein-Barhoom, Sima
; TITLE OF INVENTION: TRANSGENIC FUNGI EXPRESSING BCL-2 AND METHODS OF USING BCL-2 OR F
; TITLE OF INVENTION: THEREOF FOR IMPROVING BIOMASS PRODUCTION, SURVIVAL, LONGEVITY AN
; TITLE OF INVENTION: RESISTANCE OF FUNGI
; FILE REFERENCE: 30302
; CURRENT APPLICATION NUMBER: US/11/201,322
; CURRENT FILING DATE: 2005-08-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-11-201-322-2

Query Match      66.7%; Score 16; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCCATGG 21
    |||||
Db 20 CCAGCGTGGCCATGG 5

RESULT 5
US-10-310-914A-1185838
; Sequence 1185838, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1185838
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1185838

Query Match      65.8%; Score 15.8; DB 7; Length 22;
Best Local Similarity 84.2%; Pred. No. 6.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCCATGGGG 24
    |||||
Db 1 CCAGCGGGCCCCAUGGGG 19
```

```

RESULT 6
US-11-121-849-235244/c
; Sequence 235244, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 235244
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-235244

Query Match      65.8%; Score 15.8; DB 11; Length 25;
Best Local Similarity 89.5%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCCATGGGG 24
    |||||
Db 25 CCAGCGTGGCAGATGAGGG 7

RESULT 7
US-10-310-914A-34498/c
; Sequence 34498, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34498
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-34498

Query Match      63.3%; Score 15.2; DB 7; Length 24;
Best Local Similarity 85.0%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 TCCAGCGTGGCCATGGGG 24
    |||||
Db 24 TCCAGCTTGGCGCATGGGG 5

RESULT 8
US-11-127-654-84
; Sequence 84, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
```

; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 84  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-84

Query Match 62.5%; Score 15; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGCCTCAT 19  
|||||  
Db 1 TCCAGCGTGCCTCAT 15

RESULT 9  
US-10-310-914A-94891/c  
; Sequence 94891, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Krizat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CFUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 94891  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-94891

Query Match 62.5%; Score 15; DB 7; Length 23;  
Best Local Similarity 78.3%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCCTCATGGGG 24  
|||||  
Db 23 GGGTCTGTGTGCCACAGGGG 1

RESULT 10  
US-11-121-849-23997/c  
; Sequence 23997, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 23997  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-23997

Query Match 62.5%; Score 15; DB 11; Length 25;

Best Local Similarity 78.3%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 GGGTCCAGCGTGCCTCATGGGG 24  
|||||  
Db 25 GGGCCACGCTCCACCTTGTGG 3  
RESULT 11  
US-11-121-849-46868  
; Sequence 46868, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 46868  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-46868

Query Match 62.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGCCTCATGGGG 23  
|||||  
Db 3 GGGGACCAGTGTGTGCCAGCGG 25

RESULT 12  
US-11-121-849-46869  
; Sequence 46869, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 46869  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-46869

Query Match 62.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGCCTCATGGGG 23  
|||||  
Db 2 GGGGACCAGTGTGTGCCAGCGG 24

RESULT 13  
US-10-310-914A-45418/c  
; Sequence 45418, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

```

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45418
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-45418

Query Match      60.8%; Score 14.6; DB 7; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGG 21
Db 21 GGGCTCAGCGTGGCCCATGG 1

RESULT 14
US-10-310-914A-402274
; Sequence 402274, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 402274
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-402274

Query Match      60.8%; Score 14.6; DB 7; Length 21;
Best Local Similarity 71.4%; Pred. No. 2.1e+03;
Matches 15; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGG 21
Db 1 GGGGCCAGCGUCCACCUUGG 21

RESULT 15
US-10-310-914A-38276
; Sequence 38276, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38276
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-38276
```

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Query Match      60.8%; Score 14.6; DB 7; Length 24;
Best Local Similarity 71.4%; Pred. No. 2.1e+03;
Matches 15; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GTCCAGCGTGGCCCATGGGG 24
Db 1 GUCCAGGCGCGCAUGGGCG 21

RESULT 16
US-10-310-914A-895311/c
; Sequence 895311, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 895311
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-895311

Query Match      60.8%; Score 14.6; DB 7; Length 26;
Best Local Similarity 81.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GTCCAGCGTGGCCCATGGGG 24
Db 21 GTCTGGGCGCGCATGGGAG 1

RESULT 17
US-10-310-914A-650086/c
; Sequence 650086, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 650086
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-650086

Query Match      60.0%; Score 14.4; DB 7; Length 21;
Best Local Similarity 93.8%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCG 16
Db 20 GGGGTCCAGCGTGCAC 5

RESULT 18
US-10-310-914A-721320/c
; Sequence 721320, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
```

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; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 721320
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-721320

Query Match      59.2%; Score 14.2; DB 7; Length 24;
Best Local Similarity 84.2%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4  GTCCAGCGTGGCCCATGGG 22
        ||||| ||||| |||||
Db      19  GTCCACCCCTGGGCGCATGGG 1

RESULT 19
US-10-994-213-7/c
; Sequence 7, Application US/10994213
; Publication No. US20060019911A1
; GENERAL INFORMATION:
; APPLICANT: Papisov, Mikhail. I.
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
; FILE OF INVENTION: USE THEREOF
; FILE REFERENCE: 0838.1003-001
; CURRENT APPLICATION NUMBER: US/10/994,213
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: US/09/634,320
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/147,919
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-994-213-7

Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  CCAGCGTGGCCCAT 19
        ||||| ||||| |||||
Db      14  CCAGCGTGGCCCAT 1

RESULT 20
US-10-918-638-24
; Sequence 24, Application US/10918638
; Publication No. US20050249663A1
; GENERAL INFORMATION:
; APPLICANT: Copharos
; TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEIC ACIDS, ANALOGS
; FILE OF INVENTION: AND
; FILE REFERENCE: COP1010
; CURRENT APPLICATION NUMBER: US/10/918,638
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US/10/246,300
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide-- G3139 Genta
US-10-918-638-24

Query Match      58.3%; Score 14; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  CCAGCGTGGCCCAT 19
        ||||| ||||| |||||
Db      5  CCAGCGTGGCCCAT 18

RESULT 21
US-10-658-947-14
; Sequence 14, Application US/10658947
; Publication No. US20050255153A1
; GENERAL INFORMATION:
; APPLICANT: Inex Pharmaceuticals Inc.
; TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic
; FILE OF INVENTION: Agents in
; FILE REFERENCE: Lipid Vesicles
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson LLP
; STREET: PO Box 5068
; CITY: Dillon
; STATE: CO
; COUNTRY: US
; ZIP: 80435
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/658,947
; FILING DATE: 09-Sep-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,480
; FILING DATE: 29-Jun-2001
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: <Unknown>
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: <Unknown>
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-658-947-14

Query Match      58.3%; Score 14; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  CCAGCGTGGCCCAT 19
        ||||| ||||| |||||
```





```
US-11-127-654-85
; Sequence 85, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-85

Query Match      58.3%; Score 14; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCACGGTGGCCCAT 19
Db      5 CCACGGTGGCCCAT 18
|||||

RESULT 27
US-11-081-140-6
; Sequence 6, Application US/11081140
; Publication No. US20050261225A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Cy A
; APPLICANT: Benimetkaya, Lyuba
; APPLICANT: Guzzo-Pernelli, Nancy
; TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWNR
; FILE REFERENCE: 0575/63293
; CURRENT APPLICATION NUMBER: US/11/081,140
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: US/10/002,884
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: ANTISENSE OLIGONUCLEOTIDE
US-11-081-140-6

Query Match      58.3%; Score 14; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCACGGTGGCCCAT 19
Db      5 CCACGGTGGCCCAT 18
|||||

US-11-134-918-55
; Sequence 55, Application US/11134918
; Publication No. US20050267064A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/134,918
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-031-460-55

Query Match      58.3%; Score 14; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCACGGTGGCCCAT 19
Db      5 CCACGGTGGCCCAT 18
|||||

US-11-031-460-55
; Sequence 55, Application US/11031460
; Publication No. US20050277609A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/031,460
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-031-460-55

Query Match      58.3%; Score 14; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCACGGTGGCCCAT 19
Db      5 CCACGGTGGCCCAT 18
|||||
```

RESULT 30  
US-11-067-587-55  
; Sequence 55, Application US/11067587  
; Publication No. US20060003955A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Kline, Joel N.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules  
; FILE REFERENCE: C1039/7048 (AWS)  
; CURRENT APPLICATION NUMBER: US/11/067,587  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR APPLICATION NUMBER: US/09/818,918  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 08/276,358  
; PRIOR FILING DATE: 1994-07-15  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; PRIOR APPLICATION NUMBER: US 08/738,652  
; PRIOR FILING DATE: 1996-10-30  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 55  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-067-587-55

Query Match 58.3%; Score 14; DB 11; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCCAT 18

RESULT 31  
US-11-099-683-131  
; Sequence 131, Application US/11099683  
; Publication No. US20060019916A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES  
; FILE REFERENCE: C1037.70047US01  
; CURRENT APPLICATION NUMBER: US/11/099,683  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 60/558,951  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 131  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-099-683-131

Query Match 58.3%; Score 14; DB 11; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCCAT 18

RESULT 32  
US-11-099-683-132  
; Sequence 132, Application US/11099683  
; Publication No. US20060019916A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES  
; FILE REFERENCE: C1037.70047US01  
; CURRENT APPLICATION NUMBER: US/11/099,683  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 60/558,951  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 132  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-099-683-132

Query Match 58.3%; Score 14; DB 11; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCCAT 18

RESULT 33  
US-10-994-213-8  
; Sequence 8, Application US/10994213  
; Publication No. US20060019911A1  
; GENERAL INFORMATION:  
; APPLICANT: Papilov, Mikhail, I.  
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF  
; FILE REFERENCE: 0838.1003-001  
; CURRENT APPLICATION NUMBER: US/10/994,213  
; CURRENT FILING DATE: 2004-11-19  
; PRIOR APPLICATION NUMBER: US/09/634,320  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: US 60/147,919  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
; FEATURE:  
; OTHER INFORMATION: c indicates an RNA base  
US-10-994-213-8

Query Match 58.3%; Score 14; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCCAT 18

RESULT 34  
US-10-994-213-9/c  
; Sequence 9, Application US/10994213  
; Publication No. US20060019911A1

; GENERAL INFORMATION:  
; APPLICANT: Papisov, Mikhail, I.  
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/994,213  
; CURRENT FILING DATE: 2004-11-19  
; PRIOR APPLICATION NUMBER: US/09/634,320  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: US 60/147,919  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
; FEATURE:  
; OTHER INFORMATION: c indicates an RNA base  
US-10-994-213-9

Query Match 58.3%; Score 14; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 14 CCAGCGTGGCCAT 1

## RESULT 35

US-11-127-654-81  
; Sequence 81, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Beig, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 81  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-81

Query Match 58.3%; Score 14; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 36

US-10-310-914A-100840/c  
; Sequence 100840, Application US/10310914A  
; Publication No. US2006000322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 100840  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-100840

Query Match 58.3%; Score 14; DB 7; Length 22;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGGCCATGGGG 23  
Db 22 GGGGCCAGCGCTCGGCATGGCG 1

## RESULT 37

US-10-994-213-1  
; Sequence 1, Application US/10994213  
; Publication No. US20060019911A1  
; GENERAL INFORMATION:  
; APPLICANT: Papisov, Mikhail, I.  
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF  
; FILE REFERENCE: 0838.1003-001  
; CURRENT APPLICATION NUMBER: US/10/994,213  
; CURRENT FILING DATE: 2004-11-19  
; PRIOR APPLICATION NUMBER: US/09/634,320  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: US 60/147,919  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-994-213-1

Query Match 58.3%; Score 14; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 8 CCAGCGTGGCCAT 21

## RESULT 38

US-10-994-213-2/c  
; Sequence 2, Application US/10994213  
; Publication No. US20060019911A1  
; GENERAL INFORMATION:  
; APPLICANT: Papisov, Mikhail, I.  
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF  
; FILE REFERENCE: 0838.1003-001  
; CURRENT APPLICATION NUMBER: US/10/994,213  
; CURRENT FILING DATE: 2004-11-19  
; PRIOR APPLICATION NUMBER: US/09/634,320  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: US 60/147,919  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
; FEATURE:  
; OTHER INFORMATION: t = amino modified T  
US-10-994-213-2

Query Match 58.3%; Score 14; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
|||  
Db 16 CCAGCGTGGCCAT 3

RESULT 39  
US-10-310-914A-903934  
; Sequence 903934, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 903934  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-903934

Query Match 58.3%; Score 14; DB 7; Length 23;  
Best Local Similarity 63.6%; Pred. No. 3.7e+03;  
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGGCCATGGGG 24  
|:|||||:|:|:|  
Db 2 GCUCAGCGGCGGCAUGAGGG 23

RESULT 40  
US-10-310-914A-989919/c  
; Sequence 989919, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 989919  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-989919

Query Match 58.3%; Score 14; DB 7; Length 25;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCATGGG 22  
|||||:|:|:|  
Db 22 GGGGTCCAGGTGGGACATGGG 1

RESULT 41  
US-11-121-849-46867  
; Sequence 46867, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 46867  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-46867

Query Match 58.3%; Score 14; DB 11; Length 25;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCATGGG 22  
|||||:|:|:|  
Db 4 GGGGACCAGTGTGTGCCAGGCG 25

RESULT 42  
US-11-121-849-46870  
; Sequence 46870, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 46870  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-46870

Query Match 58.3%; Score 14; DB 11; Length 25;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGGCCATGGGG 23  
|||||:|:|:|  
Db 1 GGGACCAGTGTGTGCCAGGCGG 22

RESULT 43  
US-10-310-914A-1042200/c  
; Sequence 1042200, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1042200  
; LENGTH: 26  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1042200

Query Match 58.3%; Score 14; DB 7; Length 26;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTCGCCCATGGG 22  
Db 24 GTGGTCCAGCGTCGCCCGGG 3

RESULT 44

US-10-939-294A-19743/c  
; Sequence 19743, Application US/10939294A  
; Publication No. US20050266417A1  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Turner, Daniel  
; APPLICANT: Pingler, Maneesh  
; APPLICANT: Pincas, Hanna  
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules  
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)  
; CURRENT APPLICATION NUMBER: US/10/939,294A  
; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: US 60/502/731  
; PRIOR FILING DATE: 2003-09-12  
; NUMBER OF SEQ ID NOS: 38895  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 19743  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide probe  
US-10-939-294A-19743

Query Match 58.3%; Score 14; DB 7; Length 32;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTCGCCCATGGG 23  
Db 23 GGCTCCGCGTCGCTCTGTAGG 2

RESULT 45

US-10-310-914A-906465/c  
; Sequence 906465, Application US/10310914A  
; Publication No. US2006000322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 906465  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human

Query Match 57.5%; Score 13.8; DB 7; Length 23;  
Best Local Similarity 76.5%; Pred. No. 4.5e+03;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTCGCC 17  
Db 2 GGGGUCCAGGGUGCACC 18

RESULT 46

US-11-121-849-330122  
; Sequence 330122, Application US/11121849  
; Publication No. US20050272080A1

US-10-310-914A-906465

Query Match 57.5%; Score 13.8; DB 7; Length 18;  
Best Local Similarity 88.2%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CCAGCGTCGCCCATGGG 22  
Db 18 CCAGCGTCGCCCGGG 2

RESULT 46

US-10-310-914A-775551/c  
; Sequence 775551, Application US/10310914A  
; Publication No. US2006000322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 775551  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-775551

Query Match 57.5%; Score 13.8; DB 7; Length 21;  
Best Local Similarity 88.2%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTCGCCCA 18  
Db 17 GGGTCCAGACTGCCCA 1

RESULT 47

US-10-310-914A-321695  
; Sequence 321695, Application US/10310914A  
; Publication No. US2006000322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 321695  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-321695

Query Match 57.5%; Score 13.8; DB 7; Length 23;  
Best Local Similarity 76.5%; Pred. No. 4.5e+03;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTCGCC 17  
Db 2 GGGGUCCAGGGUGCACC 18

RESULT 48

US-11-121-849-330122  
; Sequence 330122, Application US/11121849  
; Publication No. US20050272080A1

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; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 330122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-121-849-330122

Query Match      57.5%; Score 13.8; DB 11; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2  GGGTCCAGCGTGCGCCA 18
        |||||
Db      9  GGGTCCAGTGTCCGCCA 25

RESULT 49
US-11-131-212-40/c
; Sequence 40, Application US/11131212
; Publication No. US20050262593A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: Motoo YAMASAKI
; APPLICANT: Nobuo HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/131,212
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-11-131-212-40

Query Match      57.5%; Score 13.8; DB 11; Length 45;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8  AGCGTGGCCCATGGGG 24
        |||||
Db     27  AGCGTGAGCCATGGTGG 11

RESULT 50
US-10-310-914A-222305
; Sequence 222305, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 222305
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-222305

Query Match      56.7%; Score 13.6; DB 7; Length 20;
Best Local Similarity 70.0%; Pred. No. 5.5e+03;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1  GGGGTCCAGCGTGCGCCATG 20
        |||||
Db      1  GGGGUCGCGCGGGGUCCUG 20

Search completed: February 16, 2006, 02:53:03
Job time : 226.736 secs
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| 21 | 29.8 | 78.4 | 44 | 6  | AR473523  | Sequence    |
| 22 | 29.8 | 78.4 | 44 | 6  | AR542759  | Sequence    |
| 23 | 29.2 | 76.8 | 45 | 6  | AR027239  | Sequence    |
| 24 | 29.2 | 76.8 | 45 | 6  | AR035447  | Sequence    |
| 25 | 29.2 | 76.8 | 45 | 6  | AR035451  | Sequence    |
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| 27 | 29   | 76.3 | 46 | 6  | AR035449  | Sequence    |
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| 29 | 29   | 76.3 | 46 | 6  | AR035455  | Sequence    |
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| 31 | 28.8 | 75.8 | 36 | 6  | AR149733  | Sequence    |
| 32 | 28.8 | 75.8 | 36 | 6  | AR404853  | Sequence    |
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| 36 | 28   | 73.7 | 33 | 6  | BD081630  | Inhibito    |
| 37 | 28   | 73.7 | 34 | 6  | I09458    | Sequence 2  |
| 38 | 28   | 73.7 | 35 | 6  | BD249738  | Intracell   |
| 39 | 28   | 73.7 | 35 | 6  | AR532727  | Sequence    |
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| 41 | 27.6 | 72.6 | 45 | 6  | AR035454  | Sequence    |
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| 43 | 27.4 | 72.1 | 35 | 6  | AR589386  | Sequence    |
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| 46 | 26.4 | 69.5 | 35 | 6  | CQ846478  | Sequence    |
| 47 | 26.4 | 69.5 | 35 | 6  | AR585153  | Sequence    |
| 48 | 26.4 | 69.5 | 35 | 6  | AR589385  | Sequence    |
| 49 | 26   | 68.4 | 32 | 6  | AR397504  | Sequence    |
| 50 | 26   | 68.4 | 32 | 6  | AR575406  | Sequence    |
| 51 | 26   | 68.4 | 33 | 6  | AR032342  | Sequence    |
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| 53 | 25.8 | 67.9 | 35 | 6  | AR585154  | Sequence    |
| 54 | 25.2 | 66.3 | 48 | 6  | AR035458  | Sequence    |
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| 56 | 24   | 63.2 | 25 | 6  | AX299019  | Sequence    |
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| 60 | 24   | 63.2 | 27 | 6  | AR035436  | Sequence    |
| 61 | 24   | 63.2 | 27 | 6  | E61343    | Probe for d |
| 62 | 24   | 63.2 | 27 | 6  | I82942    | Sequence 44 |
| 63 | 24   | 63.2 | 27 | 6  | I83022    | Sequence 12 |
| 64 | 24   | 63.2 | 27 | 6  | AR352029  | Sequence    |
| 65 | 24   | 63.2 | 27 | 6  | AR431128  | Sequence    |
| 66 | 24   | 63.2 | 27 | 6  | AR431208  | Sequence    |
| 67 | 24   | 63.2 | 27 | 6  | AX828921  | Sequence    |
| 68 | 24   | 63.2 | 27 | 6  | AX829001  | Sequence    |
| 69 | 24   | 63.2 | 28 | 6  | A40180    | Sequence 2  |
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| 71 | 24   | 63.2 | 29 | 6  | BD085996  | Tumor nec   |
| 72 | 24   | 63.2 | 29 | 6  | BD090957  | Apo-3 lig   |
| 73 | 24   | 63.2 | 29 | 6  | BD132797  | Apo-2 DGR   |
| 74 | 24   | 63.2 | 29 | 6  | AR183747  | Sequence    |
| 75 | 24   | 63.2 | 29 | 6  | AR236056  | Sequence    |
| 76 | 24   | 63.2 | 29 | 6  | AR241295  | Sequence    |
| 77 | 24   | 63.2 | 29 | 6  | AX099766  | Sequence    |
| 78 | 24   | 63.2 | 29 | 6  | AX188648  | Sequence    |
| 79 | 24   | 63.2 | 29 | 6  | AX188649  | Sequence    |
| 80 | 24   | 63.2 | 29 | 11 | CS001237  | Sequence    |
| 81 | 24   | 63.2 | 37 | 6  | A40179    | Sequence 1  |
| 82 | 23   | 60.5 | 23 | 6  | AR106267  | Sequence    |
| 83 | 23   | 60.5 | 23 | 6  | BD008835  | Uses of a   |
| 84 | 22.4 | 58.9 | 25 | 6  | I72377    | Sequence 8  |
| 85 | 22   | 57.9 | 22 | 6  | AX13989   | Synthetic H |
| 86 | 22   | 57.9 | 22 | 6  | AR131408  | Sequence    |
| 87 | 22   | 57.9 | 22 | 6  | BD001814  | Immunogen   |
| 88 | 21.4 | 55.3 |    |    |           |             |

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| 92    | 20.2 | 53.2 | 42 | 6  | AX798848  | Sequence            | 165   | 14.4 | 37.9 | 38 | 6 | AR351569   | Sequence           |
| 93    | 19.8 | 52.1 | 26 | 6  | AR035444  | Sequence            | 166   | 14.4 | 37.9 | 38 | 6 | AX492879   | Sequence           |
| 94    | 19.2 | 50.5 | 26 | 6  | AR035437  | Sequence            | 167   | 14.4 | 37.9 | 39 | 6 | AX135021   | Sequence           |
| 95    | 19.2 | 50.5 | 26 | 6  | AR035437  | Sequence            | c 168 | 14.4 | 37.9 | 45 | 6 | AX068147   | Sequence           |
| c 96  | 19   | 50.0 | 24 | 6  | AR654113  | Sequence            | 169   | 14.4 | 37.9 | 46 | 6 | AR275619   | Sequence           |
| 97    | 19   | 50.0 | 26 | 6  | AR035438  | Sequence            | 170   | 14.4 | 37.9 | 46 | 6 | AR278099   | Sequence           |
| 98    | 19   | 50.0 | 26 | 6  | AR035442  | Sequence            | 171   | 14.4 | 37.9 | 46 | 6 | AR409070   | Sequence           |
| 99    | 18.6 | 48.9 | 39 | 6  | AR005187  | Sequence            | 172   | 14.4 | 37.9 | 46 | 6 | AR616918   | Sequence           |
| c 100 | 18.6 | 48.9 | 39 | 6  | AR005188  | Sequence            | 173   | 14.4 | 37.9 | 46 | 6 | AX082449   | Sequence           |
| 101   | 18.6 | 48.9 | 39 | 6  | AR038397  | Sequence            | 174   | 14.4 | 37.9 | 46 | 6 | AX084800   | Sequence           |
| c 102 | 18.6 | 48.9 | 39 | 6  | AR038398  | Sequence            | 175   | 14.4 | 37.9 | 46 | 6 | AX817878   | Sequence           |
| 103   | 18.6 | 48.9 | 39 | 6  | AR088704  | Sequence            | 176   | 14.2 | 37.4 | 28 | 6 | BD176640   | Promoter           |
| 104   | 18.6 | 48.9 | 39 | 6  | AR178133  | Sequence            | c 177 | 14.2 | 37.4 | 31 | 6 | AX248800   | Sequence           |
| c 105 | 18.6 | 48.9 | 39 | 6  | AR178134  | Sequence            | c 178 | 14.2 | 37.4 | 32 | 6 | BD161889   | Kl Gene            |
| c 106 | 18.6 | 48.9 | 39 | 6  | I58473    | Sequence 45         | c 179 | 14.2 | 37.4 | 32 | 6 | BD161898   | Nonhuman           |
| c 107 | 18.6 | 48.9 | 39 | 6  | I58474    | Sequence 46         | c 180 | 14.2 | 37.4 | 33 | 6 | AX084276   | Sequence           |
| c 108 | 18.6 | 48.9 | 39 | 6  | I66591    | Sequence 45         | 181   | 14.2 | 37.4 | 33 | 8 | AF505525   | Homo sapi          |
| c 109 | 18.6 | 48.9 | 39 | 6  | I66592    | Sequence 46         | c 182 | 14.2 | 37.4 | 35 | 6 | AX686396   | Sequence           |
| c 110 | 18.6 | 48.9 | 39 | 6  | I68238    | Sequence 45         | c 183 | 14.2 | 37.4 | 37 | 6 | BD161877   | Kl gene            |
| c 111 | 18.6 | 48.9 | 39 | 6  | I68239    | Sequence 46         | c 184 | 14.2 | 37.4 | 39 | 6 | AX306642   | Sequence           |
| c 112 | 18.2 | 47.9 | 26 | 6  | AR004563  | Sequence            | 185   | 14.2 | 37.4 | 40 | 6 | A79625     | Sequence 5         |
| c 113 | 17.6 | 46.3 | 26 | 6  | AR004564  | Sequence            | 186   | 14.2 | 37.4 | 40 | 6 | AR003558   | Sequence           |
| 114   | 17.6 | 46.3 | 26 | 6  | AR035441  | Sequence            | 187   | 14.2 | 37.4 | 40 | 6 | AR041144   | Sequence           |
| 115   | 17.4 | 45.8 | 47 | 6  | A61803    | Sequence 26         | 188   | 14.2 | 37.4 | 40 | 6 | AR075338   | Sequence           |
| 116   | 17.2 | 45.3 | 26 | 6  | AR035440  | Sequence            | 189   | 14.2 | 37.4 | 40 | 6 | AR087848   | Sequence           |
| c 117 | 17   | 44.7 | 17 | 6  | AR438117  | Sequence            | 190   | 14.2 | 37.4 | 40 | 6 | AR1119903  | Sequence           |
| c 118 | 16.8 | 44.2 | 26 | 6  | AR035439  | Sequence            | 191   | 14.2 | 37.4 | 40 | 6 | AR154200   | Sequence           |
| c 119 | 16.6 | 43.7 | 47 | 6  | AR583119  | Sequence            | 192   | 14.2 | 37.4 | 40 | 6 | AR169478   | Sequence           |
| 120   | 16.4 | 43.2 | 38 | 6  | A79871    | Sequence 28         | 193   | 14.2 | 37.4 | 40 | 6 | AR175527   | Sequence           |
| 121   | 16.4 | 43.2 | 38 | 6  | AR011592  | Sequence            | 194   | 14.2 | 37.4 | 40 | 6 | AR179302   | Sequence           |
| 122   | 16.4 | 43.2 | 38 | 6  | AR028015  | Sequence            | 195   | 14.2 | 37.4 | 40 | 6 | BD134764   | Thermoana          |
| 123   | 16.4 | 43.2 | 38 | 6  | AR157607  | Sequence            | 196   | 14.2 | 37.4 | 40 | 6 | BD190485   | AMPLIPICA          |
| 124   | 16.4 | 43.2 | 41 | 6  | AX514212  | Sequence            | 197   | 14.2 | 37.4 | 40 | 6 | BD191470   | Nucleic a          |
| 125   | 16.4 | 43.2 | 41 | 6  | AX520358  | Sequence            | 198   | 14.2 | 37.4 | 40 | 6 | BD240946   | Self-cont          |
| 126   | 16.2 | 42.6 | 40 | 6  | AR004621  | Sequence            | 199   | 14.2 | 37.4 | 40 | 6 | BD249410   | Electroni          |
| 127   | 16.2 | 42.6 | 41 | 6  | AX514803  | Sequence            | 200   | 14.2 | 37.4 | 40 | 6 | I25354     | Sequence 3         |
| 128   | 16.2 | 42.6 | 41 | 6  | AX520698  | Sequence            | 201   | 14.2 | 37.4 | 40 | 6 | AR195022   | Sequence           |
| c 129 | 16.2 | 42.6 | 46 | 6  | E11769    | Primer for          | 202   | 14.2 | 37.4 | 40 | 6 | AR352409   | Sequence           |
| c 130 | 16.2 | 42.6 | 46 | 6  | I82413    | Sequence 5          | 203   | 14.2 | 37.4 | 40 | 6 | AR352438   | Sequence           |
| 131   | 16.2 | 42.6 | 48 | 8  | HSBFA1B   | X72146 H.sapiens    | 204   | 14.2 | 37.4 | 40 | 6 | AR3430589  | Sequence           |
| c 132 | 15.8 | 41.6 | 28 | 6  | AX431437  | Sequence            | 205   | 14.2 | 37.4 | 40 | 6 | AR642772   | Sequence           |
| c 133 | 15.8 | 41.6 | 47 | 6  | AR219307  | Sequence            | 206   | 14.2 | 37.4 | 40 | 6 | AR648091   | Sequence           |
| c 134 | 15.6 | 41.1 | 50 | 6  | CQ004477  | Sequence            | 207   | 14.2 | 37.4 | 40 | 6 | AX135666   | Sequence           |
| c 135 | 15.4 | 40.5 | 25 | 6  | AR203357  | Sequence            | c 208 | 14.2 | 37.4 | 42 | 8 | HSDDTCRV01 | Z27179 H.sapiens   |
| c 136 | 15.2 | 40.0 | 32 | 6  | AX306632  | Sequence            | 209   | 14.2 | 37.4 | 44 | 6 | AR172768   | Sequence           |
| c 137 | 15   | 39.5 | 15 | 6  | AR035432  | Sequence            | 210   | 14.2 | 37.4 | 44 | 6 | AR178712   | Sequence           |
| 138   | 15   | 39.5 | 31 | 6  | AX249048  | Sequence            | 211   | 14.2 | 37.4 | 44 | 6 | AR181283   | Sequence           |
| 139   | 15   | 39.5 | 32 | 6  | AX350351  | Sequence            | 212   | 14.2 | 37.4 | 44 | 6 | AR199964   | Sequence           |
| 140   | 15   | 39.5 | 33 | 6  | I34944    | Sequence 30         | 213   | 14.2 | 37.4 | 44 | 6 | AR231912   | Sequence           |
| c 141 | 15   | 39.5 | 40 | 6  | E08945    | E08945 Probe, 9/19  | 214   | 14.2 | 37.4 | 44 | 6 | AR343387   | Sequence           |
| c 142 | 15   | 39.5 | 45 | 6  | A18604    | H. sapiens          | 215   | 14.2 | 37.4 | 44 | 6 | AR349705   | Sequence           |
| c 143 | 15   | 39.5 | 45 | 6  | AR063614  | Sequence            | 216   | 14.2 | 37.4 | 44 | 6 | AR391176   | Sequence           |
| 144   | 14.8 | 38.9 | 31 | 6  | I37241    | Sequence 25         | 217   | 14.2 | 37.4 | 44 | 6 | AR431619   | Sequence           |
| 145   | 14.8 | 38.9 | 31 | 6  | I37242    | Sequence 25         | c 218 | 14.2 | 37.4 | 47 | 6 | AR290084   | Sequence           |
| 146   | 14.8 | 38.9 | 31 | 6  | I37243    | Sequence 25         | 219   | 14.2 | 37.4 | 50 | 6 | AR077264   | Sequence           |
| 147   | 14.8 | 38.9 | 31 | 6  | I94091    | Sequence 25         | 220   | 14.2 | 37.4 | 50 | 6 | CQ006807   | Sequence           |
| 148   | 14.8 | 38.9 | 31 | 6  | I94092    | Sequence 25         | c 221 | 14.2 | 37.4 | 50 | 6 | CQ009108   | Sequence           |
| 149   | 14.8 | 38.9 | 31 | 6  | I94093    | Sequence 25         | 222   | 14.2 | 37.4 | 50 | 8 | HUMTCRVU46 | L39584 Homo sapien |
| 150   | 14.8 | 38.9 | 34 | 6  | CQ816228  | Sequence            | 223   | 14   | 36.8 | 21 | 6 | AR148640   | Sequence           |
| c 151 | 14.6 | 38.4 | 23 | 6  | AX023995  | Sequence            | 224   | 14   | 36.8 | 21 | 6 | BD124012   | Neuroprot          |
| c 152 | 14.6 | 38.4 | 24 | 6  | AX443948  | Sequence            | 225   | 14   | 36.8 | 21 | 6 | AR404019   | Sequence           |
| c 153 | 14.6 | 38.4 | 25 | 6  | AX447923  | Sequence            | 226   | 14   | 36.8 | 23 | 6 | CS048086   | Sequence           |
| c 154 | 14.6 | 38.4 | 27 | 6  | CS063410  | Sequence            | 227   | 14   | 36.8 | 25 | 6 | AX650582   | Sequence           |
| c 155 | 14.6 | 38.4 | 27 | 6  | CS081191  | Sequence            | 228   | 14   | 36.8 | 25 | 6 | AX650583   | Sequence           |
| 156   | 14.6 | 38.4 | 31 | 6  | AX249568  | Sequence            | 229   | 14   | 36.8 | 25 | 6 | AX650584   | Sequence           |
| 157   | 14.6 | 38.4 | 45 | 13 | MLMLTTRA2 | M10542 M-MuLV unlin | 230   | 14   | 36.8 | 25 | 6 | AX650585   | Sequence           |
| c 158 | 14.6 | 38.4 | 47 | 6  | AR284612  | Sequence            | c 231 | 14   | 36.8 | 27 | 8 | S62577     | lamp-2-Lyso        |
| c 159 | 14.6 | 38.4 | 47 | 6  | AX093025  | Sequence            | c 232 | 14   | 36.8 | 30 | 6 | AX590776   | Sequence           |
| c 160 | 14.6 | 38.4 | 48 | 6  | AX223706  | Sequence            | 233   | 14   | 36.8 | 31 | 9 | MUSCD3E2   | M23371 Mus musculi |
| c 161 | 14.6 | 38.4 | 50 | 6  | AR392726  | Sequence            | 234   | 14   | 36.8 | 32 | 6 | AX766988   | Sequence           |
| 162   | 14.4 | 37.9 | 24 | 6  | BD211083  | Quantitat           | c 235 | 14   | 36.8 | 33 | 6 | AR021014   | Sequence           |
| 163   | 14.4 | 37.9 | 37 | 6  | I42582    | Sequence 8          | c 236 | 14   | 36.8 | 33 | 6 | AR043429   | Sequence           |
| 164   | 14.4 | 37.9 | 38 | 6  | BD177921  | Sequence            | c 237 | 14   | 36.8 | 33 | 6 | AR062344   | Sequence           |



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| C 238 | 14   | 36.8 | 33 | 6 | AR183803   | AR183803 Sequence |
| C 239 | 14   | 36.8 | 33 | 6 | AR368186   | AR368186 Sequence |
| C 240 | 14   | 36.8 | 37 | 6 | E10784     | PCR primer        |
| C 241 | 14   | 36.8 | 38 | 6 | I38420     | Sequence 5        |
| C 242 | 14   | 36.8 | 40 | 6 | AR053668   | Sequence          |
| C 243 | 14   | 36.8 | 40 | 6 | CQ918211   | Sequence          |
| C 244 | 14   | 36.8 | 40 | 6 | AR258603   | Sequence          |
| C 245 | 14   | 36.8 | 40 | 6 | AR364432   | Sequence          |
| C 246 | 14   | 36.8 | 41 | 6 | AX513944   | Sequence          |
| C 247 | 14   | 36.8 | 41 | 6 | AX519283   | Sequence          |
| C 248 | 14   | 36.8 | 45 | 6 | AR157675   | Sequence          |
| C 249 | 14   | 36.8 | 45 | 6 | AR157676   | Sequence          |
| C 250 | 14   | 36.8 | 45 | 8 | S69452     | TCR V gamma       |
| C 251 | 14   | 36.8 | 46 | 6 | BD268660   | Isolation         |
| C 252 | 14   | 36.8 | 47 | 6 | A43615     | Sequence 5        |
| C 253 | 14   | 36.8 | 47 | 6 | AR288379   | Sequence          |
| C 254 | 14   | 36.8 | 47 | 6 | AR289545   | Sequence          |
| C 255 | 14   | 36.8 | 47 | 6 | AR290662   | Sequence          |
| C 256 | 14   | 36.8 | 50 | 6 | AR214693   | Sequence          |
| C 257 | 14   | 36.8 | 50 | 6 | AR282147   | Sequence          |
| C 258 | 13.8 | 36.3 | 18 | 6 | CS120586   | Sequence          |
| C 259 | 13.8 | 36.3 | 19 | 6 | CS120544   | Sequence          |
| C 260 | 13.8 | 36.3 | 20 | 6 | AR315359   | Sequence          |
| C 261 | 13.8 | 36.3 | 20 | 6 | AX293963   | Sequence          |
| C 262 | 13.8 | 36.3 | 21 | 6 | BD266036   | Universal         |
| C 263 | 13.8 | 36.3 | 24 | 6 | AX289330   | Sequence          |
| C 264 | 13.8 | 36.3 | 26 | 6 | AR239768   | Sequence          |
| C 265 | 13.8 | 36.3 | 26 | 6 | AX279570   | Sequence          |
| C 266 | 13.8 | 36.3 | 27 | 6 | AR091132   | Sequence          |
| C 267 | 13.8 | 36.3 | 27 | 6 | AR198167   | Sequence          |
| C 268 | 13.8 | 36.3 | 29 | 6 | AR260321   | Sequence          |
| C 269 | 13.8 | 36.3 | 29 | 6 | CQ827928   | Sequence          |
| C 270 | 13.8 | 36.3 | 29 | 6 | CQ831062   | Sequence          |
| C 271 | 13.8 | 36.3 | 32 | 6 | I82400     | Sequence 48       |
| C 272 | 13.8 | 36.3 | 36 | 6 | AR001104   | Sequence          |
| C 273 | 13.8 | 36.3 | 36 | 6 | AR343272   | Sequence          |
| C 274 | 13.8 | 36.3 | 36 | 6 | AR401634   | Sequence          |
| C 275 | 13.8 | 36.3 | 36 | 6 | AR439958   | Sequence          |
| C 276 | 13.8 | 36.3 | 36 | 6 | AR576588   | Sequence          |
| C 277 | 13.8 | 36.3 | 36 | 6 | AR609191   | Sequence          |
| C 278 | 13.8 | 36.3 | 38 | 6 | AR078082   | Sequence          |
| C 279 | 13.8 | 36.3 | 38 | 6 | E35663     | Detection o       |
| C 280 | 13.8 | 36.3 | 38 | 6 | I76164     | Sequence 8        |
| C 281 | 13.8 | 36.3 | 38 | 6 | AR287028   | Sequence          |
| C 282 | 13.8 | 36.3 | 38 | 6 | AR399018   | Sequence          |
| C 283 | 13.8 | 36.3 | 38 | 6 | AR601747   | Sequence          |
| C 284 | 13.8 | 36.3 | 38 | 8 | HUMTCVDIES |                   |
| C 285 | 13.8 | 36.3 | 39 | 6 | I82405     | Sequence 55       |
| C 286 | 13.8 | 36.3 | 39 | 6 | I82406     | Sequence 56       |
| C 287 | 13.8 | 36.3 | 40 | 6 | AR3621     | Sequence 50       |
| C 288 | 13.8 | 36.3 | 41 | 6 | AR206162   | Sequence          |
| C 289 | 13.8 | 36.3 | 41 | 6 | AR595445   | Sequence          |
| C 290 | 13.8 | 36.3 | 41 | 6 | AX516152   | Sequence          |
| C 291 | 13.8 | 36.3 | 41 | 6 | AX517555   | Sequence          |
| C 292 | 13.8 | 36.3 | 42 | 6 | I82396     | Sequence 43       |
| C 293 | 13.8 | 36.3 | 42 | 6 | I82397     | Sequence 44       |
| C 294 | 13.8 | 36.3 | 42 | 6 | AX538890   | Sequence          |
| C 295 | 13.8 | 36.3 | 42 | 6 | AX538891   | Sequence          |
| C 296 | 13.8 | 36.3 | 42 | 8 | S80775     | gamma Delta       |
| C 297 | 13.8 | 36.3 | 47 | 6 | AR291782   | Sequence          |
| C 298 | 13.8 | 36.3 | 50 | 6 | CQ003473   | Sequence          |
| C 299 | 13.8 | 36.3 | 50 | 6 | CQ005360   | Sequence          |
| C 300 | 13.8 | 36.3 | 50 | 6 | CQ008574   | Sequence          |

ALIGNMENTS

|            |          |                                    |     |        |                 |
|------------|----------|------------------------------------|-----|--------|-----------------|
| RESULT 1   | AR088703 | 38 bp                              | DNA | linear | PAT 07-SEP-2000 |
| LOCUS      | AR088703 | Sequence 2 from patent US 5990090. |     |        |                 |
| DEFINITION | AR088703 |                                    |     |        |                 |
| ACCESSION  | AR088703 |                                    |     |        |                 |

|  |  |                                    |
|--|--|------------------------------------|
| VERSION  | AR088703.1   | GI:10015467                        |
| KEYWORDS   | Unknown.   |                                    |
| SOURCE   | Unknown.   |                                    |
| ORGANISM   | Unclassified.  |                                    |
| REFERENCE  | 1 (bases 1 to 38)  |                                    |
| AUTHORS  | Nabel,G.Jan.   |                                    |
| TITLE  | Methods and compositions for treatment of diseases             |                                    |
| JOURNAL  | Patent: US 5990090-A 2 23-NOV-1999;                            |                                    |
| FEATURES   | Location/Qualifiers  |                                    |
| source   | 1..38  |                                    |
| /organism="unknown"  |  |                                    |
| /mol_type="unassigned DNA"   |  |                                    |
| ORIGIN   |  |                                    |
| Query Match  | 100.0%;  | Score 38; DB 6; Length 38;         |
| Best Local Similarity  | 100.0%;  | Pred. No. 2.3e-05;                 |
| Matches  | 38; Conservative   | 0; Mismatches 0; Indels 0; Gaps 0; |
| QY   | 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38                     |                                    |
| Db   | 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38                     |                                    |
| RESULT 2   |  |                                    |
| LOCUS  | AX103956   | 38 bp DNA linear PAT 30-APR-2001   |
| DEFINITION   | Sequence 148 from Patent WO0122972.                            |                                    |
| ACCESSION  | AX103956   |                                    |
| VERSION  | AX103956.1   | GI:13920153                        |
| KEYWORDS   | synthetic construct  |                                    |
| SOURCE   | other sequences; artificial sequences.                         |                                    |
| ORGANISM   |  |                                    |
| REFERENCE  | 1  |                                    |
| AUTHORS  | Krieg,A.M., Schetter,C. and Vollmer,J.C.                       |                                    |
| TITLE  | Immunostimulatory nucleic acids                                |                                    |
| JOURNAL  | Patent: WO 0122972-A 148 05-APR-2001;                          |                                    |
| UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical |  |                                    |
| GmbH (DB)  |  |                                    |
| FEATURES   | Location/Qualifiers  |                                    |
| source   | 1..38  |                                    |
| /organism="synthetic construct"                                    |  |                                    |
| /mol_type="unassigned DNA"   |  |                                    |
| /db_xref="taxon:32630"   |  |                                    |
| ORIGIN   |  |                                    |
| Query Match  | 100.0%;  | Score 38; DB 6; Length 38;         |
| Best Local Similarity  | 100.0%;  | Pred. No. 2.3e-05;                 |
| Matches  | 38; Conservative   | 0; Mismatches 0; Indels 0; Gaps 0; |
| QY   | 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38                     |                                    |
| Db   | 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38                     |                                    |
| RESULT 3   |  |                                    |
| LOCUS  | AX355389   | 38 bp DNA linear PAT 06-FEB-2002   |
| DEFINITION   | Sequence 417 from Patent WO0197843.                            |                                    |
| ACCESSION  | AX355389   |                                    |
| VERSION  | AX355389.1   | GI:18620057                        |
| KEYWORDS   | synthetic construct  |                                    |
| SOURCE   | other sequences; artificial sequences.                         |                                    |
| ORGANISM   |  |                                    |
| REFERENCE  | 1  |                                    |
| AUTHORS  | Weiner,G. and Hartmann,G.                                      |                                    |
| TITLE  | Methods for enhancing antibody-induced cell lysis and treating |                                    |
| JOURNAL  | Patent: WO 0197843-A 417 27-DEC-2001;                          |                                    |
| UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)                        |  |                                    |
| FEATURES   | Location/Qualifiers  |                                    |

|                                 |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
|---------------------------------|---|---------------------------------------|----|--------------------------------------|--|----------------------------|--|------------------------|--|---|--|
| source                          |   | 1. .38                                |    | /organism="synthetic construct"      |  | /mol_type="unassigned DNA" |  | /db_xref="taxon:32630" |  | /note="Synthetic oligonucleotide chimeric phosphorothioate/phosphodiester backbone with phosphorothioate at 5' and 3' ends" |  |
| ORIGIN                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| Query Match                     |   | 100.0%; Score 38; DB 6; Length 38;    |    | Best Local Similarity                |  | 100.0%; Pred. No. 2.3e-05; |  | Matches                |  | 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   |  |
| Qy                              | 1 | GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC | 38 |                                      |  |                            |  |                        |  |   |  |
| Db                              | 1 | GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC | 38 |                                      |  |                            |  |                        |  |   |  |
| RESULT 4                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| AX547009                        |   | AX547009                              |    | Sequence 148 from Patent WO20053141. |  | 38 bp                      |  | DNA                    |  | linear  |  |
| DEFINITION                      |   | AX547009                              |    | Sequence 148 from Patent WO20053141. |  | 38 bp                      |  | DNA                    |  | linear  |  |
| ACCESSION                       |   | AX547009                              |    | Sequence 148 from Patent WO20053141. |  | 38 bp                      |  | DNA                    |  | linear  |  |
| VERSION                         |   | AX547009.1                            |    | GI:25812153                          |  |                            |  |                        |  |   |  |
| KEYWORDS                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| SOURCE                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| ORGANISM                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| REFERENCE                       |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| AUTHORS                         |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| TITLE                           |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| JOURNAL                         |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| FEATURES                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| source                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| 1. .38                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| /organism="synthetic construct" |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| /mol_type="unassigned DNA"      |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| /db_xref="taxon:32630"          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| /note="Synthetic Sequence"      |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| ORIGIN                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| Query Match                     |   | 100.0%; Score 38; DB 6; Length 38;    |    | Best Local Similarity                |  | 100.0%; Pred. No. 2.3e-05; |  | Matches                |  | 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   |  |
| Qy                              | 1 | GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC | 38 |                                      |  |                            |  |                        |  |   |  |
| Db                              | 1 | GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC | 38 |                                      |  |                            |  |                        |  |   |  |
| RESULT 5                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| AR035457                        |   | AR035457                              |    | Sequence 29 from patent US 5871902.  |  | 43 bp                      |  | DNA                    |  | linear  |  |
| DEFINITION                      |   | AR035457                              |    | Sequence 29 from patent US 5871902.  |  | 43 bp                      |  | DNA                    |  | linear  |  |
| ACCESSION                       |   | AR035457                              |    | Sequence 29 from patent US 5871902.  |  | 43 bp                      |  | DNA                    |  | linear  |  |
| VERSION                         |   | AR035457.1                            |    | GI:5952125                           |  |                            |  |                        |  |   |  |
| KEYWORDS                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| SOURCE                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| ORGANISM                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| REFERENCE                       |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| AUTHORS                         |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| TITLE                           |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| JOURNAL                         |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| FEATURES                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| source                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| 1. .43                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| /organism="unknown"             |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| /mol_type="unassigned DNA"      |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| ORIGIN                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| Query Match                     |   | 81.1%; Score 30.8; DB 6; Length 43;   |    | Best Local Similarity                |  | 86.8%; Pred. No. 0.061;    |  | Matches                |  | 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;   |  |
| Qy                              | 1 | GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC | 38 |                                      |  |                            |  |                        |  |   |  |
| Db                              | 1 | GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC | 38 |                                      |  |                            |  |                        |  |   |  |
| RESULT 6                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| AR035456                        |   | AR035456                              |    | Sequence 28 from patent US 5871902.  |  | 46 bp                      |  | DNA                    |  | linear  |  |
| DEFINITION                      |   | AR035456                              |    | Sequence 28 from patent US 5871902.  |  | 46 bp                      |  | DNA                    |  | linear  |  |
| ACCESSION                       |   | AR035456                              |    | Sequence 28 from patent US 5871902.  |  | 46 bp                      |  | DNA                    |  | linear  |  |
| VERSION                         |   | AR035456.1                            |    | GI:5952124                           |  |                            |  |                        |  |   |  |
| KEYWORDS                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| SOURCE                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| ORGANISM                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| REFERENCE                       |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| AUTHORS                         |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| TITLE                           |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| JOURNAL                         |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| FEATURES                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| source                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| 1. .46                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| /organism="unknown"             |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| /mol_type="unassigned DNA"      |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| ORIGIN                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| Query Match                     |   | 79.5%; Score 30.2; DB 6; Length 46;   |    | Best Local Similarity                |  | 91.4%; Pred. No. 0.051;    |  | Matches                |  | 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;   |  |
| Qy                              | 1 | GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTT   | 35 |                                      |  |                            |  |                        |  |   |  |
| Db                              | 6 | GGGGACTTTCCGCTGGGGACTTTCCAGGGGAGCGT   | 40 |                                      |  |                            |  |                        |  |   |  |
| RESULT 7                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| AR005185                        |   | AR005185                              |    | Sequence 43 from patent US 5747641.  |  | 39 bp                      |  | DNA                    |  | linear  |  |
| DEFINITION                      |   | AR005185                              |    | Sequence 43 from patent US 5747641.  |  | 39 bp                      |  | DNA                    |  | linear  |  |
| ACCESSION                       |   | AR005185                              |    | Sequence 43 from patent US 5747641.  |  | 39 bp                      |  | DNA                    |  | linear  |  |
| VERSION                         |   | AR005185.1                            |    | GI:3966064                           |  |                            |  |                        |  |   |  |
| KEYWORDS                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| SOURCE                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| ORGANISM                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| REFERENCE                       |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| AUTHORS                         |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| TITLE                           |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| JOURNAL                         |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| FEATURES                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| source                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| 1. .39                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| /organism="unknown"             |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| /mol_type="unassigned DNA"      |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| ORIGIN                          |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| Query Match                     |   | 78.9%; Score 30; DB 6; Length 39;     |    | Best Local Similarity                |  | 86.8%; Pred. No. 0.061;    |  | Matches                |  | 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;   |  |
| Qy                              | 1 | GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC | 38 |                                      |  |                            |  |                        |  |   |  |
| Db                              | 1 | GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC | 38 |                                      |  |                            |  |                        |  |   |  |
| RESULT 8                        |   |                                       |    |                                      |  |                            |  |                        |  |   |  |
| AR005186/c                      |   | AR005186                              |    | Sequence 44 from patent US 5747641.  |  | 39 bp                      |  | DNA                    |  | linear  |  |
| DEFINITION                      |   | AR005186                              |    | Sequence 44 from patent US 5747641.  |  | 39 bp                      |  | DNA                    |  | linear  |  |

ACCESSION AR005186  
VERSION AR005186.1 GI:3966065  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 39)  
TITLE Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
JOURNAL Tat-derived transport polypeptide conjugates  
FEATURES Patent: US 5747641-A 44 05-MAY-1998;  
Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2  
|||||

RESULT 9  
LOCUS AR038395  
DEFINITION Sequence 43 from patent US 5804604.  
ACCESSION AR038395  
VERSION AR038395.1 GI:5957112  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 39)  
TITLE Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
JOURNAL Tat-derived transport polypeptides and fusion proteins  
FEATURES Patent: US 5804604-A 43 08-SEP-1998;  
Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2  
|||||

RESULT 10  
LOCUS AR038396/c  
DEFINITION Sequence 44 from patent US 5804604.  
ACCESSION AR038396  
VERSION AR038396.1 GI:5957113  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 39)  
TITLE Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
JOURNAL Tat-derived transport polypeptides and fusion proteins  
FEATURES Patent: US 5804604-A 44 08-SEP-1998;  
Location/Qualifiers  
source 1. .39

ORIGIN

Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||

RESULT 11  
LOCUS AR178131  
DEFINITION Sequence 43 from patent US 6316003.  
ACCESSION AR178131  
VERSION AR178131.1 GI:17921024  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 39)  
TITLE Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
JOURNAL Tat-derived transport polypeptides  
FEATURES Patent: US 6316003-A 43 13-NOV-2001;  
Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||

RESULT 12  
LOCUS AR178132/c  
DEFINITION Sequence 44 from patent US 6316003.  
ACCESSION AR178132  
VERSION AR178132.1 GI:17921025  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 39)  
TITLE Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
JOURNAL Tat-derived transport polypeptides  
FEATURES Patent: US 6316003-A 44 13-NOV-2001;  
Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||

RESULT 13  
LOCUS AR178133  
DEFINITION Sequence 43 from patent US 6316003.  
ACCESSION AR178133  
VERSION AR178133.1 GI:17921024  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 39)  
TITLE Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
JOURNAL Tat-derived transport polypeptides  
FEATURES Patent: US 6316003-A 43 13-NOV-2001;  
Location/Qualifiers  
source 1. .39  
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/mol\_type="unassigned DNA"

ORIGIN

Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2  
|||||

ORIGIN

Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2  
|||||

RESULT 11  
LOCUS AR178131  
DEFINITION Sequence 43 from patent US 6316003.  
ACCESSION AR178131  
VERSION AR178131.1 GI:17921024  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 39)  
TITLE Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
JOURNAL Tat-derived transport polypeptides  
FEATURES Patent: US 6316003-A 43 13-NOV-2001;  
Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||

RESULT 12  
LOCUS AR178132/c  
DEFINITION Sequence 44 from patent US 6316003.  
ACCESSION AR178132  
VERSION AR178132.1 GI:17921025  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 39)  
TITLE Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
JOURNAL Tat-derived transport polypeptides  
FEATURES Patent: US 6316003-A 44 13-NOV-2001;  
Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||

RESULT 13  
LOCUS AR178133  
DEFINITION Sequence 43 from patent US 6316003.  
ACCESSION AR178133  
VERSION AR178133.1 GI:17921024  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 39)  
TITLE Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
JOURNAL Tat-derived transport polypeptides  
FEATURES Patent: US 6316003-A 43 13-NOV-2001;  
Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2  
|||||

RESULT 13  
158471  
LOCUS 158471 39 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 43 from patent US 5652122.  
ACCESSION 158471  
VERSION 158471.1 GI:2477709  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
Pepinsky,R.Blake.  
TITLE Nucleic acids encoding and methods of making tat-derived transport  
polypeptides  
JOURNAL Patent: US 5652122-A 43 29-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTCCGCTGGGACTTTCACAGGGGACTTTC 38  
Db 1 GGGGACTTCCGCTGGGACTTTCACAGGGGACTTTC 38  
RESULT 14  
158472/c  
LOCUS 158472 39 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 44 from patent US 5652122.  
ACCESSION 158472  
VERSION 158472.1 GI:2477710  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
Pepinsky,R.Blake.  
TITLE Nucleic acids encoding and methods of making tat-derived transport  
polypeptides  
JOURNAL Patent: US 5652122-A 44 29-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTCCGCTGGGACTTTCACAGGGGACTTTC 38  
Db 1 GGGGACTTCCGCTGGGACTTTCACAGGGGACTTTC 38  
RESULT 15  
16589  
LOCUS 16589 39 bp DNA linear PAT 29-DEC-1997  
DEFINITION Sequence 43 from patent US 5670617.  
ACCESSION 16589  
VERSION 16589.1 GI:2724566  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)

AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
Pepinsky,R.Blake.  
TITLE Nucleic acid conjugates of tat-derived transport polypeptides  
JOURNAL Patent: US 5670617-A 43 23-SEP-1997;  
FEATURES Location/Qualifiers  
source 1..39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTCCGCTGGGACTTTCACAGGGGACTTTC 38  
Db 1 GGGGACTTCCGCTGGGACTTTCACAGGGGACTTTC 38  
RESULT 16  
166590/c  
LOCUS 166590 39 bp DNA linear PAT 29-DEC-1997  
DEFINITION Sequence 44 from patent US 5670617.  
ACCESSION 166590  
VERSION 166590.1 GI:2724567  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
Pepinsky,R.Blake.  
TITLE Nucleic acid conjugates of tat-derived transport polypeptides  
JOURNAL Patent: US 5670617-A 44 23-SEP-1997;  
FEATURES Location/Qualifiers  
source 1..39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTCCGCTGGGACTTTCACAGGGGACTTTC 38  
Db 39 GGGGACTTCCGCTGGGACTTTCACAGGGGACTTTC 2  
RESULT 17  
168236  
LOCUS 168236 39 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 43 from patent US 5674980.  
ACCESSION 168236  
VERSION 168236.1 GI:2830358  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
Pepinsky,R.Blake.  
TITLE Fusion protein comprising tat-derived transport moiety  
JOURNAL Patent: US 5674980-A 43 07-OCT-1997;  
FEATURES Location/Qualifiers  
source 1..39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 38
|||||
Db 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 38
|||||

RESULT 18
168237/c
LOCUS 168237
DEFINITION Sequence 44 from patent US 5674980.
ACCESSION 168237
VERSION 168237.1 GI:2830359
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 39)
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and
Pepinsky,R.Blake.
TITLE Fusion protein comprising tat-derived transport moiety
JOURNAL Patent: US 5674980-A 44 07-OCT-1997;
FEATURES
source
1..39
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 78.9%; Score 30; DB 6; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.061;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 38
|||||
Db 39 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 2
|||||

RESULT 19
BD261195
LOCUS BD261195
DEFINITION Triterpen compositions and methods for use thereof.
ACCESSION BD261195
VERSION BD261195.1 GI:33070965
KEYWORDS JP 2002515430-A/9.
SOURCE synthetic construct
ORGANISM other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 44)
AUTHORS Arntzen,C.J., Tracey,M.B., Gutterman,J.U., Hoffmann,J.J.,
Bailey,D.T. and Jayatilake,G.S.
TITLE Triterpen compositions and methods for use thereof
JOURNAL Patent: JP 2002515430-A 9 28-MAY-2002;
COMMENT RESEARCH DEVELOPMENT FOUNDATION
OS Artificial Sequence
PN JP 2002515430-A/9
PD 28-MAY-2002
PF 19-MAY-1999 JP 2000549243
PR 19-MAY-1998 US 60/085997,03-SEP-1998 US 60/090666 PI
CHARLES J ARNTZEN, MARY BLAKE TRACEY, JORDAN U GUTTERMAN, JOSEPH PI
J HOFFMANN,
PI DAVID T BAILEY, GAMINI S JAYATILAKE
PC A61K35/78,A61K35/78,A61K31/7028,A61K31/704,A61P35/00,A61P43/00, PC
C12N5/04//
PC C07H15/18,C07H15/256,C12N5/00
CC Description of Artificial Sequence:SYNTHETIC PRIMER FH Key
Location/Qualifiers
FT source
1..44
FT Location/Qualifiers
1..44
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 78.4%; Score 29.8; DB 6; Length 44;
Best Local Similarity 93.9%; Pred. No. 0.076;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 34
|||||
Db 10 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 42
|||||

RESULT 20
AR225344
LOCUS AR225344
DEFINITION Sequence 9 from patent US 6444233.
ACCESSION AR225344
VERSION AR225344.1 GI:27263287
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Arntzen,C.J., Blake,M.E., Gutterman,J.U., Hoffmann,J.J.,
Jayatilake,G.S. and Bailey,D.T.
TITLE Triterpene compositions and methods for use thereof
JOURNAL Patent: US 644233-A 9 03-SEP-2002;
FEATURES
source
1..44
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 78.4%; Score 29.8; DB 6; Length 44;
Best Local Similarity 93.9%; Pred. No. 0.076;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 34
|||||
Db 10 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 42
|||||

RESULT 21
AR473523
LOCUS AR473523
DEFINITION Sequence 9 from patent US 6689398.
ACCESSION AR473523
VERSION AR473523.1 GI:42711810
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Haridas,V. and Gutterman,J.U.
TITLE Triterpene compositions and methods for use thereof
JOURNAL Patent: US 6689398-A 9 10-FEB-2004;
FEATURES
source
1..44
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 78.4%; Score 29.8; DB 6; Length 44;
Best Local Similarity 93.9%; Pred. No. 0.076;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 34
|||||
Db 10 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 42
|||||

RESULT 22
Query Match 78.4%; Score 29.8; DB 6; Length 44;
Best Local Similarity 93.9%; Pred. No. 0.076;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 34
|||||
Db 10 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 42
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AR542759  
LOCUS AR542759 44 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 9 from patent US 6746696.  
ACCESSION AR542759  
VERSION AR542759.1 GI:53935323  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 44)  
AUTHORS Arnzen,C.J. and Gutterman,J.U.  
TITLE Triterpene compositions and methods for use thereof  
JOURNAL Patent: US 6746696-A 9 08-JUN-2004;  
Research Development Foundation; Carson City, NV  
FEATURES  
source  
1..44  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 78.4%; Score 29.8; DB 6; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.076; 2; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGGACT 34  
|||||  
Db 10 GGGACTTTCGGCTGGGACTTTCAGGGGGCT 42  
|||||

RESULT 23  
LOCUS AR027239 45 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 12 from patent US 5856161.  
ACCESSION AR027239  
VERSION AR027239.1 GI:5938079  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 45)  
AUTHORS Aggarwal,B.B. and Darnay,B.G.  
TITLE Tumor necrosis factor receptor-I-associated protein kinase and methods for its use  
JOURNAL Patent: US 5856161-A 12 05-JAN-1999;  
FEATURES  
source  
1..45  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 76.8%; Score 29.2; DB 6; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.14; 3; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGGACTT 35  
|||||  
Db 10 GGGACTTTCGGCTGGGACTTTCAGGGGGCT 43  
|||||

RESULT 24  
LOCUS AR035447 45 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 19 from patent US 5871902.  
ACCESSION AR035447  
VERSION AR035447.1 GI:5952115  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 45)  
AUTHORS Weininger,S. and Weininger,A.M.  
TITLE Sequence-specific detection of nucleic acid hybrids using a DNA-binding molecule or assembly capable of discriminating perfect

hybrids from non-perfect hybrids  
Patent: US 5871902-A 19 16-FEB-1999;  
Location/Qualifiers  
1..45  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 76.8%; Score 29.2; DB 6; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.14; 3; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGGACTT 35  
|||||  
Db 7 GGGACTTTCGGCTGGGACTTTCAGGGAGGCGT 40  
|||||

RESULT 25  
LOCUS AR035451 45 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 23 from patent US 5871902.  
ACCESSION AR035451  
VERSION AR035451.1 GI:5952119  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 45)  
AUTHORS Weininger,S. and Weininger,A.M.  
TITLE Sequence-specific detection of nucleic acid hybrids using a DNA-binding molecule or assembly capable of discriminating perfect hybrids from non-perfect hybrids  
JOURNAL Patent: US 5871902-A 23 16-FEB-1999;  
FEATURES  
source  
1..45  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 76.8%; Score 29.2; DB 6; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.14; 3; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGGACTT 35  
|||||  
Db 7 GGGACTTTCGGCTGGGACTTTCAGGGAGGCGT 40  
|||||

RESULT 26  
LOCUS AR035448 46 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 20 from patent US 5871902.  
ACCESSION AR035448  
VERSION AR035448.1 GI:5952116  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 46)  
AUTHORS Weininger,S. and Weininger,A.M.  
TITLE Sequence-specific detection of nucleic acid hybrids using a DNA-binding molecule or assembly capable of discriminating perfect hybrids from non-perfect hybrids  
JOURNAL Patent: US 5871902-A 20 16-FEB-1999;  
FEATURES  
source  
1..46  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 76.3%; Score 29; DB 6; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 GGGACTTTCGCTGGGACTTTCCAGGG 30
    |||||
Db 7 GGGACTTTCGCTGGGACTTTCCAGGG 35

RESULT 27
AR035449
LOCUS AR035449 linear DNA 46 bp PAT 29-SEP-1999
DEFINITION Sequence 21 from patent US 5871902.
ACCESSION AR035449
VERSION AR035449.1 GI:5952117
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned DNA

REFERENCE
1 (bases 1 to 46)
AUTHORS Weininger, S. and Weininger, A.M.
TITLE Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
JOURNAL Patent: US 5871902-A 21 16-FEB-1999;
FEATURES Location/Qualifiers
source 1..46
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 76.3%; Score 29; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCCAGGG 30
    |||||
Db 7 GGGACTTTCGCTGGGACTTTCCAGGG 35

RESULT 30
AR049839
LOCUS AR049839 36 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 142 from patent US 5824770.
ACCESSION AR049839
VERSION AR049839.1 GI:5971831
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned DNA

REFERENCE
1 (bases 1 to 36)
AUTHORS Georgopoulos, K.
TITLE Ikaros polypeptides
JOURNAL Patent: US 5824770-A 142 20-OCT-1998;
FEATURES Location/Qualifiers
source 1..36
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 75.8%; Score 28.8; DB 6; Length 36;
Best Local Similarity 93.8%; Pred. No. 0.2;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCCAGGGAC 33
    |||||
Db 4 GGGACTTTCGCTGGGACTTTCCAGGGAGC 35

RESULT 31
AR149733
LOCUS AR149733 36 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 142 from patent US 6228611.
ACCESSION AR149733
VERSION AR149733.1 GI:15114324
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned DNA

REFERENCE
1 (bases 1 to 36)
AUTHORS Georgopoulos, K.
TITLE Ikaros: A T cell pathway regulatory gene
JOURNAL Patent: US 6228611-A 142 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..36
/organism="unknown"
/mol_type="unassigned DNA"
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QY 2 GGGACTTTCGCTGGGACTTTCCAGGG 30
    |||||
Db 7 GGGACTTTCGCTGGGACTTTCCAGGG 35

RESULT 28
AR035450
LOCUS AR035450 linear DNA 46 bp PAT 29-SEP-1999
DEFINITION Sequence 22 from patent US 5871902.
ACCESSION AR035450
VERSION AR035450.1 GI:5952118
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned DNA

REFERENCE
1 (bases 1 to 46)
AUTHORS Weininger, S. and Weininger, A.M.
TITLE Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
JOURNAL Patent: US 5871902-A 22 16-FEB-1999;
FEATURES Location/Qualifiers
source 1..46
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 76.3%; Score 29; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCCAGGG 30
    |||||
Db 7 GGGACTTTCGCTGGGACTTTCCAGGG 35

RESULT 29
AR035455
LOCUS AR035455 linear DNA 46 bp PAT 29-SEP-1999
DEFINITION Sequence 27 from patent US 5871902.
ACCESSION AR035455
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|                       |  |                       |   |               |           |
|-----------------------|--|-----------------------|---|---------------|-----------|
| ORIGIN                |  | AR438116              |   | AR438116      |           |
| Query Match           | 75.8%; Score 28.8; DB 6; Length 36;                                | LOCUS                 | Sequence 9 from patent US 6660906.                              | 32 bp         | DNA       |
| Best Local Similarity | 93.8%; Pred. No. 0.2;  | DEFINITION            | Sequence 9 from patent US 6660906.                              |               |           |
| Matches               | 30; Conservative   | ACCESSION             | AR438116  |               |           |
|                       |  | VERSION               | AR438116.1  | GI:40204578   |           |
| QY                    | 2 GGGACTTTCGGCTGGGGACTTTCCAGGGGAC 33                               | KEYWORDS              | Unknown.  |               |           |
| Db                    | 4 GGGACTTTCGGCTGGGGACTTTCCAGGGAGGC 35                              | SOURCE                | Unknown.  |               |           |
|                       |  | ORGANISM              | Unclassified.   |               |           |
| RESULT 32             |  | REFERENCE             | 1 (bases 1 to 32)   |               |           |
| LOCUS                 | AR404853   | AUTHORS               | Tsichlis,P.N.   |               |           |
| DEFINITION            | Sequence 142 from patent US 6630141.                               | TITLE                 | Tp12 transgenic knockout mice                                   |               |           |
| ACCESSION             | AR404853   | JOURNAL               | Patent: US 6660906-A 9 09-DEC-2003;                             |               |           |
| VERSION               | AR404853.1   |                       | Thomas Jefferson University; Philadelphia, PA;                  |               |           |
| KEYWORDS              | Unknown.   |                       | WOX;  |               |           |
| SOURCE                | Unknown.   | FEATURES              | Location/Qualifiers   |               |           |
| ORGANISM              | Unclassified.  | source                | 1..32   |               |           |
| REFERENCE             | 1 (bases 1 to 36)  |                       | /organism="unknown"   |               |           |
| AUTHORS               | Georgopoulos,K.  |                       | /mol_type="genomic DNA"   |               |           |
| TITLE                 | Isolated antibody that binds to an Ikaros polypeptide              | ORIGIN                |   |               |           |
| JOURNAL               | Patent: US 6630141-A 142 07-OCT-2003;                              | Query Match           | 73.7%; Score 28; DB 6; Length 32;                               |               |           |
|                       | The General Hospital Corporation; Boston, MA                       | Best Local Similarity | 100.0%; Pred. No. 0.44;   |               |           |
| FEATURES              | Location/Qualifiers  | Matches               | 28; Conservative  | 0; Mismatches | 0; Indels |
| source                | 1..36  | QY                    | 2 GGGACTTTCGGCTGGGGACTTTCCAGGG 29                               |               |           |
|                       | /organism="unknown"  | Db                    | 5 GGGACTTTCGGCTGGGGACTTTCCAGGG 32                               |               |           |
|                       | /mol_type="mRNA"   |                       |   |               |           |
| ORIGIN                |  | AR438118              |   | AR438118      |           |
| Query Match           | 75.8%; Score 28.8; DB 6; Length 36;                                | LOCUS                 | Sequence 11 from patent US 6660906.                             | 32 bp         | DNA       |
| Best Local Similarity | 93.8%; Pred. No. 0.2;  | DEFINITION            | Sequence 11 from patent US 6660906.                             |               |           |
| Matches               | 30; Conservative   | ACCESSION             | AR438118  |               |           |
|                       |  | VERSION               | AR438118.1  | GI:40204580   |           |
| QY                    | 2 GGGACTTTCGGCTGGGGACTTTCCAGGGGAC 33                               | KEYWORDS              | Unknown.  |               |           |
| Db                    | 4 GGGACTTTCGGCTGGGGACTTTCCAGGGAGGC 35                              | SOURCE                | Unknown.  |               |           |
|                       |  | ORGANISM              | Unclassified.   |               |           |
| RESULT 33             |  | REFERENCE             | 1 (bases 1 to 32)   |               |           |
| LOCUS                 | AR035466   | AUTHORS               | Tsichlis,P.N.   |               |           |
| DEFINITION            | Sequence 38 from patent US 5871902.                                | TITLE                 | Tp12 transgenic knockout mice                                   |               |           |
| ACCESSION             | AR035466   | JOURNAL               | Patent: US 6660906-A 11 09-DEC-2003;                            |               |           |
| VERSION               | AR035466.1   |                       | Thomas Jefferson University; Philadelphia, PA;                  |               |           |
| KEYWORDS              | Unknown.   |                       | WOX;  |               |           |
| SOURCE                | Unknown.   | FEATURES              | Location/Qualifiers   |               |           |
| ORGANISM              | Unclassified.  | source                | 1..32   |               |           |
| REFERENCE             | 1 (bases 1 to 37)  |                       | /organism="unknown"   |               |           |
| AUTHORS               | Weininger,S. and Weininger,A.M.                                    |                       | /mol_type="genomic DNA"   |               |           |
| TITLE                 | Sequence-specific detection of nucleic acid hybrids using a        | ORIGIN                |   |               |           |
|                       | DNA-binding molecule or assembly capable of discriminating perfect | Query Match           | 73.7%; Score 28; DB 6; Length 32;                               |               |           |
|                       | hybrids from non-perfect hybrids                                   | Best Local Similarity | 100.0%; Pred. No. 0.44;   |               |           |
| JOURNAL               | Patent: US 5871902-A 38 16-FEB-1999;                               | Matches               | 28; Conservative  | 0; Mismatches | 0; Indels |
| FEATURES              | Location/Qualifiers  | QY                    | 2 GGGACTTTCGGCTGGGGACTTTCCAGGG 29                               |               |           |
| source                | 1..37  | Db                    | 5 GGGACTTTCGGCTGGGGACTTTCCAGGG 32                               |               |           |
|                       | /organism="unknown"  |                       |   |               |           |
|                       | /mol_type="unassigned DNA"   |                       |   |               |           |
| ORIGIN                |  | BD081630              |   | BD081630      |           |
| Query Match           | 74.7%; Score 28.4; DB 6; Length 37;                                | LOCUS                 | Inhibition of human immunodeficiency virus (HIV-1) replication. | 33 bp         | DNA       |
| Best Local Similarity | 96.7%; Pred. No. 0.3;  | DEFINITION            | Inhibition of human immunodeficiency virus (HIV-1) replication. |               |           |
| Matches               | 29; Conservative   | ACCESSION             | BD081630  |               |           |
|                       |  | VERSION               | BD081630.1  | GI:22627233   |           |
| QY                    | 2 GGGACTTTCGGCTGGGGACTTTCCAGGGG 31                                 | KEYWORDS              | JP 2001520017-A/4.  |               |           |
| Db                    | 7 GGGACTTTCGGCTGGGGACTTTCCAGGGAG 36                                | SOURCE                | synthetic construct   |               |           |
|                       |  | ORGANISM              | other sequences; artificial sequences.                          |               |           |
| RESULT 34             |  | REFERENCE             | 1 (bases 1 to 33)   |               |           |
|                       |  | AUTHORS               | Suhadolnik,R.J., Adelson,M.E. and Iacono,K.T.                   |               |           |



TITLE Inhibition of human immunodeficiency virus (HIV-1) replication  
JOURNAL Patent: JP 2001520017-A 4 30-OCT-2001;  
COMMENT TEMPLE UNIVERSITY OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION  
OS Artificial Sequence  
PN JP 2001520017-A/4  
PD 30-OCT-2001  
PF 15-OCT-1998 JP 2000516047  
PR 16-OCT-1997 US 60/061984  
PT ROBERT J SUHADOLNIK, MARTIN E ADELSON, KATHRYN T IACONO PC  
C12N15/09, A61K31/513, A61K45/00, A61K45/06, A61K48/00, A61P31/18, PC  
A61P37/04,  
PC  
C12N1/15, C12N1/19, C12N1/21, C12N5/10, A61K35/76, C12N15/00, C12N5/ PC  
00  
CC Description of Artificial Sequence: sense probe CC  
oligonucleotide  
CC corresponding to NF-kappa beta binding site  
FH Key Location/Qualifiers  
FT source 1..33  
FT Location/Qualifiers  
1..33  
/organism="Artificial Sequence".  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Query Match 73.7%; Score 28; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCCGCTGGGACTTTCCAGG 29  
|||||  
DB 5 GGGACTTTCCGCTGGGACTTTCCAGG 32  
|||||

RESULT 37  
109458  
LOCUS I09458  
DEFINITION Sequence 2 from Patent WO 8908147.  
ACCESSION I09458  
VERSION I09458.1 GI:597836  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 34)  
AUTHORS Baeuerle, P.A. and Baltimore, D.  
TITLE ACTIVATION OF NF-KB PRECURSOR  
JOURNAL Patent: WO 8908147-A 2 08-SEP-1989;  
FEATURES Location/Qualifiers  
source 1..34  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 73.7%; Score 28; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCCGCTGGGACTTTCCAGG 29  
|||||  
DB 6 GGGACTTTCCGCTGGGACTTTCCAGG 33  
|||||

RESULT 38  
BD249738  
LOCUS BD249738  
DEFINITION Intracellular targeted delivery of compounds by 70 kD heat shock protein.  
ACCESSION BD249738  
VERSION BD249738.1 GI:33059508  
KEYWORDS JP 2002530426-A/1.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Fujihara, S.M. and Nadler, S.G.  
TITLE Intracellular targeted delivery of compounds by 70 kD heat shock protein.  
JOURNAL Patent: JP 2002530426-A 1 17-SEP-2002;  
BRISTOL MYERS SQUIBB CO  
COMMENT OS Homo sapiens (human)  
PN JP 2002530426-A/1  
PD 17-SEP-2002  
PF 17-NOV-1999 JP 2000583940  
PR 24-NOV-1998 US 60/109872  
PT SHERI M FUJIHARA, STEVEN G NADLER  
PC A61K38/00, A61K47/48, A61K48/00, A61P3/10, A61P9/00, A61P11/06, PC  
A61P19/02  
PC A61P29/00, A61P29/00, A61P35/00, C12N15/09, A61K37/02, C12N15/00 CC  
Intracellular targeted delivery of compounds by 70 kD heat shock protein  
FH Key Location/Qualifiers  
FT source 1..35  
FT Location/Qualifiers  
1..35  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 73.7%; Score 28; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGACTTTCCAGG 28  
|||||  
DB 8 GGGGACTTTCCGCTGGGACTTTCCAGG 35  
|||||

RESULT 39  
AR532727  
LOCUS AR532727  
DEFINITION Sequence 4 from patent US 6730302.  
ACCESSION AR532727  
VERSION AR532727.1 GI:53922132  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Fujihara, S.M. and Nadler, S.G.  
TITLE Intracellular targeted delivery of compounds by 70 kD heat shock protein.  
JOURNAL Patent: US 6730302-A 4 04-MAY-2004;  
Bristol-Myers Squibb Company; Princeton, NJ  
FEATURES Location/Qualifiers  
source 1..35  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 73.7%; Score 28; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGACTTTCCAGG 28  
|||||  
DB 8 GGGGACTTTCCGCTGGGACTTTCCAGG 35  
|||||

RESULT 40  
AX798846

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LOCUS AX798846 42 bp DNA linear PAT 08-OCT-2003
DEFINITION Sequence 2 from Patent WO03053468.
ACCESSION AX798846
VERSION AX798846.1 GI:37604920
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM
1
REFERENCE
AUTHORS van Lint,C., Burny,A., Quivy,V. and Adam,E.
TITLE Method for obtaining the elimination of integrated and functional
JOURNAL viruses from infected mammal cells
PATENT: WO 03053468-A 2 03-JUL-2003;
UNIVERSITE LIBRE DE BRUXELLES (BE)
FEATURES
source
1..42
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="mutagenic oligonucleotide primer"

ORIGIN
Query Match 73.7%; Score 28; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCACGGG 29
|||||
Db 15 GGGACTTTCGCTGGGGACTTTCACGGG 42

RESULT 41
AR035454
LOCUS AR035454 45 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 26 from patent US 5871902.
ACCESSION AR035454
VERSION AR035454.1 GI:5952122
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 45)
AUTHORS Weininger,S. and Weininger,A.M.
TITLE Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
JOURNAL Patent: US 5871902-A 26 16-FEB-1999;
FEATURES
source
1..45
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 72.6%; Score 27.6; DB 6; Length 45;
Best Local Similarity 88.2%; Pred. No. 0.67;
Matches 30; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCACGGGGGACTT 35
|||||
Db 7 GGGACTTTCGCTGGGGACTTTCACAGAGGCGT 40

RESULT 42
CQ846479/c
LOCUS CQ846479 35 bp DNA linear PAT 02-AUG-2004
DEFINITION Sequence 10 from Patent EP1433485.
ACCESSION CQ846479
VERSION CQ846479.1 GI:50895715
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1

LOCUS AX798846 42 bp DNA linear PAT 08-OCT-2003
DEFINITION Sequence 2 from Patent WO03053468.
ACCESSION AX798846
VERSION AX798846.1 GI:37604920
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM
1
REFERENCE
AUTHORS van Lint,C., Burny,A., Quivy,V. and Adam,E.
TITLE Method for obtaining the elimination of integrated and functional
JOURNAL viruses from infected mammal cells
PATENT: WO 03053468-A 2 03-JUL-2003;
UNIVERSITE LIBRE DE BRUXELLES (BE)
FEATURES
source
1..42
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="mutagenic oligonucleotide primer"

ORIGIN
Query Match 73.7%; Score 28; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCACGGG 29
|||||
Db 15 GGGACTTTCGCTGGGGACTTTCACGGG 42

RESULT 43
AR589386/c
LOCUS AR589386 35 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 6 from patent US 6803044.
ACCESSION AR589386
VERSION AR589386.1 GI:56636662
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Catania,A.P. and Lipton,J.M.
TITLE Antimicrobial and anti-inflammatory peptides for use in human
immunodeficiency virus
JOURNAL Patent: US 6803044-A 6 12-OCT-2004;
Zengen, Inc.; Woodland Hills, CA
FEATURES
source
1..35
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 72.1%; Score 27.4; DB 6; Length 35;
Best Local Similarity 96.6%; Pred. No. 0.8;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCACGGG 29
|||||
Db 32 GGGGACTTTCGCTGGGGACTTTCACATGG 4

RESULT 44
AR035452
LOCUS AR035452 44 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 24 from patent US 5871902.
ACCESSION AR035452
VERSION AR035452.1 GI:5952120
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Weininger,S. and Weininger,A.M.
TITLE Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
JOURNAL Patent: US 5871902-A 24 16-FEB-1999;
FEATURES
source
1..44
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 72.1%; Score 27.4; DB 6; Length 35;
Best Local Similarity 96.6%; Pred. No. 0.8;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCACGGG 29
|||||
Db 32 GGGGACTTTCGCTGGGGACTTTCACATGG 4
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Query Match 72.1%; Score 27.4; DB 6; Length 44;  
Best Local Similarity 83.8%; Pred. No. 0.81;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGACTTTC 38  
|||||  
Db 7 GGGACTTTCGGCTGGGACTTTCAGGGGACTTTC 43  
|||||

RESULT 45  
LOCUS AR035453  
DEFINITION Sequence 25 from patent US 5871902.  
ACCESSION AR035453  
VERSION AR035453.1 GI:5952121  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 44)  
AUTHORS Weininger, S. and Weininger, A. M.  
TITLE Sequence-specific detection of nucleic acid hybrids using a DNA-binding molecule or assembly capable of discriminating perfect hybrids from non-perfect hybrids  
JOURNAL Patent: US 5871902-A 25 16-FEB-1999;  
FEATURES Location/Qualifiers  
1..44  
source /organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 71.6%; Score 27.2; DB 6; Length 44;  
Best Local Similarity 90.6%; Pred. No. 0.99;  
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGAC 33  
|||||  
Db 7 GGGACTTTCGGCTGGGACTTTCAGGGGAC 38  
|||||

RESULT 46  
LOCUS CQ846478  
DEFINITION Sequence 9 from Patent EPI433485.  
ACCESSION CQ846478  
VERSION CQ846478.1 GI:50895714  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Lipton, J. and Catania, A.  
TITLE A uro-genital condition treatment system  
JOURNAL Patent: EP 1433485-A 9 30-JUN-2004;  
Zengen, Inc. (US)  
FEATURES Location/Qualifiers  
1..35  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide probe for NF-kB (sense)"

ORIGIN  
Query Match 69.5%; Score 26.4; DB 6; Length 35;  
Best Local Similarity 96.4%; Pred. No. 2.1;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACTTTCGGCTGGGACTTTCAGG 28  
|||||  
Db 8 GGGACTTTCGGCTGGGACTTTCATG 35  
|||||

RESULT 47  
LOCUS AR585153  
DEFINITION Sequence 9 from patent US 680291.  
ACCESSION AR585153  
VERSION AR585153.1 GI:56628768  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Lipton, J. M. and Catania, A. P.  
TITLE Uro-genital condition treatment system  
JOURNAL Patent: US 680291-A 9 05-OCT-2004;  
Zengen, Inc.; Woodland Hills, CA  
FEATURES Location/Qualifiers  
1..35  
source /organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 69.5%; Score 26.4; DB 6; Length 35;  
Best Local Similarity 96.4%; Pred. No. 2.1;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACTTTCGGCTGGGACTTTCAGG 28  
|||||  
Db 8 GGGACTTTCGGCTGGGACTTTCATG 35  
|||||

RESULT 48  
LOCUS AR589385  
DEFINITION Sequence 5 from patent US 6803044.  
ACCESSION AR589385  
VERSION AR589385.1 GI:56636661  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Catania, A. P. and Lipton, J. M.  
TITLE Antimicrobial and anti-inflammatory peptides for use in human immunodeficiency virus  
JOURNAL Patent: US 6803044-A 5 12-OCT-2004;  
Zengen, Inc.; Woodland Hills, CA  
FEATURES Location/Qualifiers  
1..35  
source /organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 69.5%; Score 26.4; DB 6; Length 35;  
Best Local Similarity 96.4%; Pred. No. 2.1;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACTTTCGGCTGGGACTTTCAGG 28  
|||||  
Db 8 GGGACTTTCGGCTGGGACTTTCATG 35  
|||||

RESULT 49  
LOCUS AR397504  
DEFINITION Sequence 5 from patent US 6617171.  
ACCESSION AR397504  
VERSION AR397504.1 GI:40134392  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Faustman, D. L. and Hayashi, T.

TITLE Methods for diagnosing and treating autoimmune disease  
JOURNAL Patent: US 6617171-A 5 09-SEP-2003;  
The General Hospital Corporation; Boston, MA  
FEATURES  
source 1. .32  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 68.4%; Score 26; DB 6; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGGCTGGGACTTTCCAG 27  
|||||  
Db 7 GGGACTTTCGGCTGGGACTTTCCAG 32  
RESULT 50  
AR575406  
LOCUS AR575406 32 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 1 from patent US 6773705.  
ACCESSION AR575406  
VERSION AR575406.1 GI:56576396  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Faustman,D.L. and Hayashi,T.  
TITLE Methods for diagnosing and treating autoimmune disease  
JOURNAL Patent: US 6773705-A 1 10-AUG-2004;  
General Hospital Corporation; Boston, MA  
FEATURES  
source 1. .32  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 68.4%; Score 26; DB 6; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGGCTGGGACTTTCCAG 27  
|||||  
Db 7 GGGACTTTCGGCTGGGACTTTCCAG 32

Search completed: February 15, 2006, 18:55:57  
Job time : 924.686 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:25:23 ; Search time 286.413 Seconds  
(without alignments)  
884.241 Million cell updates/sec

Title: US-09-669-187A-148  
Perfect score: 38  
Sequence: 1 ggggacttccgtgggactttccaggggactttccc 38

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

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- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 38    | 100.0       | 38     | 3  | Aaz32919 Kappa-B-P |
| 2          | 38    | 100.0       | 38     | 4  | Aaf99023 Immunosti |
| 3          | 38    | 100.0       | 38     | 6  | Ab577664 Angiogene |
| 4          | 38    | 100.0       | 38     | 6  | Ab139015 Immunosti |
| 5          | 38    | 100.0       | 38     | 9  | Acd99455 Immunosti |
| 6          | 38    | 100.0       | 38     | 9  | Adb36525 Immunosti |
| 7          | 38    | 100.0       | 38     | 13 | Adu89464 Allergic  |
| 8          | 30.8  | 81.1        | 43     | 2  | Aat30609 Target bi |
| 9          | 30.2  | 79.5        | 46     | 2  | Aat30608 Target bi |
| 10         | 30    | 78.9        | 39     | 2  | Aaq58049 Oligonucl |
| 11         | 30    | 78.9        | 39     | 2  | Aaq58050 Oligonucl |
| 12         | 30    | 78.9        | 39     | 2  | Aat84584 NF-kappa  |
| 13         | 30    | 78.9        | 39     | 2  | Aat88240 NF-kappaB |
| 14         | 30    | 78.9        | 39     | 2  | Aat88239 NF-kappaB |
| 15         | 30    | 78.9        | 39     | 2  | Aat89779 Transcrip |
| 16         | 30    | 78.9        | 39     | 2  | Aat89780 Transcrip |
| 17         | 30    | 78.9        | 39     | 2  | Aav56615 NF-kappaB |
| 18         | 30    | 78.9        | 39     | 2  | Aav56616 NF-kappaB |
| 19         | 30    | 78.9        | 39     | 6  | Aad26647 NF-kB wil |

|       |      |      |    |    |           |                     |       |      |      |    |    |          |                    |
|-------|------|------|----|----|-----------|---------------------|-------|------|------|----|----|----------|--------------------|
| 93    | 23   | 60.5 | 23 | 2  | AAT95708  | Aat95708 DNA from   | C 166 | 16.2 | 42.6 | 46 | 2  | AAT34424 | Aat34424 Primer fo |
| 94    | 23   | 60.5 | 23 | 2  | AAV04923  | Aav04923 Primer LT  | 167   | 15.8 | 41.6 | 28 | 6  | ABK94866 | Abk94866 Fat regul |
| 95    | 23   | 60.5 | 23 | 2  | AAV09864  | Aav09864 Primer LT  | 168   | 15.8 | 41.6 | 32 | 14 | ADY62240 | Ady62240 FeLV p15E |
| 96    | 23   | 60.5 | 23 | 2  | AAV15221  | Aav15221 PCR prime  | C 169 | 15.8 | 41.6 | 45 | 2  | AAT35082 | Aat35082 Human int |
| 97    | 23   | 60.5 | 23 | 3  | AAA90157  | Aaa90157 PCR prime  | C 170 | 15.8 | 41.6 | 47 | 3  | AAC87820 | Aac87820 Zymogen a |
| 98    | 23   | 60.5 | 23 | 3  | AAI72530  | Aai72530 Nested PC  | C 171 | 15.8 | 41.6 | 47 | 4  | AAF55294 | Aaf55294 Primer us |
| 99    | 23   | 60.5 | 23 | 8  | ABX11223  | Abx11223 HIV-1 PCR  | 172   | 15.6 | 41.1 | 25 | 9  | ACI53845 | Aci53845 Human mic |
| 100   | 22.4 | 58.9 | 25 | 2  | AAQ30479  | Aaq30479 Phosphorot | 173   | 15.6 | 41.1 | 37 | 10 | ADK68360 | Adk68360 HCMV glyc |
| C 101 | 22   | 57.9 | 22 | 2  | AAQ06947  | Aaq06947 Mny11 nuc  | 174   | 15.6 | 41.1 | 41 | 6  | ABV75580 | Abv75580 SR protei |
| C 102 | 22   | 57.9 | 22 | 2  | AAT98055  | Aat98055 Human or   | 175   | 15.6 | 41.1 | 50 | 4  | AAI29909 | Aai29909 Human SNP |
| 103   | 21.4 | 56.3 | 29 | 10 | AD82904   | Ad82904 EMSA prob   | C 176 | 15.4 | 40.5 | 25 | 5  | AAC85573 | Aac85573 Human S-H |
| 104   | 21.4 | 56.3 | 45 | 14 | AEA06161  | Aea06161 Mutated o  | C 177 | 15.4 | 40.5 | 25 | 9  | ACI95695 | Aci95695 Human mic |
| 105   | 21   | 55.3 | 25 | 2  | AAT91829  | Aat91829 Probe 1 u  | 178   | 15.2 | 40.0 | 23 | 2  | AAQ41413 | Aaq41413 Sequence  |
| 106   | 20.6 | 54.2 | 45 | 9  | ACF05494  | Acf05494 HIV-1 LAI  | C 179 | 15.2 | 40.0 | 32 | 6  | ABK13491 | Abk13491 DT390 mut |
| C 107 | 20.2 | 53.2 | 26 | 2  | AAT91830  | Aat91830 Probe 2 u  | 180   | 15.2 | 40.0 | 41 | 6  | ABZ43626 | Abz43626 Human car |
| C 108 | 20.2 | 53.2 | 30 | 3  | AAZ90467  | Aaz90467 NF-kappaB  | 181   | 15.2 | 40.0 | 41 | 6  | ABZ49774 | Abz49774 Human car |
| 109   | 20.2 | 53.2 | 30 | 3  | AAZ90466  | Aaz90466 NF-kappaB  | C 182 | 15.2 | 40.0 | 48 | 5  | ADV62542 | Adv62542 HBV amber |
| 110   | 20.2 | 53.2 | 31 | 12 | ADQ94608  | Adq94608 HIV-1 3'   | C 183 | 15.2 | 40.0 | 48 | 8  | ACD56028 | Acd56028 HBV amber |
| 111   | 20.2 | 53.2 | 31 | 14 | AEA11054  | Aea11054 STAT5 bin  | C 184 | 15.2 | 40.0 | 48 | 12 | ADM63789 | Adm63789 Hepatitis |
| 112   | 20.2 | 53.2 | 42 | 9  | ACF05497  | Acf05497 HIV-1 LAI  | C 185 | 15.2 | 40.0 | 50 | 6  | ABZ05973 | Abz05973 Human leu |
| 113   | 19.8 | 52.1 | 26 | 2  | AAT30596  | Aat30596 Target bi  | 186   | 15   | 39.5 | 15 | 2  | AAT30584 | Aat30584 Target bi |
| 114   | 19.2 | 50.5 | 24 | 2  | AAQ39799  | Aaq39799 HIV-1 LTR  | 187   | 15   | 39.5 | 25 | 9  | ACI89487 | Aci89487 Human mic |
| 115   | 19.2 | 50.5 | 26 | 2  | AAT30595  | Aat30595 Target bi  | 188   | 15   | 39.5 | 25 | 9  | ACI89486 | Aci89486 Human mic |
| 116   | 19.2 | 50.5 | 26 | 2  | AAT30589  | Aat30589 Target bi  | 189   | 15   | 39.5 | 32 | 6  | ABK13733 | Abk13733 Rabbt SM  |
| C 117 | 19   | 50.0 | 19 | 10 | ADG36512  | Adg36512 HIV siNA   | 190   | 15   | 39.5 | 33 | 2  | AAQ52069 | Aaq52069 Breast ca |
| C 118 | 19   | 50.0 | 19 | 10 | ADG36584  | Adg36584 HIV siNA   | 191   | 15   | 39.5 | 39 | 11 | ADM47297 | Adm47297 NOVX olig |
| C 119 | 19   | 50.0 | 19 | 10 | ADG35846  | Adg35846 HIV siNA   | C 192 | 15   | 39.5 | 39 | 14 | ABE86140 | Aeb86140 Optimized |
| 120   | 19   | 50.0 | 19 | 10 | ADG35733  | Adg35733 HIV siNA   | C 193 | 15   | 39.5 | 40 | 2  | AAQ87916 | Aaq87916 Human his |
| C 121 | 19   | 50.0 | 19 | 10 | ADG36501  | Adg36501 HIV siNA   | 194   | 15   | 39.5 | 41 | 6  | ABL42091 | Abi42091 Probe #1  |
| 122   | 19   | 50.0 | 19 | 10 | ADG35713  | Adg35713 HIV siNA   | 195   | 15   | 39.5 | 41 | 6  | ABL42090 | Abi42090 Primer #4 |
| 123   | 19   | 50.0 | 19 | 10 | ADG35774  | Adg35774 HIV siNA   | 196   | 15   | 39.5 | 41 | 6  | ABZ44217 | Abz44217 Human NDU |
| 124   | 19   | 50.0 | 19 | 10 | ADG35818  | Adg35818 HIV siNA   | 197   | 15   | 39.5 | 41 | 6  | ABZ50114 | Abz50114 Human NDU |
| C 125 | 19   | 50.0 | 19 | 10 | ADG36471  | Adg36471 HIV siNA   | 198   | 14.8 | 38.9 | 22 | 10 | ADD43631 | Ad443631 Oligonuc  |
| 126   | 19   | 50.0 | 19 | 10 | ADG35779  | Adg35779 HIV siNA   | C 199 | 14.8 | 38.9 | 25 | 9  | ACI74187 | Aci74187 Human mic |
| C 127 | 19   | 50.0 | 19 | 10 | ADG35763  | Adg35763 HIV siNA   | 200   | 14.8 | 38.9 | 31 | 2  | AAQ93717 | Aaq93717 Human str |
| C 128 | 19   | 50.0 | 19 | 10 | ADG36556  | Adg36556 HIV siNA   | 201   | 14.8 | 38.9 | 31 | 2  | AAQ93716 | Aaq93716 Human str |
| C 129 | 19   | 50.0 | 19 | 10 | ADG36517  | Adg36517 HIV siNA   | 202   | 14.8 | 38.9 | 31 | 2  | AAQ93715 | Aaq93715 Human str |
| C 130 | 19   | 50.0 | 19 | 10 | ADG36451  | Adg36451 HIV siNA   | 203   | 14.8 | 38.9 | 31 | 2  | AAQ93715 | Aaq93715 Human str |
| C 131 | 19   | 50.0 | 19 | 10 | ADG36451  | Adg36451 HIV siNA   | 204   | 14.8 | 38.9 | 31 | 2  | AAQ93715 | Aaq93715 Human str |
| 132   | 19   | 50.0 | 24 | 14 | ADZ65007  | Adz65007 HIV-1 str  | 205   | 14.8 | 38.9 | 31 | 2  | AAQ93715 | Aaq93715 Human str |
| C 133 | 19   | 50.0 | 26 | 2  | AAT30590  | Aat30590 Target bi  | 206   | 14.8 | 38.9 | 31 | 2  | AAQ93717 | Aaq93717 Human str |
| C 134 | 18.6 | 48.9 | 39 | 2  | AAQ30594  | Aaq30594 Target bi  | 207   | 14.8 | 38.9 | 34 | 14 | ADX58204 | Adx58204 Polyepeti |
| 135   | 18.6 | 48.9 | 39 | 2  | AAQ44332  | Aaq44332 Oligonuc   | C 208 | 14.8 | 38.9 | 37 | 8  | ACA07953 | Aca07953 Necrosis  |
| 136   | 18.6 | 48.9 | 39 | 2  | AAQ44331  | Aaq44331 Oligonuc   | C 209 | 14.8 | 38.9 | 39 | 12 | ADM13533 | Adm13533 GFP circu |
| 137   | 18.6 | 48.9 | 39 | 2  | AAT94585  | Aat94585 Mutant NF  | C 210 | 14.8 | 38.9 | 41 | 12 | ADP48407 | Adp48407 Green flu |
| C 138 | 18.6 | 48.9 | 39 | 2  | AAT98241  | Aat98241 NF-kappaB  | C 211 | 14.8 | 38.9 | 44 | 4  | AAI65082 | Aai65082 Oligonuc  |
| C 139 | 18.6 | 48.9 | 39 | 2  | AAT98242  | Aat98242 NF-kappaB  | 212   | 14.8 | 38.9 | 45 | 10 | ADP18224 | Adp18224 DNA-bind  |
| 140   | 18.6 | 48.9 | 39 | 2  | AAT99782  | Aat99782 Transcrip  | C 213 | 14.8 | 38.9 | 45 | 10 | ADP18224 | Adp18224 DNA-bind  |
| C 141 | 18.6 | 48.9 | 39 | 2  | AAV56618  | Aav56618 NF-kappaB  | 214   | 14.8 | 38.9 | 48 | 2  | AAQ34624 | Aaq34624 GS3A prom |
| 142   | 18.6 | 48.9 | 39 | 2  | AAV56617  | Aav56617 NF-kappaB  | C 215 | 14.6 | 38.4 | 23 | 3  | AZ88805  | Aaz88805 Human HLA |
| 143   | 18.6 | 48.9 | 39 | 3  | AAZ32920  | Aaz32920 Mutant ka  | C 216 | 14.6 | 38.4 | 24 | 6  | ABQ04752 | Abq04752 Oligonuc  |
| 144   | 18.6 | 48.9 | 39 | 6  | ADZ26649  | Adz26649 NF-kB mut  | 217   | 14.6 | 38.4 | 24 | 6  | ABQ11121 | Abq11121 Oligonuc  |
| C 145 | 18.6 | 48.9 | 39 | 6  | ADZ26650  | Adz26650 NF-kB mut  | 218   | 14.6 | 38.4 | 24 | 6  | ABQ04793 | Abq04793 Oligonuc  |
| 146   | 18.2 | 47.9 | 26 | 2  | AAQ73641  | Aaq73641 Oligonuc   | C 219 | 14.6 | 38.4 | 24 | 6  | ABQ11080 | Abq11080 Oligonuc  |
| C 147 | 17.6 | 46.3 | 45 | 14 | ABE863578 | Aeb863578 PAG PCR p | C 220 | 14.6 | 38.4 | 24 | 6  | ABQ00396 | Abq00396 Oligonuc  |
| C 148 | 17.6 | 46.3 | 26 | 2  | AAQ73642  | Aaq73642 Oligonuc   | C 221 | 14.6 | 38.4 | 25 | 6  | ABQ12616 | Abq12616 Oligonuc  |
| 149   | 17.6 | 46.3 | 26 | 2  | AAT30593  | Aat30593 Target bi  | C 222 | 14.6 | 38.4 | 25 | 6  | ABQ12657 | Abq12657 Oligonuc  |
| C 150 | 17.6 | 46.3 | 30 | 10 | ADZ28997  | Adz28997 PCR prime  | C 223 | 14.6 | 38.4 | 27 | 14 | ADZ09950 | Adz09950 Probe use |
| C 151 | 17.6 | 46.3 | 41 | 9  | ACC41977  | Acc41977 Human KCN  | 224   | 14.6 | 38.4 | 31 | 2  | AAQ06159 | Aaq06159 Human bia |
| 152   | 17.2 | 45.3 | 26 | 2  | AAT30592  | Aat30592 Target bi  | 225   | 14.6 | 38.4 | 31 | 4  | AAI31159 | Aai31159 Human sin |
| C 153 | 17   | 44.7 | 17 | 5  | AAI7456   | Aai7456 Nuclear f   | 226   | 14.6 | 38.4 | 33 | 12 | ADJ93097 | Adj93097 rpsf prom |
| 154   | 16.8 | 44.2 | 26 | 2  | AAT30591  | Aat30591 Target bi  | C 227 | 14.6 | 38.4 | 41 | 12 | ADH06035 | Adh06035 Gene poly |
| C 155 | 16.8 | 44.2 | 30 | 10 | AD828905  | Ad828905 Control p  | C 228 | 14.6 | 38.4 | 41 | 12 | ADH05189 | Adh05189 Gene poly |
| 156   | 16.8 | 44.2 | 41 | 9  | ACC41989  | Acc41989 Human HER  | C 229 | 14.6 | 38.4 | 41 | 12 | ADH90976 | Adh90976 1-beta-me |
| 157   | 16.4 | 43.2 | 18 | 6  | AD40603   | Ad40603 HIV-1 LTR   | C 230 | 14.6 | 38.4 | 41 | 12 | ADH91822 | Adh91822 1-beta-me |
| 158   | 16.4 | 43.2 | 38 | 2  | AAT31915  | Aat31915 Plasmid 1  | C 231 | 14.6 | 38.4 | 47 | 4  | AAF80304 | Aaf80304 Primer us |
| 159   | 16.4 | 43.2 | 38 | 2  | AAT59208  | Aat59208 5' primer  | C 232 | 14.6 | 38.4 | 48 | 4  | ABK09148 | Abk09148 Human CD2 |
| 160   | 16.4 | 43.2 | 38 | 2  | AAT32093  | Aat32093 5' PCR pr  | C 233 | 14.6 | 38.4 | 48 | 5  | ADV62275 | Adv62275 HBV amber |
| 161   | 16.4 | 43.2 | 38 | 2  | AAQ00768  | Aaq00768 5' nested  | C 234 | 14.6 | 38.4 | 48 | 5  | ADV61970 | Adv61970 HBV amber |
| 162   | 16.4 | 43.2 | 38 | 5  | AAQ09598  | Aaq09598 Influenza  | C 235 | 14.6 | 38.4 | 48 | 6  | ACN36290 | Acn36290 WNV minus |
| 163   | 16.4 | 43.2 | 48 | 2  | AAK35898  | Aak35898 PCR prime  | C 236 | 14.6 | 38.4 | 48 | 8  | ACA09532 | Aca09532 Necrosis  |
| 164   | 16.4 | 43.2 | 48 | 4  | ABK43418  | Abk43418 Necrosis   | C 237 | 14.6 | 38.4 | 48 | 8  | ACD55444 | Acd55444 HBV amber |
| 165   | 16.2 | 42.6 | 40 | 2  | AAV16820  | Aav16820 Mycobacte  | C 238 | 14.6 | 38.4 | 48 | 8  | ACD55761 | Acd55761 HBV amber |

|       |      |      |    |    |          |                     |
|-------|------|------|----|----|----------|---------------------|
| C 239 | 14.6 | 38.4 | 48 | 11 | ADU55277 | Adl55277 Human IKK  |
| C 240 | 14.6 | 38.4 | 48 | 12 | ADM63489 | Adm63489 Hepatitis  |
| C 241 | 14.6 | 38.4 | 48 | 12 | ADM63658 | Adm63658 Hepatitis  |
| C 242 | 14.6 | 38.4 | 50 | 2  | AAV06347 | Aav06347 Phosphatid |
| C 243 | 14.4 | 37.9 | 24 | 3  | AAZ36082 | Aaz36082 Forward p  |
| C 244 | 14.4 | 37.9 | 25 | 9  | ACI09133 | Act09133 Human mic  |
| C 245 | 14.4 | 37.9 | 25 | 9  | ACK19148 | Ack19148 Human mic  |
| C 246 | 14.4 | 37.9 | 25 | 9  | ACI55943 | Act55943 Human mic  |
| C 247 | 14.4 | 37.9 | 32 | 6  | AAI42267 | Aal42267 Human pol  |
| C 248 | 14.4 | 37.9 | 38 | 6  | ABS70875 | Abt70875 Hepatitis  |
| C 249 | 14.4 | 37.9 | 39 | 4  | AAH24489 | Aah24489 TRIM adap  |
| C 250 | 14.4 | 37.9 | 41 | 6  | ABS60719 | Abt60719 Human DNA  |
| C 251 | 14.4 | 37.9 | 41 | 6  | ABZ43358 | Abz43358 Human N-m  |
| C 252 | 14.4 | 37.9 | 41 | 6  | ABZ48698 | Abz48698 Human N-m  |
| C 253 | 14.4 | 37.9 | 45 | 4  | AAF67676 | Aaf67676 Chicken i  |
| C 254 | 14.4 | 37.9 | 46 | 4  | AAF63534 | Aaf63534 aveC muta  |
| C 255 | 14.4 | 37.9 | 46 | 5  | AAS00545 | Aas00545 S. avermi  |
| C 256 | 14.4 | 37.9 | 46 | 10 | ADG83558 | Adg83558 Streptomy  |
| C 257 | 14.4 | 37.9 | 50 | 6  | ABZ02656 | Abz02656 Human leu  |
| C 258 | 14.4 | 37.9 | 50 | 6  | ABZ00443 | Abz00443 Human leu  |
| C 259 | 14.2 | 37.4 | 21 | 13 | ADU28731 | Adu28731 Knock-dow  |
| C 260 | 14.2 | 37.4 | 28 | 6  | ABQ82499 | Abq82499 Spo11B ge  |
| C 261 | 14.2 | 37.4 | 32 | 6  | ABK87827 | Abk87827 Interleuk  |
| C 262 | 14.2 | 37.4 | 32 | 14 | ADY51614 | Ady51614 Transcrip  |
| C 263 | 14.2 | 37.4 | 33 | 4  | AAF74484 | Aaf74484 Clone 179  |
| C 264 | 14.2 | 37.4 | 34 | 10 | ADC98706 | Adc98706 Double-st  |
| C 265 | 14.2 | 37.4 | 35 | 6  | ABT08597 | Abt08597 Human nov  |
| C 266 | 14.2 | 37.4 | 35 | 12 | ADO09962 | Ado09962 Human NOV  |
| C 267 | 14.2 | 37.4 | 37 | 6  | ABK87815 | Abk87815 Human Kai  |
| C 268 | 14.2 | 37.4 | 39 | 6  | ABK13495 | Abk13495 DT390 mut  |
| C 269 | 14.2 | 37.4 | 40 | 2  | AAT39933 | Aat39933 SI primer  |
| C 270 | 14.2 | 37.4 | 40 | 2  | AAT61522 | Aat61522 Mycobacte  |
| C 271 | 14.2 | 37.4 | 40 | 2  | AAT93008 | Aat93008 M. tuberc  |
| C 272 | 14.2 | 37.4 | 40 | 2  | AAT64794 | Aat64794 Primer S2  |
| C 273 | 14.2 | 37.4 | 40 | 2  | AAT90466 | Aat90466 PCR prime  |
| C 274 | 14.2 | 37.4 | 40 | 2  | AAT61537 | Aat61537 Mycobacte  |
| C 275 | 14.2 | 37.4 | 40 | 2  | AAV18912 | Aav18912 Aval PCR   |
| C 276 | 14.2 | 37.4 | 40 | 2  | AAV71893 | Aav71893 Mycobacte  |
| C 277 | 14.2 | 37.4 | 40 | 3  | AZ94293  | Aaz94293 Composite  |
| C 278 | 14.2 | 37.4 | 40 | 3  | AAC64840 | Aac64840 Novel str  |
| C 279 | 14.2 | 37.4 | 40 | 3  | AAC63161 | Aac63161 Novel str  |
| C 280 | 14.2 | 37.4 | 40 | 3  | AAC85251 | Aac85251 Allele-ap  |
| C 281 | 14.2 | 37.4 | 40 | 3  | AAC65184 | Aac65184 Novel str  |
| C 282 | 14.2 | 37.4 | 40 | 4  | AAH27107 | Aah27107 Primer S2  |
| C 283 | 14.2 | 37.4 | 40 | 5  | AAC63642 | Aac63642 Surface a  |
| C 284 | 14.2 | 37.4 | 40 | 5  | AAC64902 | Aac64902 Novel str  |
| C 285 | 14.2 | 37.4 | 40 | 6  | ABL54131 | Ab154131 Mycobacte  |
| C 286 | 14.2 | 37.4 | 40 | 6  | ABQ78694 | Abq78694 SDA prime  |
| C 287 | 14.2 | 37.4 | 40 | 8  | ACC58630 | Acc58630 Mycobacte  |
| C 288 | 14.2 | 37.4 | 40 | 9  | ACF57180 | Acf57180 M. tuberc  |
| C 289 | 14.2 | 37.4 | 40 | 10 | ADP11059 | Adp11059 Mtb DNA P  |
| C 290 | 14.2 | 37.4 | 40 | 11 | ADY50544 | Ady50544 Novel nuc  |
| C 291 | 14.2 | 37.4 | 40 | 13 | ADU04902 | Adu04902 Composite  |
| C 292 | 14.2 | 37.4 | 41 | 6  | ABN85235 | Abn85235 Protein a  |
| C 293 | 14.2 | 37.4 | 44 | 2  | AAV39051 | Aav39051 Intronic   |
| C 294 | 14.2 | 37.4 | 48 | 5  | ADV07518 | Adv07518 Human BAC  |
| C 295 | 14.2 | 37.4 | 50 | 2  | AAT89217 | Aat89217 Specific   |
| C 296 | 14.2 | 37.4 | 50 | 4  | AAL32239 | Aal32239 Human SNP  |
| C 297 | 14.2 | 37.4 | 50 | 4  | AAL34540 | Aal34540 Human SNP  |
| C 298 | 14   | 36.8 | 19 | 13 | ADT01206 | Adt01206 Novel mut  |
| C 299 | 14   | 36.8 | 21 | 2  | AAZ25681 | Aaz25681 Transcrip  |
| C 300 | 14   | 36.8 | 21 | 12 | ADP48377 | Adp48377 NF-kappaB  |

## ALIGNMENTS

RESULT 1  
AAZ32919  
ID AAZ32919 standard; DNA; 38 BP.

XX  
AC AAZ32919;  
XX

DT 09-FEB-2000 (first entry)  
XX Kappa-B-PT sequence (SEQ ID 2), used to inhibit NF-kappa-B.  
DE Kappa-B-PT sequence; NF-kappa-B; nuclear factor kappa B; adhesion;  
XX Kappa-B-PT sequence; NF-kappa-B; nuclear factor kappa B; adhesion;  
KW differentiation; phosphorothioate; treatment; immune disorder;  
KW inflammatory disease; cancer; viral infection; immune disorder;  
KW immunoglobulin kappa B sequence; rheumatoid arthritis; ischaemia;  
KW reperfusion injury; restenosis; transplant rejection; Crohn's disease;  
KW ulcerative colitis; psoriasis; glomerulonephritis; leukaemia; melanoma;  
KW sarcoma; lymphoma; HIV; HTLV; herpes virus; poison ivy; poison oak;  
KW poison sumac; ds.  
XX Synthetic.  
OS Key  
FH modified\_base 1..10 Location/Qualifiers  
FT /tag= a  
FT /mod\_base= OTHER  
FT protein\_bind 2..11 /note= "Optionally phosphorothioate linkages"  
FT /tag= b  
FT protein\_bind 16..25 /bound\_moiety= "NF-kappa-B"  
FT /tag= b  
FT protein\_bind 29..38 /bound\_moiety= "NF-kappa-B"  
FT /tag= b  
FT /bound\_moiety= "NF-kappa-B"  
XX US990090-A.  
XX 23-NOV-1999.  
XX 27-FEB-1996; 96US-00607519.  
XX 20-SEP-1993; 93US-00123188.  
(UNMI ) UNIV MICHIGAN.  
XX Nabel GU;  
XX WPI; 2000-022803/02.  
XX Composition useful for the treatment of immune and inflammatory diseases,  
XX cancer and viral infections.  
XX Claim 1; Col 4; 14pp; English.  
XX This sequence represents the kappa-B-PT sequence (SEQ ID 2) which  
XX contains three immunoglobulin kappa-B sequences (AAZ32918) which are  
XX bound by activated NF-kappa-B (nuclear factor kappa-B). It can inhibit NF  
XX -kappa-B binding to endogenous kappa-B enhancer/promoter elements, thus  
XX inhibiting transcription of genes that comprise such elements. NF-kappa-B  
XX is involved in the induction of cell adhesion associated with  
XX differentiation or activation. For example, the human promyelotic  
XX leukaemia cell line (HL-60 cells) can be induced to differentiate into  
XX monocytoic cells with concomitant expression of the leukocyte adhesion  
XX glycoprotein CD11b by treatment with phorbol esters. However, this  
XX differentiation and adhesion can be inhibited by prior incubation of the  
XX HL-60 cells with this sequence which specifically binds NF-kappa-B. In  
XX contrast, use of a mutant kappa-B-PT sequence (AAZ32920) had no effect on  
XX differentiation and adhesion. Compositions containing the kappa-B-PT  
XX sequence may be used for the treatment of immune and inflammatory  
XX diseases, cancer and viral infections. In particular it can be used to  
XX treat rheumatoid arthritis, ischaemia/reperfusion injury, restenosis,  
XX transplant rejection, Crohn's disease, ulcerative colitis, psoriasis,  
XX glomerulonephritis, leukaemia, melanoma, sarcoma, lymphomas and HIV,  
XX HTLV, herpes virus infections and reaction to poison ivy, poison oak and  
XX poison sumac  
XX Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;





DT 16-APR-2002 (first entry)  
XX Immunostimulatory nucleic acid SEQ ID NO: 417.  
DE  
XX  
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; ss.  
XX  
XX Synthetic.  
OS  
XX WO200197843-A2.  
PN  
XX  
XX 27-DEC-2001.  
PD  
XX  
XX 22-JUN-2001; 2001WO-US020154.  
PF  
XX  
XX 22-JUN-2000; 2000US-0213346P.  
PR  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA  
XX  
XX Weiner G, Hartmann G;  
PI  
XX WPI; 2002-154611/20.  
DR  
XX  
XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.  
XX  
XX Disclosure; Page 201; 312pp; English.  
PS  
XX  
XX The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention  
XX  
XX Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 38; DB 6; Length 38;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACTTTCC 38  
DB 1 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACTTTCC 38  
RESULT 5  
ACD99455  
ID ACD99455 standard; DNA; 38 BP.  
XX  
XX ACD99455;  
AC  
XX  
XX 25-SEP-2003 (first entry)  
DT  
XX  
XX Immunostimulatory nucleic acid #141.  
DE  
XX  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX  
XX Synthetic.  
OS  
XX

PN US2003050268-A1.  
XX  
XX 13-MAR-2003.  
XX  
XX 29-MAR-2002; 2002US-00112653.  
PF  
XX  
XX 29-MAR-2001; 2001US-0279642P.  
PR  
XX  
XX (KRIE//) KRIEG A M.  
PA (BERG//) BERG D J.  
XX  
XX Krieg AM, Berg DJ;  
PI  
XX WPI; 2003-521815/49.  
DR  
XX  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX  
XX Disclosure; Page 12; 229pp; English.  
PS  
XX  
XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
XX Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 38; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACTTTCC 38  
DB 1 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACTTTCC 38  
RESULT 6  
ADB36525  
ID ADB36525 standard; DNA; 38 BP.  
XX  
XX ADB36525;  
AC  
XX  
XX 04-DEC-2003 (first entry)  
DT  
XX  
XX Immunostimulatory nucleic acid #139.  
DE  
XX  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
KW  
XX Synthetic.  
OS  
XX  
XX US2003087848-A1.  
PN  
XX  
XX 08-MAY-2003.  
PD  
XX  
XX 02-FEB-2001; 2001US-00776479.  
PF  
XX  
XX 03-FEB-2000; 2000US-0179991P.  
PR  
XX  
XX (BRAT//) BRATZLER R L.  
PA (PETE//) PETERSEN D M.  
PA (FOUR//) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
PI  
XX WPI; 2003-657977/62.  
DR  
XX  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT

PT nucleic acid alone or in combination with an asthma/allergy medicament.  
 XX  
 PS Disclosure; Page 7; 221pp; English.  
 XX  
 CC The invention relates to a method of treating or preventing allergy or  
 CC asthma which comprises administering to a subject a poly-G nucleic acid  
 CC in an aerosol formulation. The methods and compositions of the present  
 CC invention are useful for diagnosing and/or treating asthma and allergy  
 CC especially in a hypo-responsive subject. The present sequence represents  
 CC an immunostimulatory nucleic acid of the invention.  
 XX  
 SQ Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 38; DB 9; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGACTTTCCTGGGGACTTTCAGGGGGACTTTCC 38  
 Db 1 GGGGACTTTCCTGGGGACTTTCAGGGGGACTTTCC 38  
 RESULT 7  
 ID ADU89464  
 XX ADU89464 standard; DNA; 38 BP.  
 AC ADU89464;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Allergic response suppressor oligonucleotide #148.  
 XX  
 DE ss: antiasthmatic; antiallergic; dermatological; antiinflammatory;  
 KW antibacterial; virucide; immunoglobulin E antagonist; allergy;  
 KW immunostimulant; asthma; rhinitis; urticaria; dermatitis;  
 KW bacterial infection; viral infection.  
 XX  
 OS Synthetic.  
 XX  
 PN US2004235774-A1.  
 XX  
 PD 25-NOV-2004.  
 XX  
 PF 23-APR-2004; 2004US-00831778.  
 XX  
 PR 03-FEB-2000; 2000US-0179991P.  
 PR 02-FEB-2001; 2001US-00776479.  
 XX  
 PA (BRAT/) BRATZLER R L.  
 PA (PETE/) PETERSEN D M.  
 PA (FOUR/) FOURON Y.  
 XX  
 PI Bratzler RL, Petersen DM, Fouron Y;  
 XX  
 DR WPI; 2004-833006/82.  
 XX  
 XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
 PT dermatitis in a subject, comprises administering a first and second dose  
 PT of an immunostimulatory nucleic acid.  
 XX  
 PS Disclosure; SEQ ID NO 148; 235pp; English.  
 XX  
 CC The invention relates to a method of suppressing a symptom of an allergic  
 CC response in a subject by administering a first and second dose of an  
 CC immunostimulatory nucleic acid that comprises a nucleotide sequence  
 CC comprising 5'-cg-3', and where the second dose is administered from 1 day  
 CC to 8 weeks after the first dose. The methods and compositions of the  
 CC present invention are useful for the treatment or prevention of asthma  
 CC and allergy, including rhinitis, urticaria and atopic dermatitis, using  
 CC an immunostimulatory nucleic acid alone or in combination with other  
 CC medicaments. They can also be used in preventing bacterial and viral  
 CC infections. This sequence represents an oligonucleotide used in the  
 CC method of the invention.

XX  
 SQ Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 38; DB 13; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGACTTTCCTGGGGACTTTCAGGGGGACTTTCC 38  
 Db 1 GGGGACTTTCCTGGGGACTTTCAGGGGGACTTTCC 38  
 RESULT 8  
 AAT30609  
 ID AAT30609 standard; DNA; 43 BP.  
 XX  
 AC AAT30609;  
 XX  
 DT 19-FEB-1997 (first entry)  
 XX  
 DE Target binding region #29.  
 XX  
 KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;  
 KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
 KW virus; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9617956-A2.  
 XX  
 PD 13-JUN-1996.  
 XX  
 PF 07-DEC-1995; 95WO-US015944.  
 XX  
 PR 09-DEC-1994; 94US-00353476.  
 XX  
 PA (GENE-) GENE POOL INC.  
 XX  
 PI Weininger S, Weininger AM;  
 XX  
 DR WPI; 1996-287199/29.  
 XX  
 PT Probe nucleic acids, target binding assemblies, etc - for detection and  
 PT localisation of specific nucleic acid sequences, esp. HIV and HPV.  
 XX  
 PS Disclosure; Page 73; 172pp; English.  
 XX  
 CC AAT30581-T30614 represent target binding regions (TBR) of a probe of the  
 CC invention. The probe of the invention contains a TBR, a booster binding  
 CC region (BBR), and an optional support or attachment (OSA). The target  
 CC binding assembly (TBA) recognised by the probe, contains at least one  
 CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an  
 CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see  
 CC AAR95999-R36006), a nuclear localisation signal sequence (see AAR96007),  
 CC and an OSA. The assembly sequence and asymmetry sequences are responsible  
 CC for the folding and association of the NARS. The NARS (see AAR95965-  
 CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus  
 CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding  
 CC units. The linker sequence is an oligopeptide, which does not interfere  
 CC with NAR function, but provides stability and control over the spacing of  
 CC the NAR from the rest of the TBA. The OSA is an attached support or  
 CC indicator, or other means of localisation of the probe. The probe can be  
 CC used in a method for detecting or localising a specific target nucleic  
 CC acid sequence (TNA). The method is highly sensitive, and has a high  
 CC degree of specificity. The method can be used for detecting specific  
 CC nucleic acid sequences, including those found in human cells, in HIV,  
 CC HPV, and other nucleic acid containing systems, including bacteria and  
 CC viruses  
 XX  
 SQ Sequence 43 BP; 6 A; 12 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 81.1%; Score 30.8; DB 2; Length 43;  
Best Local Similarity 94.1%; Pred. No. 0.015;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGACTTCCAGGGGACT 34  
DB 6 GGGGACTTCCGCTGGGACTTCCAGGGGAGCT 39

RESULT 9  
AAAT30608  
ID AAAT30608 standard; DNA; 46 BP.  
XX AC  
XX AAT30608;  
DT 19-FEB-1997 (first entry)  
XX DE  
DE Target binding region #28.  
XX KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;  
KW TATA; human papillomavirus; HPV E2; human immunodeficiency virus;  
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
KW virus; ss.  
XX KW  
XX Synthetic.  
XX OS  
XX PN WO9617956-A2.  
XX PD  
XX PF 13-JUN-1996.  
XX PR  
XX PT 07-DEC-1995; 9SWO-US015944.  
XX PR 09-DEC-1994; 94US-00353476.  
XX PA (GENE-) GENE POOL INC.  
XX PI Weininger S, Weininger AM;  
XX DR WPI; 1996-287199/29.  
XX PT Probe nucleic acids, target binding assemblies, etc - for detection and  
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.  
XX PS Disclosure; Page 73; 172pp; English.  
XX CC  
CC AAT30581-T30614 represent target binding regions (TBR) of a probe of the  
CC invention. The probe of the invention contains a TBR, a booster binding  
CC region (BBR), and an optional support or attachment (OSA). The target  
CC binding assembly (TBA) recognised by the probe, contains at least one  
CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an  
CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see  
CC AAR95999-R95006), a nuclear localisation signal sequence (see AAR96007),  
CC and an OSA. The assembly sequence and asymmetry sequences are responsible  
CC for the folding and association of the NARs. The NARs (see AAR95995-  
CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus  
CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding  
CC units. The linker sequence is an oligopeptide, which does not interfere  
CC with NAR function, but provides stability and control over the spacing of  
CC the NAR from the rest of the TBA. The OSA is an attached support or  
CC indicator, or other means of localisation of the probe. The probe can be  
CC used in a method for detecting or localising a specific target nucleic  
CC acid sequence (TNA). The method is highly sensitive, and has a high  
CC degree of specificity. The method can be used for detecting specific  
CC nucleic acid sequences, including those found in human cells in HIV,  
CC HPV, and other nucleic acid containing systems, including bacteria and  
XX viruses  
XX SQ Sequence 46 BP; 7 A; 10 C; 20 G; 9 T; 0 U; 0 Other;

Query Match 79.5%; Score 30.2; DB 2; Length 46;  
Best Local Similarity 91.4%; Pred. No. 0.026;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGACTTTCAGGGGACTT 35  
DB 6 GGGGACTTCCGCTGGGACTTTCAGGGAGCGT 40

RESULT 10  
AAQ58049  
ID AAQ58049 standard; DNA; 39 BP.  
XX AC  
XX AAQ58049;  
DT 25-MAR-2003 (revised)  
DT 23-SEP-1994 (first entry)  
XX DE  
DE Oligonucleotide NF1.  
XX KW HIV; tat; transport; moiety; conjugate; cargo molecule;  
KW cytoplasmic delivery; nuclear delivery; cysteine-rich region;  
KW transactivation; disulphide aggregation; ss.  
XX OS  
XX Synthetic.  
XX PN WO9404686-A1.  
XX PD  
XX PF 03-MAR-1994.  
XX PR 19-AUG-1993; 93WO-US007833.  
XX PR 21-AUG-1992; 92US-00934375.  
XX PA (BIOJ ) BIOGEN INC.  
XX PI Barsoum JG, Fawell SE, Pepinsky RB;  
XX DR WPI; 1994-083202/10.  
XX PT Transport of cargo moieties into cells - using genetic fusions of  
PT chemical conjugates comprising a portion of HIV tat protein as transport  
XX peptide.  
XX PS Claim 21; Page 116; 153pp; English.  
XX CC  
CC The sequences given in AAQ58049-50 form a double stranded DNA molecule  
CC which was used as the cargo moiety in the conjugate of the invention.  
CC This oligonucleotide fragment was linked to a peptide fragment of the HIV  
CC tat protein which was used as transport moieties. These conjugates are  
CC used as cargo molecules for the efficient cytoplasmic and nuclear  
CC delivery of biologically active non-tat proteins, nucleic acids and other  
CC molecules which are not inherently capable of entering a target cell. The  
CC tat basic region amino acid sequence carries cargo molecules by covalent  
CC attachment. The reduced size of the transport peptides minimises  
CC interference with the biological activity of the cargo molecule. By  
CC virtue of the absence of the cysteine-rich region (residues 22-36) of the  
CC tat protein, problems of spurious trans- activation and disulphide  
CC aggregation are solved. The reduced transport peptide size also enhances  
CC uptake efficiency. (Updated on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.03;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGACTTTCAGGGGACTTTC 38  
DB 1 GGGGACTTCCGCTGGGACTTTCAGGGGACTTTC 38

RESULT 11  
AAQ58050/c  
ID AAQ58050 standard; DNA; 39 BP.  
XX

AC AAQ58050;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 23-SEP-1994 (first entry)  
 XX  
 DE DE  
 XX  
 XX Oligonucleotide NF2.  
 KW HIV; tat; transport; moiety; conjugate; cargo molecule;  
 KW cytoplasmic delivery; nuclear delivery; cysteine-rich region;  
 KW transactivation; disulphide aggregation; ss.  
 XX  
 OS Synthetic.  
 XX WO9404686-A1.  
 XX  
 XX PD 03-MAR-1994.  
 XX  
 XX PF 19-AUG-1993; 93WO-US007833.  
 XX  
 XX PR 21-AUG-1992; 92US-00934375.  
 XX  
 XX PA (BIOJ ) BIOGEN INC.  
 XX  
 XX PI Barsom JG, Fawell SE, Pepinsky RB;  
 XX WPI; 1994-083202/10.  
 XX  
 XX PT Transport of cargo moieties into cells - using genetic fusions of  
 PT chemical conjugates comprising a portion of HIV tat protein as transport  
 PT peptide.  
 XX  
 XX PS Claim 21; Page 116; 153pp; English.  
 CC  
 CC The sequences given in AAQ58049-50 form a double stranded DNA molecule  
 CC which was used as the cargo moiety in the conjugate of the invention.  
 CC This oligonucleotide fragment was linked to a peptide fragment of the HIV  
 CC tat protein which was used as transport moieties. These conjugates are  
 CC used as cargo molecules for the efficient cytoplasmic and nuclear  
 CC delivery of biologically active non-tat proteins, nucleic acids and other  
 CC molecules which are not inherently capable of entering a target cell. The  
 CC tat basic region amino acid sequence carries cargo molecules by covalent  
 CC attachment. The reduced size of the transport peptides minimises  
 CC interference with the biological activity of the cargo molecule. By  
 CC virtue of the absence of the cysteine-rich region (residues 22-36) of the  
 CC tat protein, problems of spurious trans- activation and disulphide  
 CC aggregation are solved. The reduced transport peptide size also enhances  
 CC uptake efficiency. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX SQ Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;  
 Query Match 78.9%; Score 30; DB 2; Length 39;  
 Best Local Similarity 86.8%; Pred. No. 0.03;  
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38  
 |||||  
 Db 39 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 2  
 |||||  
 RESULT 12  
 AAT84584  
 ID AAT84584 standard; DNA; 39 BP.  
 XX  
 XX AC AAT84584;  
 XX  
 XX DT 25-MAR-2003 (revised)  
 DT 16-DEC-1997 (first entry)  
 XX  
 XX DE NF-kappa B binding site.  
 XX HIV; tat protein; transport protein; cargo delivery;  
 KW NF-kappa B binding site; ds.  
 XX

OS Synthetic.  
 XX US5652122-A.  
 PN  
 XX 29-JUL-1997.  
 PD  
 XX  
 XX PF 25-MAY-1995; 95US-00450257.  
 XX  
 XX PR 21-DEC-1989; 89US-00454450.  
 PR 02-JAN-1991; 91US-00636662.  
 PR 21-AUG-1992; 92US-00934375.  
 PR 19-AUG-1993; 93WO-US007833.  
 PR 24-NOV-1993; 93US-00158015.  
 PR 28-APR-1994; 94US-00235403.  
 XX  
 XX (BIOJ ) BIOGEN INC.  
 PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 XX PI Pepinsky RB, Barsom JG, Pabo C, Fawell SE, Frankel A;  
 XX WPI; 1997-392943/36.  
 DR  
 XX  
 XX PT New DNA constructs for transporting molecules to cells - encode a fusion  
 PT protein comprising a modified HIV tat protein and a carboxy-terminal  
 PT cargo moiety.  
 XX  
 XX PS Example 17; Col 97; 76pp; English.  
 XX  
 CC This double-stranded DNA sequence, comprising oligonucleotides NF1 (sense  
 CC strand) and NF2 (antisense strand), corresponds to the wild-type NF-kappa  
 CC B binding site. It was used in the preparation of transport polypeptide-  
 CC DNA conjugates. Such conjugates, in which modified HIV tat protein is  
 CC used as transport polypeptide, can be used to deliver cargo molecules to  
 CC cells in vivo or in vitro. (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 XX SQ Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;  
 Query Match 78.9%; Score 30; DB 2; Length 39;  
 Best Local Similarity 86.8%; Pred. No. 0.03;  
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38  
 |||||  
 Db 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38  
 |||||  
 RESULT 13  
 AAT8240/c  
 ID AAT8240 standard; DNA; 39 BP.  
 XX  
 XX AC AAT8240;  
 XX  
 XX DT 25-MAR-2003 (revised)  
 DT 20-JAN-1998 (first entry)  
 XX  
 XX DE NF-kappaB transcriptional activation inhibitor NF2.  
 XX  
 XX KW Chemical conjugate; transport polypeptide; tat protein; nucleic acid;  
 KW delivery; cytoplasm; cell nucleus; therapy; prophylaxis; diagnosis;  
 KW spurious transactivation; HIV-1; disulphide aggregation; NF-kappaB;  
 KW inhibition; NF2; human immunodeficiency virus type 1;  
 KW transcriptional activation; ss.  
 XX  
 XX OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX XX US5670617-A.  
 XX  
 XX PD 23-SEP-1997.  
 XX  
 XX PF 25-MAY-1995; 95US-00450246.

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XX 21-DEC-1989; 89US-00454450.
PR 02-JAN-1991; 91US-00636662.
PR 21-AUG-1992; 92US-00934375.
PR 19-AUG-1993; 93WO-US007833.
PR 24-NOV-1993; 93US-00158015.
PR 28-APR-1994; 94US-00235403.
XX
XX (BIOJ ) BIOGEN INC.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
XX
XX Barsom JG, Fawell SE, Frankel A, Pepinsky RB, Pabo C;
XX WPI; 1997-479523/44.
XX
XX Conjugate for intracellular delivery - comprising transport moiety having
PT amino acids 49-57 of human immunodeficiency virus tat protein and nucleic
PT acid cargo moiety.
XX
XX Claim 3; Col 97-98; 77pp; English.
XX
XX A novel covalently linked chemical conjugate, comprises a transport
CC polypeptide moiety consisting of at least residues 49-57 of human
CC immunodeficiency virus (HIV) tat protein, but not residues 22-36 and 73-
CC 86, and a cargo moiety comprising a single or double stranded nucleic
CC acid, e.g. the present sequence. The conjugate can be used to deliver
CC cargo moieties into the cytoplasm and nuclei of cells for therapeutic,
CC prophylactic and diagnostic applications. In an example conjugates to
CC inhibit transcriptional activation by NF-kappaB were prepared, the
CC oligonucleotides used were NF1-4 (AAT88239-42). NF1 and NF2 for a duplex
CC a duplex corresponding to the wild type NF-KB binding site, while NF2 and NF4 form
CC was then reacted with bismaleimidoethane activated tat 32-72. The
CC products were tested as in Science 250, 997-1000 (1990) for inhibition of
CC NF-KB transcriptional activation. The results showed that the tat
CC transport polypeptide significantly enhanced the inhibition. The HIV tat
CC protein is readily taken up into cells and the cell nucleus. The reduced
CC size of the transport polypeptides minimises interference with the
CC biological activity of the cargo molecule. In addition, by virtue of the
CC absence of the cysteine rich region of the HIV tat protein, the transport
CC polypeptides solve the potential problems of spurious transactivation and
CC disulphide aggregation. (Updated on 25-MAR-2003 to correct PF field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
SQ
Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38
Db 39 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 2
RESULT 14
AAT88239
ID AAT88239 standard; DNA; 39 BP.
XX
XX AAT88239;
XX
XX 25-MAR-2003 (revised)
DT 20-JAN-1998 (first entry)
XX
XX NF-kappaB transcriptional activation inhibitor NF1.
DE
XX
XX Chemical conjugate; transport polypeptide; tat protein; nucleic acid;
KW delivery; cytoplasm; cell nucleus; therapy; prophylaxis; diagnosis;
KW spurious transactivation; HIV-1; disulphide aggregation; NF-kappaB;
KW inhibition; NF1; human immunodeficiency virus type 1;
KW transcriptional activation; ss.
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XX Synthetic.
OS Homo sapiens.
XX
XX US5670617-A.
XX
XX 23-SEP-1997.
XX
XX 25-MAY-1995; 95US-00450246.
XX
XX 21-DEC-1989; 89US-00454450.
PR 02-JAN-1991; 91US-00636662.
PR 21-AUG-1992; 92US-00934375.
PR 19-AUG-1993; 93WO-US007833.
PR 24-NOV-1993; 93US-00158015.
PR 28-APR-1994; 94US-00235403.
XX
XX (BIOJ ) BIOGEN INC.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
XX
XX Barsom JG, Fawell SE, Frankel A, Pepinsky RB, Pabo C;
XX WPI; 1997-479523/44.
XX
XX Conjugate for intracellular delivery - comprising transport moiety having
PT amino acids 49-57 of human immunodeficiency virus tat protein and nucleic
PT acid cargo moiety.
XX
XX Claim 3; Col 97-98; 77pp; English.
XX
XX A novel covalently linked chemical conjugate, comprises a transport
CC polypeptide moiety consisting of at least residues 49-57 of human
CC immunodeficiency virus (HIV) tat protein, but not residues 22-36 and 73-
CC 86, and a cargo moiety comprising a single or double stranded nucleic
CC acid, e.g. the present sequence. The conjugate can be used to deliver
CC cargo moieties into the cytoplasm and nuclei of cells for therapeutic,
CC prophylactic and diagnostic applications. In an example conjugates to
CC inhibit transcriptional activation by NF-kappaB were prepared, the
CC oligonucleotides used were NF1-4 (AAT88239-42). NF1 and NF2 for a duplex
CC a duplex corresponding to the wild type NF-KB binding site, while NF2 and NF4 form
CC was then reacted with bismaleimidoethane activated tat 32-72. The
CC products were tested as in Science 250, 997-1000 (1990) for inhibition of
CC NF-KB transcriptional activation. The results showed that the tat
CC transport polypeptide significantly enhanced the inhibition. The HIV tat
CC protein is readily taken up into cells and the cell nucleus. The reduced
CC size of the transport polypeptides minimises interference with the
CC biological activity of the cargo molecule. In addition, by virtue of the
CC absence of the cysteine rich region of the HIV tat protein, the transport
CC polypeptides solve the potential problems of spurious transactivation and
CC disulphide aggregation. (Updated on 25-MAR-2003 to correct PF field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
SQ
Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38
Db 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38
RESULT 15
AAT89779
ID AAT89779 standard; DNA; 39 BP.
XX
XX AAT89779;
AC
XX 25-MAR-2003 (revised)
DT
```

```

DT 20-MAR-1998 (first entry)
DE
DE Transcription factor NF-kappaB oligonucleotide NF1.
XX
XX Human Immunodeficiency Virus; HIV Type 1; Tat protein; cargo molecule;
KW intracellular delivery; fusion protein; therapeutic; prophylactic;
KW diagnostic; transport polypeptide; E2 repressor protein; ss.
XX
XX Synthetic.
OS
XX
XX US5674980-A.
PN
XX
XX 07-OCT-1997.
PD
XX
XX 25-MAY-1995; 95US-00450098.
PF
XX
XX 21-DEC-1989; 89US-00454450.
PR
XX 02-JAN-1991; 91US-00636662.
PR
XX 21-AUG-1992; 92US-00934375.
PR
XX 19-AUG-1993; 93WO-US007833.
PR
XX 24-NOV-1993; 93US-00158015.
PR
XX 28-APR-1994; 94US-00235403.
XX
XX (PABO/) PABO C.
PA (FRAN/) FRANKEL A.
PA (FAWE/) FAWELL S E.
PA (PEPI/) PEPINSKY R B.
PA (BARS/) BARSOUM J G.
XX
XX Barsoum JG, Fawell SE, Frankel A, Pepinsky RB, Pabo C;
PI WPI; 1997-502388/46.
XX
XX Fusion proteins containing truncated HIV tat sequences - useful for
PT intracellular delivery of viral repressor proteins.
XX
XX Example 17; Col 95-96; 77pp; English.
XX
XX This oligonucleotide primer is used with AAT89780 to form a duplex
CC corresponding to the wild type transcription factor NF-kappaB binding
CC site which is used in the construction of a transport polypeptide-DNA
CC conjugate. This conjugate is used in a novel method for delivery of
CC biologically active cargo molecules into the cytoplasm and nuclei of
CC eukaryotic cells. The tat protein from immunodeficiency virus (e.g. HIV-
CC 1, HIV-2, SIV) is readily taken up into cells when present
CC extracellularly and can be modified to covalently link to cargo proteins
CC e.g. E2 repressor proteins producing a fusion protein without the
CC problems of spurious trans-activation and disulphide aggregation. These
CC transport polypeptides also minimise interference with the biological
CC activity of the cargo molecule. This is applicable for therapeutic,
CC prophylactic or diagnostic intracellular delivery of small molecules and
CC macromolecules e.g. proteins, nucleic acids and polysaccharides. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
XX Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
SQ
Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCTCGCTGGGGACTTTCCAGGGGGACTTTCC 38
Db 1 GGGGACTTTCCTCGCTGGGGACTTTCCAGGGGGACTTTCC 38

RESULT 16
AAT89780/c
ID AAT89780 standard; DNA; 39 BP.
XX
XX AAT89780;
AC
XX 25-MAR-2003 (revised)
DT

DT 20-MAR-1998 (first entry)
DE
DE Transcription factor NF-kappaB oligonucleotide NF2.
XX
XX Human Immunodeficiency Virus; HIV Type 1; Tat protein; cargo molecule;
KW intracellular delivery; fusion protein; therapeutic; prophylactic;
KW diagnostic; transport polypeptide; E2 repressor protein; ss.
XX
XX Synthetic.
OS
XX
XX US5674980-A.
PN
XX
XX 07-OCT-1997.
PD
XX
XX 25-MAY-1995; 95US-00450098.
PF
XX
XX 21-DEC-1989; 89US-00454450.
PR
XX 02-JAN-1991; 91US-00636662.
PR
XX 21-AUG-1992; 92US-00934375.
PR
XX 19-AUG-1993; 93WO-US007833.
PR
XX 24-NOV-1993; 93US-00158015.
PR
XX 28-APR-1994; 94US-00235403.
XX
XX (PABO/) PABO C.
PA (FRAN/) FRANKEL A.
PA (FAWE/) FAWELL S E.
PA (PEPI/) PEPINSKY R B.
PA (BARS/) BARSOUM J G.
XX
XX Barsoum JG, Fawell SE, Frankel A, Pepinsky RB, Pabo C;
PI WPI; 1997-502388/46.
XX
XX Fusion proteins containing truncated HIV tat sequences - useful for
PT intracellular delivery of viral repressor proteins.
XX
XX Example 17; Col 95-96; 77pp; English.
XX
XX This oligonucleotide primer is used with AAT89779 to form a duplex
CC corresponding to the wild type transcription factor NF-kappaB binding
CC site which is used in the construction of a transport polypeptide-DNA
CC conjugate. This conjugate is used in a novel method for delivery of
CC biologically active cargo molecules into the cytoplasm and nuclei of
CC eukaryotic cells. The tat protein from immunodeficiency virus (e.g. HIV-
CC 1, HIV-2, SIV) is readily taken up into cells when present
CC extracellularly and can be modified to covalently link to cargo proteins
CC e.g. E2 repressor proteins producing a fusion protein without the
CC problems of spurious trans-activation and disulphide aggregation. These
CC transport polypeptides also minimise interference with the biological
CC activity of the cargo molecule. This is applicable for therapeutic,
CC prophylactic or diagnostic intracellular delivery of small molecules and
CC macromolecules e.g. proteins, nucleic acids and polysaccharides. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
XX Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
SQ
Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCTCGCTGGGGACTTTCCAGGGGGACTTTCC 38
Db 39 GGGGACTTTCCTCGCTGGGGACTTTCCAGGGGGACTTTCC 2

RESULT 17
AAV56615
ID AAV56615 standard; DNA; 39 BP.
XX
XX AAV56615;
AC
XX 25-MAR-2003 (revised)
DT

```

```
DT 24-NOV-1998 (first entry)
DE NF-kappaB binding site phosphorothioate primer NF1.
XX
XX
XX TAT protein; cargo molecule; therapy; diagnosis; transport protein;
KW fusion protein; human papillomavirus E2 repressor; target cell;
KW phosphorothioate; primer; ss.
XX
XX Synthetic.
XX
XX US5804604-A.
XX
XX 08-SEP-1998.
XX
XX 25-MAY-1995; 95US-00450236.
XX
XX 21-DEC-1989; 89US-00454450.
XX 02-JAN-1991; 91US-00636662.
XX 19-AUG-1993; 93WO-US0007833.
XX 24-NOV-1993; 93US-00158015.
XX 28-APR-1994; 94US-00235403.
XX
XX (BIOJ ) BIOGEN INC.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
XX
XX Fawell SE, Barsoum JG, Pepinsky RB, Pabo C, Frankel A;
XX WPI; 1998-505702/43.
XX
XX HIV tat-derived transport fusion proteins - used to deliver biological
PT active molecules e.g. peptide(s) or nucleic acids, specifically into
PT cytoplasm or nuclei of cells.
XX
XX Example 17; Col 95-96; 83pp; English.
XX
XX This sequence is a phosphorothioate primer used in a method for the
CC delivery of biologically active cargo molecules into the cytoplasm and
CC nuclei of cells, for therapeutic, prophylactic or diagnostic purposes.
CC This is accomplished by the presence of a small, basic section of the tat
CC transport protein from human immunodeficiency virus (HIV) Type I. This is
CC used as it is this protein which is observed to cause human cells in
CC culture to take up HIV. The method involves the use of a cargo moiety in
CC combination with a transport moiety usually in the form of a fusion
CC protein. The cargo moiety is a human papillomavirus E2 repressor that
CC retains its biological activity after delivery into a target cell and
CC where the transport moiety is one of following HIV tat protein fragments
CC (a) aa 47-58, (b) aa 47-72, (c) 38-72, (d) aa 38-58, (e) aa 37-58, (f) aa
CC 1-21 and 38-72, (g) aa 47-62 or aa 38-62. The proteins allow delivery of
CC specific peptides into cells at high concentrations due to use of
CC existing transporters. Previous methods of delivery include bombardment
CC and transforming, which only allow a fraction of the cell population to
CC be infected and can additionally damage cells as they cause physical
CC opening of the cell walls/membranes to allow entry. (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
XX Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
SQ
Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTCC 38
DB 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38
RESULT 18
AAV56616/c
ID AAV56616 standard; DNA; 39 BP.
XX
XX AAV56616;
AC
XX
```

```
DT 25-MAR-2003 (revised)
DT 24-NOV-1998 (first entry)
XX
XX NF-kappaB binding site phosphorothioate primer NF2.
DE
XX
XX TAT protein; cargo molecule; therapy; diagnosis; transport protein;
KW fusion protein; human papillomavirus E2 repressor; target cell;
KW phosphorothioate; primer; ss.
XX
XX Synthetic.
XX
XX US5804604-A.
XX
XX 08-SEP-1998.
XX
XX 25-MAY-1995; 95US-00450236.
XX
XX 21-DEC-1989; 89US-00454450.
XX 02-JAN-1991; 91US-00636662.
XX 19-AUG-1993; 93WO-US0007833.
XX 24-NOV-1993; 93US-00158015.
XX 28-APR-1994; 94US-00235403.
XX
XX (BIOJ ) BIOGEN INC.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
XX
XX Fawell SE, Barsoum JG, Pepinsky RB, Pabo C, Frankel A;
XX WPI; 1998-505702/43.
XX
XX HIV tat-derived transport fusion proteins - used to deliver biological
PT active molecules e.g. peptide(s) or nucleic acids, specifically into
PT cytoplasm or nuclei of cells.
XX
XX Example 17; Col 97-98; 83pp; English.
XX
XX This sequence is a phosphorothioate primer used in a method for the
CC delivery of biologically active cargo molecules into the cytoplasm and
CC nuclei of cells, for therapeutic, prophylactic or diagnostic purposes.
CC This is accomplished by the presence of a small, basic section of the tat
CC transport protein from human immunodeficiency virus (HIV) Type I. This is
CC used as it is this protein which is observed to cause human cells in
CC culture to take up HIV. The method involves the use of a cargo moiety in
CC combination with a transport moiety usually in the form of a fusion
CC protein. The cargo moiety is a human papillomavirus E2 repressor that
CC retains its biological activity after delivery into a target cell and
CC where the transport moiety is one of following HIV tat protein fragments
CC (a) aa 47-58, (b) aa 47-72, (c) 38-72, (d) aa 38-58, (e) aa 37-58, (f) aa
CC 1-21 and 38-72, (g) aa 47-62 or aa 38-62. The proteins allow delivery of
CC specific peptides into cells at high concentrations due to use of
CC existing transporters. Previous methods of delivery include bombardment
CC and transforming, which only allow a fraction of the cell population to
CC be infected and can additionally damage cells as they cause physical
CC opening of the cell walls/membranes to allow entry. (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
XX Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
SQ
Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTCC 38
DB 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2
RESULT 19
AAD26647
ID AAD26647 standard; DNA; 39 BP.
XX
XX AAD26647;
AC
```

```
XX 26-MAR-2002 (first entry)
XX NF-kB wild type binding site generating NF1 phosphorothioate oligo.
XX
XX Human immunodeficiency virus; HIV-1; tat; therapeutic; toxin; enzyme;
XX regulatory factor; prophylactic; extracellular fusion protein; drug;
XX NFkB; nuclear factor kappa B; phosphorothioate backbone; ds.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1..39
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX
XX US6316003-B1.
XX
XX 13-NOV-2001.
XX
XX 28-APR-1994; 94US-00235403.
XX
XX 21-DEC-1989; 89US-00454450.
XX 02-JAN-1991; 91US-00636662.
XX 21-AUG-1992; 92US-00934375.
XX 19-AUG-1993; 93WO-US007833.
XX 24-NOV-1993; 93US-00158015.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (UYUO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX (BIOJ ) BIOGEN INC.
XX
XX Frankel A, Pabo C, Barsom JG, Fawell SE, Pepinsky RB;
XX WPI; 2002-088872/12.
XX
XX Delivering biologically active cargo molecules such as polypeptides,
XX nucleic acids into cells by using transport polypeptides which comprise
XX human immunodeficiency virus transactivator protein linked to cargo
XX molecules.
XX
XX Example 17; Col 95; 78pp; English.
XX
XX The invention relates to a method for delivering a biologically active
XX cargo molecule of interest into a cell. The method comprises presenting
XX to the cell an extracellular fusion protein or a covalently linked
XX conjugate consisting of a cargo moiety and a transport moiety having
XX amino acids 49-57 of human immunodeficiency virus (HIV) transactivator
XX (tat) protein and lacking amino acids 22-36 and 73-86 of HIV tat protein.
XX The method is useful for delivering a molecule of interest such as
XX polypeptides, antigen, monoclonal antibody, single- or double-stranded
XX nucleic acid, a therapeutic, prophylactic and diagnostic molecule to a
XX cell in vitro or in vivo. The method delivers proteins or peptides,
XX including regulatory factors, enzymes, drugs or toxins into the cytoplasm
XX and cell nucleus. The method is useful for diagnostic, prophylactic or
XX therapeutic intracellular delivery of small and macro molecules. The
XX present sequence is a phosphorothioate oligonucleotide used for generating
XX nuclear factor kappa B (NFkB) wild type binding site used in the
XX exemplification of the invention
XX
XX Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 78.9%; Score 30; DB 6; Length 39;
XX Best Local Similarity 86.8%; Pred.No. 0.03;
XX Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
XX
XX 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
XX
```

```

AAD26648/c
ID AAD26648 standard; DNA; 39 BP.
XX
XX AAD26648;
AC
XX
XX 26-MAR-2002 (first entry)
XX
XX NF-kB wild type binding site generating NF2 phosphorothioate oligo.
XX
XX Human immunodeficiency virus; HIV-1; tat; therapeutic; toxin; enzyme;
XX regulatory factor; prophylactic; extracellular fusion protein; drug;
XX NFkB; nuclear factor kappa B; phosphorothioate backbone; ds.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1..39
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX
XX US6316003-B1.
XX
XX 13-NOV-2001.
XX
XX 28-APR-1994; 94US-00235403.
XX
XX 21-DEC-1989; 89US-00454450.
XX 02-JAN-1991; 91US-00636662.
XX 21-AUG-1992; 92US-00934375.
XX 19-AUG-1993; 93WO-US007833.
XX 24-NOV-1993; 93US-00158015.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (UYUO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX (BIOU ) BIOGEN INC.
XX
XX Frankel A, Pabo C, Barsom JG, Fawell SE, Pepinsky RB;
XX WPI; 2002-088872/12.
XX
XX Delivering biologically active cargo molecules such as polypeptides,
XX nucleic acids into cells by using transport polypeptides which comprise
XX human immunodeficiency virus transactivator protein linked to cargo
XX molecules.
XX
XX Example 17; Col 97; 78pp; English.
XX
XX The invention relates to a method for delivering a biologically active
XX cargo molecule of interest into a cell. The method comprises presenting
XX to the cell an extracellular fusion protein or a covalently linked
XX conjugate consisting of a cargo moiety and a transport moiety having
XX amino acids 49-57 of human immunodeficiency virus (HIV) transactivator
XX (tat) protein and lacking amino acids 22-36 and 73-86 of HIV tat protein.
XX The method is useful for delivering a molecule of interest such as
XX polypeptides, antigen, monoclonal antibody, single- or double-stranded
XX nucleic acid, a therapeutic, prophylactic and diagnostic molecule to a
XX cell in vitro or in vivo. The method delivers proteins or peptides,
XX including regulatory factors, enzymes, drugs or toxins into the cytoplasm
XX and cell nucleus. The method is useful for diagnostic, prophylactic or
XX therapeutic intracellular delivery of small and macro molecules. The
XX present sequence is a phosphorothioate oligonucleotide used for generating
XX nuclear factor kappa B (NFkB) wild type binding site used in the
XX exemplification of the invention
XX
XX Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 78.9%; Score 30; DB 6; Length 39;
XX Best Local Similarity 86.8%; Pred.No. 0.03;
XX Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
XX
XX 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
XX
```



Db 39 GGGGACTTTCGGCTGGGACTTTCACGGGGGACTTTC 2

RESULT 21

AA248474

ID AAZ48474 standard; DNA; 44 BP.

XX AC AAZ48474;

XX AC

XX AC

DT 15-SEP-2003 (revised)

DT 28-MAR-2000 (first entry)

XX HIV LTR NF-kB oligonucleotide.

XX Triterpene glycoside; antitumor; cytotoxic; antioxidant; contraceptive; antihelminthic; expectorant; diuretic; anti-inflammatory; cardiac; anti-ulcer; analgesic; sedative; immunomodulator; antipyretic; cancer; vasotropic; Acacia victoriae; angiogenesis; antifungal; cholesterol; cardiovascular effector; HIV; NF-kappaB; ds.

XX Human immunodeficiency virus 1.

OS W0959578-A1.

PN 25-NOV-1999.

PD 19-MAY-1999; 99WO-US011041.

PF 19-MAY-1998; 98US-0085997P.

PR 03-SEP-1998; 98US-0099066P.

XX (RERE-) RES DEV FOUND.

XX Arntzen CJ, Tracey MB, Guterman JU, Hoffmann JJ, Bailey DT;

PI Jayatilake GS;

XX WPI; 2000-105567/09.

XX Mixture containing triterpene glycosides, useful for treating variety of tumor cells.

XX Example 27; Page 199; 312pp; English.

XX The invention relates to a mixture comprising one or more triterpene glycosides isolated from Acacia victoriae. The composition is used for the treatment of cancer, inhibiting the initiation and promotion of mammalian epithelial cells (such as skin, colon, uterine, ovarian, pancreatic, prostate, renal, lung, bladder or breast cells), for preventing the abnormal proliferation of mammalian epithelial cells (such as crypt or colon cells), and/or regulating angiogenesis. The triterpene glycosides may also be used as a solvent, an antioxidant, antifungal or antiviral agent, piscicide, molluscicides, contraceptive, antihelminthic, angiogenesis regulator, UV-protectant, expectorant, diuretic, anti-inflammatory agent, regulator of cholesterol metabolism, cardiovascular effector, anti-ulcer agent, analgesic, sedative, immunomodulator, antipyretic, as an agent for decreasing capillary fragility, combating the effects of aging, increasing skin collagen, enhancing penile function and improving cognition and memory. The present sequence represents an 32P-labelled NF-kappaB oligo from HIV long terminal repeat used in electrophoretic mobility shift assay. (Updated on 15-SEP-2003 to standardise OS field)

XX Sequence 44 BP; 7 A; 9 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 78.4%; Score 29.8; DB 3; Length 44;

Best Local Similarity 93.9%; Pred. No. 0.037; Mismatches 0; Gaps 0;

Matches 31; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACGGGGGACT 34

Db 10 GGGACTTTCGGCTGGGACTTTCACGGGGGACT 42

RESULT 22

ABL61552

XX ABL61552 standard; DNA; 44 BP.

XX AC ABL61552;

XX DT 20-SEP-2002 (first entry)

XX HIV-LTR NFkappaB DNA.

XX NFkappaB; antiinflammatory; antiarteriosclerotic; antirheumatic;

XX antiarthritic; osteopathic; antiparkinsonian; nootropic; monoterpene;

XX neuroprotective; antiparkinsonian. Barretts esophagitis; osteoarthritis;

XX inflammatory bowel disease; chronic pancreatitis; chronic prostatitis;

XX familial polyposis; actinic keratosis; rheumatoid arthritis;

XX multiple sclerosis; Parkinson's disease; Alzheimer's disease; ds.

XX Human immunodeficiency virus.

XX Key modified\_base 1 Location/Qualifiers

FT /\*tag= a /mod\_base= OTHER

FT /note= "32P labelled"

XX WO200255016-A2.

XX 18-JUL-2002.

XX 19-NOV-2001; 2001WO-US043286.

XX 17-NOV-2000; 2000US-0249710P.

XX 17-SEP-2001; 2001US-0322859P.

XX (RERE-) RES DEV FOUND.

XX Guterman JU, Haridas V;

XX WPI; 2002-557793/59.

XX Inhibiting inflammation used for treating e.g. osteoarthritis and multiple sclerosis comprises administering monoterpene composition inhibiting nuclear factor kappaB.

XX Example 28; Page 349; 349pp; English.

XX This sequence represents a novel method for inhibiting inflammation which comprises administering a monoterpene composition that inhibits NFkappaB. The products of the invention have antiinflammatory, antiarthritic, osteopathic, antiarteriosclerotic, antirheumatic, antiarthritic, osteopathic, antiparkinsonian, nootropic, neuroprotective and antiparkinsonian activity. The method described can be used for treating inflammatory diseases, particularly premalignant inflammatory disease (e.g. Barretts esophagitis, inflammatory bowel disease, chronic pancreatitis, chronic prostatitis, familial polyposis and actinic keratosis), arteriosclerosis, rheumatoid arthritis, osteoarthritis, multiple sclerosis, Parkinson's disease and Alzheimer's disease. This sequence represents a 32P-labelled NFkappaB oligonucleotide used in an electrophoretic mobility shift assay to detect the biological characteristics of active triterpenes

XX Sequence 44 BP; 7 A; 9 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 78.4%; Score 29.8; DB 6; Length 44;

Best Local Similarity 93.9%; Pred. No. 0.037; Mismatches 0; Gaps 0;

Matches 31; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACGGGGGACT 34

Db 10 GGGACTTTCGGCTGGGACTTTCACGGGGGACT 42

RESULT 23

AAT30599

```

ID AAT30599 standard; DNA; 45 BP.
XX
AC AAT30599;
XX
XX 19-FEB-1997 (first entry)
XX
DE Target binding region #19.
XX
XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;
KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
KW virus; ss.
XX
OS Synthetic.
XX
PN WO9617956-A2.
XX
XX 13-JUN-1996.
XX
PD 07-DEC-1995; 95WO-US015944.
XX
PF 09-DEC-1994; 94US-00353476.
XX
PR (GENE-) GENE POOL INC.
XX
PA Weininger S, Weininger AM;
XX PI WPI; 1996-287199/29.
XX
XX Probe nucleic acids, target binding assemblies, etc - for detection and
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.
XX
XX Disclosure; Page 70; 172pp; English.
XX
CC AAT30581-T30614 represent target binding regions (TBR) of a probe of the
CC invention. The probe of the invention contains a TBR, a booster binding
CC region (BBR), and an optional support or attachment (OSA). The target
CC binding assembly (TBA) recognised by the probe, contains at least one
CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an
CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see
CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),
CC and an OSA. The assembly sequence and asymmetry sequences are responsible
CC for the folding and association of the NARs. The NARs (see AAR95965-
CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus
CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding
CC units. The linker sequence is an oligopeptide, which does not interfere
CC with NAR function, but provides stability and control over the spacing of
CC the NAR from the rest of the TBA. The OSA is an attached support or
CC indicator, or other means of localisation of the probe. The probe can be
CC used in a method for detecting or localising a specific target nucleic
CC acid sequence (TNA). The method is highly sensitive, and has a high
CC degree of specificity. The method can be used for detecting specific
CC nucleic acid sequences, including those found in human cells, in HIV,
CC HPV, and other nucleic acid containing systems, including bacteria and
CC viruses
XX
XX Sequence 45 BP; 7 A; 12 C; 16 G; 10 T; 0 U; 0 Other;
SQ
Query Match 76.8%; Score 29.2; DB 2; Length 45;
Best Local Similarity 91.2%; Pred. No. 0.064;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCCAGGGGACTT 35
| | | | | | | | | | | | | | | | | | | |
Db 7 GGGACTTTCGGCTGGGACTTTCCAGGGGAGCGT 40
| | | | | | | | | | | | | | | | | | | |

RESULT 24
AAT30603
ID AAT30603 standard; DNA; 45 BP.
XX
XX AAT30603;
AC

19-FEB-1997 (first entry)
Target binding region #23.
Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;
TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
virus; ss.
Synthetic.
WO9617956-A2.
13-JUN-1996.
07-DEC-1995; 95WO-US015944.
09-DEC-1994; 94US-00353476.
(GENE-) GENE POOL INC.
Weininger S, Weininger AM;
WPI; 1996-287199/29.
Probe nucleic acids, target binding assemblies, etc - for detection and
localisation of specific nucleic acid sequences, esp. HIV and HPV.
Disclosure; Page 71; 172pp; English.
AAT30581-T30614 represent target binding regions (TBR) of a probe of the
invention. The probe of the invention contains a TBR, a booster binding
region (BBR), and an optional support or attachment (OSA). The target
binding assembly (TBA) recognised by the probe, contains at least one
nucleic acid recognition unit (NAR), and optionally a linker sequence, an
assembly sequence (see AAR95994-R95998), an asymmetry sequence (see
AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),
and an OSA. The assembly sequence and asymmetry sequences are responsible
for the folding and association of the NARs. The NARs (see AAR95965-
R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus
(HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding
units. The linker sequence is an oligopeptide, which does not interfere
with NAR function, but provides stability and control over the spacing of
the NAR from the rest of the TBA. The OSA is an attached support or
indicator, or other means of localisation of the probe. The probe can be
used in a method for detecting or localising a specific target nucleic
acid sequence (TNA). The method is highly sensitive, and has a high
degree of specificity. The method can be used for detecting specific
nucleic acid sequences, including those found in human cells, in HIV,
HPV, and other nucleic acid containing systems, including bacteria and
viruses
Sequence 45 BP; 8 A; 11 C; 16 G; 10 T; 0 U; 0 Other;
Query Match 76.8%; Score 29.2; DB 2; Length 45;
Best Local Similarity 91.2%; Pred. No. 0.064;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCCAGGGGACTT 35
| | | | | | | | | | | | | | | | | | | |
Db 7 GGGACTTTCGGCTGGGACTTTCCAGGGGAGCGT 40
| | | | | | | | | | | | | | | | | | | |

RESULT 25
AAX28079
ID AAX28079 standard; DNA; 45 BP.
XX
XX AAX28079;
AC
XX 17-OCT-2003 (revised)
DT 10-JUN-1999 (first entry)
DT
```

XX HIV-LTR oligonucleotide.  
 DE Inhibitor; activator; NF-kappaB transcription factor; toxic shock;  
 XX septic shock; graft versus host disease; curcumin; diferuloylmethane;  
 KW radiation damage; atherosclerosis; cancer; HIV infection; HIV-LTR; ss.  
 KW  
 XX Human immunodeficiency virus 1.  
 OS  
 XX  
 XX US5891924-A.  
 PN  
 XX  
 XX 06-APR-1999.  
 PD  
 XX  
 XX 26-SEP-1996; 96US-00712932.  
 PF  
 XX  
 XX 26-SEP-1996; 96US-00712932.  
 PR  
 XX  
 XX (RERE-) RES DEV FOUND.  
 PA  
 XX Aggarwal BB;  
 PI  
 XX WPI; 1999-253918/21.  
 DR  
 XX  
 XX Inhibiting activation of NFkappaB with curcumin used for treatment of  
 PT e.g. septic shock or guest versus host reaction.  
 PT  
 XX  
 XX Example 3; Col 5; 21pp; English.  
 PS  
 XX  
 CC This sequence represents a HIV-LTR oligonucleotide used to test the  
 CC method of the invention. The method is for inhibition of activation of  
 CC the NF-kappaB transcription factor (A), for treatment of toxic or septic  
 CC shock or graft versus host reactions in humans, comprises administration  
 CC of curcumin (I; diferuloylmethane). (I) is used to treat toxic or septic  
 CC shock and graft versus host reactions in humans. (I) may be used to  
 CC inhibit activation of (A) e.g. in cases of radiation damage,  
 CC atherosclerosis, cancer and human immune deficiency virus (HIV)  
 CC infection. (Updated on 17-OCT-2003 to standardise OS field)  
 CC  
 XX  
 XX Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;  
 SQ  
 Query Match 76.8%; Score 29.2; DB 2; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.064;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GGGACTTTCCGCTGGGACTTTCCAGGGGACTT 35  
 Db 10 GGGACTTTCCGCTGGGACTTTCCAGGGGCGT 43  
 RESULT 26  
 ADH12178  
 ID ADH12178 standard; DNA; 45 BP.  
 XX  
 AC ADH12178;  
 XX  
 XX 11-MAR-2004 (first entry)  
 DT  
 XX  
 XX HIV-1 LTR NF-kappa-B sequence used as EMSA probe.  
 DE  
 XX  
 XX Multiple myeloma; proliferation inhibition; apoptosis induction;  
 KW curcumin; diferuloylmethane; chemotherapy potentiator;  
 KW I-kappa-B kinase inhibitor; I-kappa-B-alpha phosphorylation suppressor;  
 KW NF-kappa-B suppressor; I-kappa-B-alpha; Bcl-2; Bcl-XL; cyclin D1;  
 KW interleukin-6; IL-6; cell cycle arrest; cytosstatic; NF-kappa-B;  
 KW HIV-1 LTR; long terminal repeat; electrophoretic mobility shift assay;  
 KW EMSA; probe; ds.  
 XX  
 XX Human immunodeficiency virus 1.  
 OS  
 XX  
 XX WO200400229-A2.  
 PN  
 XX  
 XX 31-DEC-2003.  
 PD  
 XX

PF 24-JUN-2003; 2003WO-US019837.  
 XX  
 PR 24-JUN-2002; 2002US-0390926P.  
 XX  
 PA (RERE-) RES DEV FOUND.  
 XX  
 PI Aggarwal B;  
 XX  
 XX WPI; 2004-156362/15.  
 DR  
 XX  
 XX Inhibiting proliferation of multiple myeloma cells comprises  
 PT administering curcumin and optionally with vincristine,  
 PT bichloroethylnitrosourea, melphalan, cyclophosphamide, adriamycin,  
 PT prednisone or dexamethasone.  
 XX  
 XX Example 3; SEQ ID NO 4; 77pp; English.  
 PS  
 XX  
 CC The invention relates to a method for inhibiting the proliferation of,  
 CC and inducing apoptosis in multiple myeloma cells comprising  
 CC administration of curcumin (diferuloylmethane). The invention also  
 CC relates to a method for increasing the cytotoxic effects of a  
 CC chemotherapeutic agent (e.g., vincristine, bichloroethylnitrosourea,  
 CC melphalan, cyclophosphamide, adriamycin, prednisone or dexamethasone)  
 CC against multiple myeloma cells (preferably CD138+ plasma cells) comprises  
 CC administration of the chemotherapeutic agent and curcumin. Curcumin  
 CC increases the cytotoxic effects of the chemotherapeutic agent against  
 CC multiple myeloma cells. It suppresses constitutive I-kappa-B-alpha  
 CC phosphorylation through inhibition of I-kappa-B kinase activity, and  
 CC downregulates the expression of NF-kappa-B-regulated gene products (e.g.  
 CC I-kappa-B-alpha, Bcl-2, Bcl-XL, cyclin D1 and interleukin-6), leading to  
 CC suppression of proliferation and arrest of cells at the G1/S phase of the  
 CC cell cycle. The methods of the invention are used for the treatment of  
 CC multiple myeloma. The present sequence represents an NF-kappa-B binding  
 CC sequence derived from the HIV-1 long terminal repeat (LTR) which was used  
 CC as a probe in electrophoretic mobility shift assay (EMSA) of NF-kappa-B  
 CC in an example of the invention.  
 CC  
 XX  
 XX Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;  
 SQ  
 Query Match 76.8%; Score 29.2; DB 12; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.064;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GGGACTTTCCGCTGGGACTTTCCAGGGGACTT 35  
 Db 10 GGGACTTTCCGCTGGGACTTTCCAGGGGCGT 43  
 RESULT 27  
 ADZ00136  
 ID ADZ00136 standard; DNA; 45 BP.  
 XX  
 AC ADZ00136;  
 XX  
 XX 30-JUN-2005 (first entry)  
 DT  
 XX  
 XX EMSA probe for detecting NF-kappaB activation in curcumin treated cells.  
 DE  
 XX  
 XX osteopathic; osteogenesis; nuclear factor kappa B; cancer; breast tumor;  
 KW myeloma; osteoporosis; Paget's disease; rheumatoid arthritis;  
 KW head and neck tumor; probe; ss.  
 XX  
 XX Human immunodeficiency virus 1.  
 OS  
 XX  
 XX US2005080023-A1.  
 PN  
 XX  
 XX 14-APR-2005.  
 PD  
 XX  
 XX 25-AUG-2004; 2004US-00925608.  
 PF  
 XX  
 XX 26-AUG-2003; 2003US-0497841P.  
 PR  
 XX  
 XX (AGGA/) AGGARWAL B B.  
 PA

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XX Aggarwal BB;
XX
XX WPI; 2005-295074/30.
XX
XX Use of compounds comprising diferuloylmethane, guggulsterone, 1'-
XX acetoxychavicol or their analogues to e.g. reduce/inhibit osteoclast
XX development induced by the receptor for activation of nuclear factor
XX kappa B ligand.
XX
XX Example 7; SEQ ID NO 1; 43pp; English.
XX
XX The invention relates to a method of reducing or inhibiting osteoclast
XX development induced by the receptor for activation of nuclear factor
XX kappa B ligand (RANKL) by contacting the osteoclast or its precursor with
XX compounds (i) comprising diferuloylmethane, guggulsterone, 1'-
XX acetoxychavicol or their analogues. (i) is useful for reducing or
XX inhibiting osteoclast development induced by RANKL, inhibiting the
XX formation of osteoclasts in an individual and reducing osteolytic
XX activity and bone loss in an individual having breast cancer, multiple
XX myeloma, post-menopausal osteoporosis, Paget's disease, rheumatoid
XX arthritis or head and neck squamous cell carcinoma. The diferuloylmethane
XX (curcumin) is safe to humans. This sequence corresponds to an
XX electrophoresis shift assay (EMSA) probe used to analyze NF-kappaB
XX activation in curcumin-treated or untreated cells. The sequence is
XX derived from the human immunodeficiency virus 1 long terminal repeat.
XX
XX Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 76.8%; Score 29.2; DB 14; Length 45;
XX Best Local Similarity 91.2%; Pred. No. 0.064;
XX Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 GGGACTTTCGCTGGGACTTTCAGGGGACTT 35
XX |||||
XX Db 10 GGGACTTTCGCTGGGACTTTCAGGGGACTT 43
XX
XX RESULT 28
XX AEA06160
XX ID AEA06160 standard; DNA; 45 BP.
XX
XX AC AEA06160;
XX
XX DT 28-JUL-2005 (first entry)
XX
XX DE Oligo from HIV long terminal repeat containing NF-kappaB binding site.
XX
XX KW Nuclear factor-kappa B; NF-kappaB; NF-kappaB inhibitor;
XX apoptosis stimulation; cancer; cytostatic; HIV long terminal repeat; ss.
XX
XX OS Human immunodeficiency virus.
XX
XX FH Key Location/Qualifiers
XX protein_bind 10..17
XX /*tag= a
XX /bound_moiety= "NF-kappaB"
XX protein_bind 24..32
XX /*tag= b
XX /bound_moiety= "NF-kappaB"
XX
XX WO2005046708-A1.
XX
XX PN 26-MAY-2005.
XX
XX PD
XX
XX PF 04-NOV-2004; 2004WO-US036777.
XX
XX PR 06-NOV-2003; 2003US-0517852P.
XX
XX PA (RERE-) RES DEV FOUND.
XX
XX PI Aggarwal BB, Singh S;
XX
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DR WPI; 2005-372280/38.
XX
XX New cell permeable nuclear factor kappaB inhibitor comprising a peptide
XX fragment and a protein transduction domain, useful for treating cancer.
XX
XX Example 2; SEQ ID NO 1; 47pp; English.
XX
XX The present invention relates to cell permeable nuclear factor (NF)-
XX kappaB, and specifically to polypeptides that selectively inhibit NF-
XX kappaB activation, downregulate NF-kappaB mediated gene expression and
XX enhance apoptosis induced by TNF and other apoptotic stimuli. The
XX inhibitor comprises (i) a peptide fragment of the p65 subunit of NF-
XX kappaB, where the peptide comprises phosphorylation site(s) of the p65
XX subunit and (ii) a protein transduction domain which is able to transport
XX the polypeptide across cell membrane. The protein transduction domain is
XX derived from a protein or domain selected from third helix of the
XX antenapedia homeodomain (SEQ ID NO:3), herpes virus structural protein,
XX or HIV tat protein. Also disclosed is an isolated DNA encoding the
XX inhibitor. Provided is a method of inhibiting the DNA binding activity of
XX NF-kappaB; a method of increasing the level of apoptosis; and a method of
XX treating cancer. Inhibiting the DNA binding activity of NF-kappaB in a
XX cell comprises contacting a cell with the inhibitor above, where the
XX inhibitor suppresses NF-kappaB binding to DNA. Activity is induced by an
XX agent, e.g. TNF, LPS, IL-1, okadaic acid, phorbol myristate acetate
XX (PMA), hydrogen peroxide, cigarette smoke condensate, TNF receptor 1, TNF
XX receptor-associated death domain (TRADD), TNF receptor-associated factor-
XX 2 (TRAF2), NF-kappaB-inducing kinase (NIK), or IkappaBalpha kinase (IKK).
XX The present sequence is a 45-mer double-stranded oligonucleotide from the
XX HIV long terminal repeat containing NF-kappaB binding site, used to form
XX a DNA-protein complex to examine the specificity of binding of NF-kappaB
XX to the DNA.
XX
XX Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 76.8%; Score 29.2; DB 14; Length 45;
XX Best Local Similarity 91.2%; Pred. No. 0.064;
XX Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 2 GGGACTTTCGCTGGGACTTTCAGGGGACTT 35
XX |||||
XX Db 10 GGGACTTTCGCTGGGACTTTCAGGGGACTT 43
XX
XX RESULT 29
XX AAT30607
XX ID AAT30607 standard; DNA; 46 BP.
XX
XX AC AAT30607;
XX
XX DT 19-FEB-1997 (first entry)
XX
XX DE Target binding region #27.
XX
XX KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;
XX TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
XX HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
XX nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
XX virus; ss.
XX
XX OS Synthetic.
XX
XX PN WO9617956-A2.
XX
XX PD 13-JUN-1996.
XX
XX PF 07-DEC-1995; 95WO-US015944.
XX
XX PR 09-DEC-1994; 94US-00353476.
XX
XX PA (GENE-) GENE POOL INC.
XX
XX PI Weininger S, Weininger AM;
XX
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XX AAT30581-T30614 represent target binding regions (TBR) of a probe of the
CC invention. The probe of the invention contains a TBR, and a booster binding
CC region (BBR), and an optional support or attachment (OSA). The target
CC binding assembly (TBA) recognised by the probe, contains at least one
CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an
CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see
CC AAR95999-R96006), a nuclear localisation signal sequence (see
CC AAR95993) for the folding and association of the NARs. The NARs (see AAR95965-
CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus
CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding
CC units. The linker sequence is an oligopeptide, which does not interfere
CC with NAR function, but provides stability and control over the spacing of
CC the NAR from the rest of the TBA. The OSA is an attached support or
CC indicator, or other means of localisation of the probe. The probe can be
CC used in a method for detecting or localising a specific target nucleic
CC acid sequence (TNA). The method is highly sensitive, and has a high
CC degree of specificity. The method can be used for detecting specific
CC nucleic acid sequences, including those found in human cells, in HIV,
CC HPV, and other nucleic acid containing systems, including bacteria and
CC viruses
XX
SQ Sequence 46 BP; 7 A; 11 C; 17 G; 11 T; 0 U; 0 Other;

Query Match          76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGAGCTTTCACGGGG 30
Db 7 GGGACTTTCGGCTGGGGAGCTTTCACGGGG 35

RESULT 32
AAT30600
ID AAT30600 standard; DNA; 46 BP.
XX
AC AAT30600;
XX
DT 19-FEB-1997 (first entry)
DE Target binding region #20.
XX
KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;
KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
KW virus; ss.
XX
OS Synthetic.
XX
FN WO9617956-A2.
XX
PD 13-JUN-1996.
XX
PF 07-DEC-1995; 95WO-US015944.
XX
PR 09-DEC-1994; 94US-00353476.
XX
PA (GENE-) GENE POOL INC.
XX
PI Weininger S, Weininger AM;
XX
DR WPI; 1996-287199/29.
XX
PT Probe nucleic acids, target binding assemblies, etc - for detection and
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.
XX
PS Disclosure; Page 70; 172pp; English.
XX
SS AAT30581-T30614 represent target binding regions (TBR) of a probe of the
CC invention. The probe of the invention contains a TBR, a booster binding

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CC region (BBR), and an optional support or attachment (OSA). The target
CC binding assembly (TBA) recognised by the probe, contains at least one
CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an
CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see
CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),
CC and an OSA. The assembly sequence and asymmetry sequences are responsible
CC for the folding and association of the NARs. The NARs (see AAR95965-
CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus
CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding
CC units. The linker sequence is an oligopeptide, which does not interfere
CC with NAR function, but provides stability and control over the spacing of
CC the NAR from the rest of the TBA. The OSA is an attached support or
CC indicator, or other means of localisation of the probe. The probe can be
CC used in a method for detecting or localising a specific target nucleic
CC acid sequence (TNA). The method is highly sensitive, and has a high
CC degree of specificity. The method can be used for detecting specific
CC nucleic acid sequences, including those found in human cells, in HIV,
CC HPV, and other nucleic acid containing systems, including bacteria and
CC viruses
XX
SQ Sequence 46 BP; 7 A; 11 C; 18 G; 10 T; 0 U; 0 Other;

Query Match          76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGAGCTTTCACGGGG 30
Db 7 GGGACTTTCGGCTGGGGAGCTTTCACGGGG 35

RESULT 33
AAT67098
ID AAV67098 standard; cDNA; 36 BP.
XX
AC AAV67098;
XX
DT 14-JAN-1999 (first entry)
DE HIV LTR #2.
XX
KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
KW differentiation marker; immune system; corpus striatum; AIDS;
KW Alzheimer's disease; ss.
XX
OS Human immunodeficiency virus 1.
OS Synthetic.
XX
PN US5824770-A.
XX
PD 20-OCT-1998.
XX
PF 05-JUN-1995; 95US-00465590.
XX
PR 14-SEP-1992; 92US-00946233.
PR 14-SEP-1993; 93US-00121438.
PR 02-MAY-1994; 94US-00238212.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI Georgopoulos K;
XX
DR WPI; 1998-582621/49.
XX
PT Ikaros poly:peptide(s) - useful for treating disorders of immune system
PT or corpus striatum.
XX
PS Disclosure; Col 27; 111pp; English.
XX
CC The present invention describes a purified peptide having at least one of
CC the following properties: (a) it stimulates transcription of a DNA
CC sequence under the control of a delta A element, an NFkB element or an
CC Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of

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CC a delta A element, an NFkB element or an Ikaros binding oligonucleotide  
 CC consensus sequence; (c) it competitively inhibits the binding of a  
 CC naturally occurring Ikaros isoform to any of a delta A element, an NFkB  
 CC element or an Ikaros binding oligonucleotide consensus sequence; (d) it  
 CC competitively inhibits Ikaros binding to Ikaros responsive elements; or  
 CC (e) it inhibits protein-protein interactions of transcriptional complexes  
 CC formed with naturally occurring Ikaros isoforms. The proteins, provided  
 CC that they stimulate gene transcription under the control of delta A  
 CC elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to  
 CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,  
 CC competitively inhibit binding of naturally occurring Ikaros isoforms to  
 CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,  
 CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or  
 CC inhibit protein-protein interactions of transcriptional complexes with  
 CC naturally occurring Ikaros isoforms, can be used to treat immune system  
 CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.  
 CC Alzheimer's disease. AAV66975 to AAV67118 represent oligonucleotides  
 CC given in the present invention  
 XX  
 SQ Sequence 36 BP; 6 A; 9 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 75.8%; Score 28.8; DB 2; Length 36;  
 Best Local Similarity 93.8%; Pred. No. 0.088; Indels 2; Gaps 0;  
 Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACGGGGAC 33  
 |||||  
 DB 4 GGGACTTTCGGCTGGGACTTTCACGGGGAC 35

RESULT 34  
 AAQ61543  
 ID AAQ61543 standard; cDNA; 37 BP.  
 XX  
 AC AAQ61543;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-OCT-1994 (first entry)  
 XX  
 DE HIV long terminal repeat sequence comprising Ikaros binding site.  
 XX  
 KW Ikaros; zinc finger; protein; immune disorder; therapy; treatment;  
 KW corpus striatum; regulatory gene; enhancer; regulatory element;  
 KW gene expression; HIV; human immunodeficiency virus; ss.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 PN WO9406814-A1.  
 XX  
 PD 31-MAR-1994.  
 XX  
 PF 14-SEP-1993; 93WO-US008743.  
 XX  
 PR 14-SEP-1992; 92US-00946233.  
 XX  
 PA (GENO ) GEN HOSPITAL CORP.  
 XX  
 PI Georgopoulos K;  
 XX  
 DR WPI; 1994-118387/14.  
 XX  
 PT I-cell pathway regulatory gene, Ikaros - encodes family of unique zinc  
 PT finger proteins, useful for treating immune system disorders.  
 XX  
 PS Disclosure; Page 29; 112pp; English.

XX The Ikaros gene encodes a zinc finger protein which can be used in a  
 CC therapeutic composition to treat animals with an immune system disorder.  
 CC It may also be used for assessing whether a subject is at risk for an  
 CC immune disorder. It is of particular use in treating a disorder of the  
 CC corpus striatum. Heterologous genes may be expressed by placing them  
 CC under the control of an Ikaros responsive control element and contacting  
 CC the element with an Ikaros protein. Potential high affinity binding sites

CC for the Ikaros proteins were found in the enhancer and promoter regions  
 CC of the TCR-alpha, -beta and -delta, the CD3-delta, -epsilon and -gamma  
 CC genes, the SL3 and HIV long terminal repeat and in the regulatory domains  
 CC of other T cell restricted antigens. Related sequences to the Ikaros  
 CC motif were also found in the purine boxes of the IL2 gene in the in the  
 CC LYP site of the TBT promoter as well as in the NFkB variant sites of the  
 CC HIV long terminal repeat. See also AAQ61504-Q61543. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX

SQ Sequence 37 BP; 6 A; 9 C; 15 G; 7 T; 0 U; 0 Other;

Query Match 74.7%; Score 28.4; DB 2; Length 37;  
 Best Local Similarity 96.7%; Pred. No. 0.13; Indels 1; Gaps 0;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACGGGGG 31  
 |||||  
 DB 4 GGGACTTTCGGCTGGGACTTTCACGGGGG 33

RESULT 35  
 AAT30615  
 ID AAT30615 standard; cDNA; 37 BP.  
 XX  
 AC AAT30615;  
 XX  
 DT 21-FEB-1997 (first entry)  
 XX  
 DE Probe nucleic acid PNA1.

XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;  
 KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
 KW virus; ss.

XX Synthetic.  
 XX WO9617956-A2.  
 XX  
 PD 13-JUN-1996.  
 XX  
 PF 07-DEC-1995; 95WO-US015944.  
 XX  
 PR 09-DEC-1994; 94US-00353476.  
 XX  
 PA (GENE-) GENE POOL INC.  
 XX  
 PI Weininger S, Weininger AM;  
 XX  
 DR WPI; 1996-287199/29.

XX Probe nucleic acids, target binding assemblies, etc - for detection and  
 PT localisation of specific nucleic acid sequences, esp. HIV and HPV.

XX Disclosure; Page 76; 172pp; English.

XX AAT30615-T30634 represent probe nucleic acids of the invention. The probe  
 CC of the invention contains a target binding region (TBR), a booster  
 CC binding region (BBR), and an optional support or attachment (OSA). The  
 CC target binding assembly (TBA) recognised by the TBR (see AAR30581-T30614)  
 CC of the probe, contains at least one nucleic acid recognition unit (NAR),  
 CC and optionally a linker sequence, an assembly sequence (see AAR95994-  
 CC R95998), an asymmetry sequence (see AAR95999-R96006), a nuclear  
 CC localisation signal sequence (see AAR96007), and an OSA. The assembly  
 CC sequence and asymmetry sequences are responsible for the folding and  
 CC association of the NARs. The NARs (see AAR95965-R95993) are selected from  
 CC NF-kappa-B, SP1, TATA, human papillomavirus (HPV) E2, HPV LTR, human  
 CC immunodeficiency virus (HIV) LTR and Tat binding units. The linker  
 CC sequence is an oligopeptide, which does not interfere with NAR function,  
 CC but provides stability and control over the spacing of the NAR from the  
 CC rest of the TBA. The OSA is an attached support or indicator, or other  
 CC means of localisation of the probe. The probe can be used in a method for

CC detecting or localising a specific target nucleic acid sequence (TNA).  
 CC The method is highly sensitive, and has a high degree of specificity. The  
 CC method can be used for detecting specific nucleic acid sequences,  
 CC including those found in human cells, in HIV, HPV, and other nucleic acid  
 CC containing systems, including bacteria and viruses  
 XX  
 SQ Sequence 37 BP; 7 A; 9 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 74.7%; Score 28.4; DB 2; Length 37;  
 Best Local Similarity 96.7%; Pred. No. 0.13;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCACGGGG 31  
 |||||  
 DB 7 GGGACTTTCGCTGGGACTTTCACGGAG 36  
 |||||

RESULT 36  
 AAV45402  
 ID AAV45402 standard; DNA; 37 BP.  
 XX  
 AC AAV45402;  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE HIV LTR binding site for Ikaros.

XX Ikaros; mIK; transcription factor; mouse; lymphocyte;  
 KW cell differentiation; T cell; cancer; immunodeficiency;  
 KW Alzheimer's disease; therapy; diagnosis; HIV; ss.  
 XX

OS Human immunodeficiency virus.  
 XX  
 PN CA2194256-A.

XX  
 PD 05-MAR-1998.  
 XX  
 XX 02-JAN-1997; 97CA-02194256.

XX  
 PR 05-SEP-1996; 96US-00711417.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.

XX Georgopoulos K;  
 XX  
 XX WPI; 1998-378292/33.

XX New nucleic acid encoding Ikaros protein involved in early  
 PT differentiation of lymphocytes - existing in several isoforms, and  
 PT related products, used to treat e.g. immune diseases or cancer and to  
 PT control cell differentiation.  
 XX

PS Disclosure; Page 39; 158pp; English.

XX This oligonucleotide from the HIV long terminal repeat was identified as  
 CC a potential high affinity binding site for Ikaros (see AAW70963-71). It  
 CC partially includes a core motif GGAA found in consensus recognition  
 CC sites of murine Ikaros isoforms mIK-1, mIK-2 and mIK-3 (see AAV52830-32).  
 CC High affinity binding sites for Ikaros have been found in enhancer and  
 CC promoter regions of the regulatory domains of the TCR antigen complex,  
 CC the CD3 genes, the SL3 and HIV long terminal repeat and in the regulatory  
 CC domains of other T cell restricted antigens (see AAV45358-402) by gel  
 CC retardation assay. Ikaros is involved in early differentiation of  
 CC lymphocytes. The invention provides Ikaros nucleic acids (see AAV42805-11  
 CC and AAV42840) and polypeptides, vectors and host cells. These are used to  
 CC treat T and B cell diseases, to control expression of heterologous genes  
 CC placed under control of an Ikaros-responsive element, to treat nervous  
 CC system diseases and to modulate cell division, amplification or  
 CC differentiation, especially in haematopoietic cells  
 XX

SQ Sequence 37 BP; 6 A; 9 C; 15 G; 7 T; 0 U; 0 Other;

Query Match 74.7%; Score 28.4; DB 2; Length 37;

Best Local Similarity 96.7%; Pred. No. 0.13;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GGGACTTTCGCTGGGACTTTCACGGGG 31  
 |||||  
 DB 4 GGGACTTTCGCTGGGACTTTCACGGAG 33  
 |||||

RESULT 37  
 AAD17457  
 ID AAD17457 standard; DNA; 32 BP.  
 XX  
 AC AAD17457;  
 XX  
 DT 10-DEC-2001 (first entry)

XX Human immunodeficiency virus LTR NF-kB-specific double-stranded oligo.  
 XX  
 DE  
 XX  
 KW Tpl2; serine threonine kinase; tumour necrosis factor; TNFalpha; NF-kB;  
 KW inflammatory disease; therapy; rheumatoid arthritis; endotoxin shock;  
 KW research tool; LPS; lipopolysaccharide; nuclear factor kappa B; HIV;  
 KW Human immunodeficiency virus; ds.  
 XX

OS Human immunodeficiency virus.

XX WO200166559-A1.

PN  
 XX  
 PD 13-SEP-2001.

XX  
 PF 08-MAR-2001; 2001WO-US007588.

XX  
 PR 08-MAR-2000; 2000US-00522775.

XX (UYJE-) UNIV JEFFERSON THOMAS.

PA  
 XX  
 PI Tsichlis PN;

XX WPI; 2001-582266/65.

XX Knock-out animal resistant to lipopolysaccharide-induced endotoxin shock  
 PT and tumor necrosis factor alpha-mediated inflammatory disease, comprises  
 PT a functionally disrupted endogenous Tpl2 gene.  
 XX

PS Example 8; Page 55; 98pp; English.

XX The invention relates to an animal with a structurally intact Tpl2 gene  
 CC but functionally disrupted endogenous Tpl2 (a protooncogene which encodes  
 CC a cytoplasmic serine threonine protein kinase). The animal has increased  
 CC resistance to lipopolysaccharide-induced endotoxin shock or tumour  
 CC necrosis factor (TNF) alpha-mediated inflammatory diseases. Tpl2 protein  
 CC and DNA are useful for identifying compounds that agonise or inhibit the  
 CC function of Tpl2 protein. Tpl2 is useful for treating rheumatoid  
 CC arthritis. TNFalpha-mediated inflammatory diseases or LPS induced  
 CC endotoxin shock, may be treated by transfecting bone marrow derived cells  
 CC invitro with a DNA construct which encodes sequences that interferes with  
 CC the expression of function of the endogenous Tpl2 in the cells and  
 CC administering the cells to an animal. The knock out animals and the  
 CC constructs used to generate the animals are useful in the development of  
 CC compositions and methods of treating inflammation. Tpl2 agonist and  
 CC antagonist are useful as targets for the development of novel therapeutic  
 CC agents which eliminate the functional role of Tpl2 and as research tools  
 CC to facilitate the elucidation of the mechanistic action of the novel  
 CC genetic and protein interactions involved in inflammatory disorders. Tpl2  
 CC polynucleotide sequences facilitate the discovery and development of anti  
 CC endotoxin shock and/or antiinflammatory compounds. The present sequence  
 CC is human immunodeficiency virus LTR NF-kB-specific (nuclear factor kappa  
 CC B) double-stranded oligonucleotide used in the exemplification of the  
 CC invention  
 XX

SQ Sequence 32 BP; 6 A; 8 C; 11 G; 7 T; 0 U; 0 Other;

Query Match 73.7%; Score 28; DB 5; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 0.18;



```
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGCTGGGACTTTCAGGG 29
Db 5 GGGACTTTCGCTGGGACTTTCAGGG 32
RESULT 38
AADI7455
ID AAD17455 standard; DNA; 32 BP.
XX AAD17455,
XX
DT 10-DEC-2001 (first entry)
DE Nuclear factor kappa B binding site probe generating oligo #1.
XX
KW Tpl2; serine threonine kinase; tumour necrosis factor; TNFalpha; NF-kB;
KW inflammatory disease; therapy; rheumatoid arthritis; endotoxin shock;
KW research tool; LPS; lipopolysaccharide; nuclear factor kappa B; ss.
XX
OS Unidentified.
XX
PN WO20016559-A1.
XX
PD 13-SEP-2001.
XX
PF 08-MAR-2001; 2001WO-US007588.
XX
PR 08-MAR-2000; 2000US-00522775.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Tschlis PN;
XX
DR WPI; 2001-582266/65.
XX
PT Knock-out animal resistant to lipopolysaccharide-induced endotoxin shock
PT and tumor necrosis factor alpha-mediated inflammatory disease, comprises
PT a functionally disrupted endogenous Tpl2 gene.
XX
PS Example 8; Page 50; 98pp; English.
XX
CC The invention relates to an animal with a structurally intact Tpl2 gene
CC but functionally disrupted endogenous Tpl2 (a protooncogene which encodes
CC a cytoplasmic serine threonine protein kinase). The animal has increased
CC resistance to lipopolysaccharide-induced endotoxin shock or tumour
CC necrosis factor (TNF) alpha-mediated inflammatory diseases. Tpl2 protein
CC and DNA are useful for identifying compounds that agonise or inhibit the
CC function of Tpl2 protein. Tpl2 is useful for treating rheumatoid
CC arthritis. TNFalpha-mediated inflammatory diseases or LPS induced
CC endotoxin shock, may be treated by transfecting bone marrow derived cells
CC invitro with a DNA construct which encodes sequences that interferes with
CC the expression of function of the endogenous Tpl2 in the cells and
CC administering the cells to an animal. The knock out animals and the
CC constructs used to generate the animals are useful in the development of
CC compositions and methods of treating inflammation. Tpl2 agonist and
CC antagonist are useful as targets for the development of novel therapeutic
CC agents which eliminate the functional role of Tpl2 and as research tools
CC to facilitate the elucidation of the mechanistic action of the novel
CC genetic and protein interactions involved in inflammatory disorders. Tpl2
CC polynucleotide sequences facilitate the discovery and development of anti
CC endotoxin shock and/or antiinflammatory compounds. The present sequence
CC is an oligonucleotide used for generating nuclear factor kappa B (NF-kB)
CC DNA binding site probe used in the exemplification of the invention
XX
SQ Sequence 32 BP; 6 A; 8 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 73.7%; Score 28; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGCTGGGACTTTCAGGG 29
```

```
Db 5 GGGACTTTCGCTGGGACTTTCAGGG 32
RESULT 39
AAX34336
ID AAX34336 standard; DNA; 33 BP.
XX
AC AAX34336;
XX
DT 06-JUL-1999 (first entry)
XX
DE HIV probe corresponding to NF-kappaB binding site.
XX
KW Primer; PCR; amplification; HIV-1; genome; vector; inhibition;
KW replication; gene expression; infection; probe; hybridisation; ss.
XX
OS Synthetic.
OS Human immunodeficiency virus 1.
XX
PN WO9919496-A1.
XX
PD 22-APR-1999.
XX
PF 15-OCT-1998; 98WO-US021880.
XX
PR 16-OCT-1997; 97US-0061984P.
XX
PA (UTEM) UNIV TEMPLE.
XX
PI Suhadolnik RJ, Adelson ME, Iacono KT;
XX
DR WPI; 1999-277646/23.
XX
PT New vectors for inhibiting HIV replication.
XX
PS Example 1; Page 25; 65pp; English.
XX
CC Primers AAX34333-X34336 were used to amplify region of the human
CC immunodeficiency virus type 1 (HIV-1) genome for the construction of new
CC vectors for inhibiting HIV replication comprise a PKR or 2',5'-
CC oligoadenylate synthetase coding region and a regulatory element
CC activated in the presence of HIV trans-acting factors. Using the
CC constructs, antiviral gene expression is activated upon HIV infection
CC resulting in the death of HIV infected cells, thus preventing viral
CC replication and the subsequent infection of neighbouring cells
XX
SQ Sequence 33 BP; 7 A; 8 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 73.7%; Score 28; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGCTGGGACTTTCAGGG 29
Db 5 GGGACTTTCGCTGGGACTTTCAGGG 32
RESULT 40
AAN90922
ID AAN90922 standard; DNA; 34 BP.
XX
AC AAN90922;
XX
DT 09-SEP-2004 (revised)
DT 25-MAR-2003 (revised)
DT 30-JAN-1990 (first entry)
XX
DE Part of the kappa light chain enhancer.
XX
KW Nuclear factor kappa B inhibitor complex; HIV enhancer;
KW immunoglobulin kappa light chain enhancer; transcription factor; ds.
XX
```

```
OS Homo sapiens.
OS Unidentified.
PN WO8908147-A.
XX
XX
PD 08-SEP-1989.
XX
XX 01-MAR-1989; 89WO-US000820.
XX
XX 01-MAR-1988; 88US-00162680.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA
XX
XX
DR WPI; 1989-278306/38.
XX
XX Altering gene expression in a cell - by controlling dissociation of
PT nuclear factor kappa B inhibitor complex to prevent or cause binding to
PT an enhancer, e.g. HIV-dna.
XX
XX Disclosure; Fig 1; 69pp; English.
XX
XX The sequence is part of the HIV LTR enhancer. Tag a and tag b represent
CC binding sites for NF-KB. (Updated on 25-MAR-2003 to correct PA field.)
CC
CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX
XX Sequence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;
SQ
Query Match 73.7%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGGCTGGGGACTTTCACGGG 29
Db 6 GGGACTTTCGGCTGGGGACTTTCACGGG 33
RESULT 41
AAC66959
ID AAC66959 standard; DNA; 34 BP.
XX
AC AAC66959;
XX
DT 27-MAR-2001 (first entry)
XX
XX Lymphoid cell nuclear factor related sequence #6.
DE
XX Lymphoid cell nuclear factor; immunoglobulin gene transcription; Ig gene;
KW IgNF-A; IgNF-E; IgNF-B; IgNF-kappaB; PCR primer; ss.
XX
OS Unidentified.
XX
XX US6150090-A.
PN
XX
XX 21-NOV-2000.
PD
XX
XX 05-JUN-1995; 95US-00463397.
PF
XX
XX 09-JAN-1986; 86US-00817441.
PR
XX 24-DEC-1986; 86US-00946365.
PR
XX 12-FEB-1988; 88US-00155207.
PR
XX 01-MAR-1988; 88US-00162680.
PR
XX 05-DEC-1988; 88US-00280173.
PR
XX 03-MAR-1989; 89US-00318901.
PR
XX 21-APR-1989; 89US-00341436.
PR
XX 13-NOV-1991; 91US-00791898.
PR
XX 06-APR-1995; 95US-00418266.
XX
XX (HARD ) HARVARD COLLEGE.
PA
XX (WASI ) MASSACHUSETTS INST TECHNOLOGY.
PA
XX (WHED ) WHITEHEAD INST.
XX
XX Sharp PA, Singh H, Sen R, Baldwin AS, Clerc RG, Baltimore D;
PI
```

```
PI Fan C, Maniatis TP, Baeuerle PA, Lebowitz JH, Lenardo MJ;
PI Corcoran LM, Staudt L;
XX
XX WPI; 2001-060011/07.
XX
XX Identifying an NF-kappa B modulator, useful for analyzing protein DNA
PT interactions in cells or in identifying transcriptional regulatory
PT factors by detecting NF-kappa B or Ikb DNA binding activity level or
PT cytoplasmic localization.
XX
XX Disclosure; Fig 14; 66pp; English.
XX
XX The present invention provides assays for identifying compounds which
CC modulate NF-kappaB. NF-kappaB, along with IgNF-A, IgNF-E and IgNF-B, is a
CC lymphoid cell nuclear factor which regulates the transcription of the
CC immunoglobulin genes. The modulators are useful in the control of
CC activation of host cells
XX
XX Sequence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;
SQ
Query Match 73.7%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGGCTGGGGACTTTCACGGG 29
Db 6 GGGACTTTCGGCTGGGGACTTTCACGGG 33
RESULT 42
ADT77252
ID ADT77252 standard; DNA; 34 BP.
XX
AC ADT77252;
XX
DT 13-JAN-2005 (first entry)
XX
XX HIV enhancer NF-KB binding site.
DE
XX
XX necrosis factor kappa B; NF-kappaB;
KW transcriptional regulatory DNA element; immunoglobulin;
KW transcription enhancer; immunoassay; IgNF-B; HIV enhancer; ds.
XX
XX Human immunodeficiency virus.
OS
XX
XX US2004214757-A1.
PN
XX
XX 28-OCT-2004.
PD
XX
XX 04-JAN-2002; 2002US-00037341.
PF
XX
XX 09-JAN-1986; 86US-00817441.
PR
XX 24-DEC-1986; 86US-00946365.
PR
XX 12-FEB-1988; 88US-00155207.
PR
XX 01-MAR-1988; 88US-00162680.
PR
XX 05-DEC-1988; 88US-00280173.
PR
XX 03-MAR-1989; 89US-00318901.
PR
XX 21-APR-1989; 89US-00341436.
PR
XX 13-NOV-1991; 91US-00791898.
PR
XX 06-APR-1995; 95US-00418266.
PR
XX 05-JUN-1995; 95US-00464364.
XX
XX (BALT/) BALTIMORE D.
PA
XX (SENR/) SEN R.
PA
XX (SHAR/) SHARP P A.
PA
XX (SING/) SINGH H.
PA
XX (STAU/) STAUDT L.
PA
XX (LEBO/) LEBOWITZ J H.
PA
XX (BALD/) BALDWIN A S.
PA
XX (CLER/) CLERC R G.
PA
XX (CORC/) CORCORAN L M.
PA
XX (BAEU/) BAEUERLE P A.
PA
XX (LENA/) LENARDO M J.
```

PA (FANC/) FAN C.  
 PA (MANI/) MANIATIS T P.  
 XX  
 PI Baltimore D, Sen R, Sharp PA, Singh H, Staudt L, Lebowitz JH;  
 PI Baldwin AS, Clerc RG, Corcoran LM, Baeuerle PA, Lenardo MJ, Fan C;  
 PI Maniatis TP;  
 XX  
 DR WPI; 2004-774818/76.  
 XX  
 XX Novel isolated nuclear protein NF-kappaB that binds in sequence specific  
 PT manner to transcriptional regulatory DNA element of immunoglobulin light  
 PT or heavy chain genes, or both, useful for enhancing transcription of gene  
 PT of interest.  
 XX  
 PS Disclosure; SEQ ID NO 53; 136pp; English.  
 XX  
 CC The invention describes an isolated nuclear protein NF-kappaB (I) which  
 CC binds: in a sequence specific manner, to a transcriptional regulatory DNA  
 CC element of an immunoglobulin light or heavy chain genes, or both; in a  
 CC sequence specific manner, to enhance DNA sequences of the kappa light  
 CC chain gene; or to DNA sequences in the upstream region of both mouse  
 CC heavy and kappa light chain gene promoters, and to DNA sequences of mouse  
 CC heavy chain gene enhancer. (I) is useful for enhancing the transcription  
 CC of the gene of interest, and for screening for expression of sequence-  
 CC specific binding protein. A polyclonal or monoclonal antibody (II)  
 CC specifically reactive with a nuclear protein which binds, in sequence  
 CC specific manner, to a transcriptional regulatory DNA element of an  
 CC immunoglobulin light or heavy chain gene, or both is useful in an  
 CC immunoassay for detection of a transcriptional regulatory factor such as  
 CC IgNF-B or NF-kappaB in a biological fluid, where (II) is specifically  
 CC reacts with IgNF-B or NF-kappaB. DNA (III) encoding the DNA binding  
 CC domain of (I) is useful for specifically stimulating gene transcription  
 CC in a cell, which involves providing an expressible gene construct  
 CC comprising (III) linked to DNA encoding an activator of the RNA  
 CC polymerase for the gene, and introducing the construct into the cell.  
 CC This sequence represents the NF-KB binding site of a HIV enhancer.  
 XX  
 SQ Sequence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;  
 Query Match 73.7%; Score 28; DB 13; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Gaps 0;  
 Matches 28; Conservative 0; Indels 0; Gaps 0;  
 QY 2 GGGACTTCCGCTGGGGACTTTCCAGG 29  
 Db 6 GGGACTTCCGCTGGGGACTTTCCAGG 33  
 RESULT 43  
 AAA61055  
 ID AAA61055 standard; DNA; 35 BP.  
 XX  
 AC AAA61055;  
 XX  
 XX 06-NOV-2000 (first entry)  
 DT  
 XX Electrophoretic mobility shift assay protein concentration primer #1.  
 DE  
 XX Heat shock protein 70; Hsp70; NF-kappaB; transplant rejection;  
 KW autoimmune disease; inflammatory disease; cancer; vascular disease;  
 KW primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200031113-A1.  
 XX  
 XX 02-JUN-2000.  
 PD  
 XX 17-NOV-1999; 99WO-US027244.  
 PF  
 XX 24-NOV-1998; 98US-0109872P.  
 PR  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Fujihara SM, Nadler SG;  
 PI WPI; 2000-400029/34.  
 DR  
 XX Intracellular targeted delivery of compounds using the 70 kilodalton heat  
 PT shock protein, useful in the treatment of transplant rejection,  
 PT autoimmune diseases and cancer.  
 XX  
 XX Example 6; Page 21; 37pp; English.  
 PS  
 XX The present sequence is a primer which was used to determine the  
 CC concentration of a fusion protein in an electrophoretic mobility shift  
 CC assay. The fusion protein comprised the C-terminus of the 70kD heat  
 CC shock protein (Hsp70), and the p50 subunit of transcription factor NF-  
 CC kappaB. The fusion protein was created in order to determine the ability  
 CC of the Hsp70 sequence to direct other proteins into the cell. It was  
 CC shown that Hsp70 fragments are able to direct other proteins into the  
 CC cell, a feature which can be used in the treatment of transplant  
 CC rejection, autoimmune diseases such as rheumatoid arthritis, multiple  
 CC sclerosis, diabetes, asthma, inflammatory bowel disease, psoriasis,  
 CC hepatitis, Graves' disease and vitelligo, inflammatory diseases including  
 CC osteoarthritis, pancreatitis and adult respiratory distress syndrome,  
 CC cancer, vascular diseases (such as restenosis and atherosclerosis) and  
 CC DNA and RNA viral replication diseases (including herpes)  
 XX  
 SQ Sequence 35 BP; 5 A; 9 C; 13 G; 8 T; 0 U; 0 Other;  
 Query Match 73.7%; Score 28; DB 3; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Gaps 0;  
 Matches 28; Conservative 0; Indels 0; Gaps 0;  
 QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGG 28  
 Db 8 GGGGACTTTCCGCTGGGGACTTTCCAGG 35  
 RESULT 44  
 ACF05495  
 ID ACF05495 standard; DNA; 42 BP.  
 XX  
 AC ACF05495;  
 XX  
 XX 06-NOV-2003 (first entry)  
 DT  
 XX HIV-1 LAI long terminal repeat 5' PCR primer.  
 DE  
 XX HIV-1; long terminal repeat; virus elimination; PCR; primer; ss.  
 KW  
 XX Human immunodeficiency virus type 1.  
 OS Synthetic.  
 OS  
 XX WO2003053468-A1.  
 PN  
 XX 03-JUL-2003.  
 PD  
 XX 23-DEC-2002; 2002WO-BE000197.  
 PF  
 XX 21-DEC-2001; 2001EP-00870289.  
 PR  
 XX (ULBR ) UNIV LIBRE BRUXELLES.  
 PA  
 XX Van Lint C, Burny A, Quivy V, Adam E;  
 PI WPI; 2003-569183/53.  
 DR  
 XX Use of deacetylase inhibitor combined with one or more compounds used in  
 PT viral treatment, for manufacturing medicament for obtaining elimination  
 PT of integrated, functional and pathogenic virus e.g. HIV-1 in mammal cell.  
 XX  
 PS Disclosure; Page 10; 56pp; English.  
 XX  
 XX The present sequence is that of a primer corresponding to nucleotides 344

CC to 377 of the coding strand sequence of the HIV-1 LAI 5' long terminal  
CC repeat (LTR), and including an added KpnI restriction site. This was used  
CC as 5' primer, with the 3' primer given in ACP05496, to amplify a 186 bp  
CC fragment of the 5' LTR (nucleotides 345-531) for use in the plasmid  
CC construct pLTR(345-531)-luc. This plasmid was used to demonstrate the  
CC trichostatin-A (TSA) inducibility of HIV-1 LTRs and also to show that  
CC intact kappaB sites are required for maximal TSA inducibility of the HIV-  
CC 1 promoter. The invention relates to the use of a deacetylase inhibitor  
CC (e.g. TSA) combined with one or more compounds used in a viral treatment  
CC for the manufacture of a medicament for obtaining elimination of  
CC integrated, functional and pathogenic viruses, e.g. HIV-1, in a mammal  
CC cell, including a human cell. This allows significant elimination and  
CC possible suppression of the presence of virus in a patient and therefore  
CC improves long-term control of viral infections in patients receiving  
CC highly active antiretroviral therapy (HAART) treatment

XX  
SQ Sequence 42 BP; 7 A; 11 C; 15 G; 9 T; 0 U; 0 Other;

Query Match 73.7%; Score 28; DB 9; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACAGG 29  
|||||  
DB 15 GGGACTTTCGGCTGGGACTTTCACAGG 42

## RESULT 45

AAAT30606  
ID AAT30606 standard; DNA; 45 BP.

XX  
AC AAT30606;

DT 19-FEB-1997 (first entry)

XX  
DE Target binding region #26.

XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SPI;  
KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
KW virus; ss.

XX Synthetic.

XX WO9617956-A2.

XX 13-JUN-1996.

XX 07-DEC-1995; 95WO-US015944.

XX 09-DEC-1994; 94US-00353476.

XX (GENE-) GENE POOL INC.

XX Weininger S, Weininger AM;

XX WPI; 1996-287199/29.

PT Probe nucleic acids, target binding assemblies, etc - for detection and  
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.

XX Disclosure; Page 72; 172pp; English.

XX AAT30581-T30614 represent target binding regions (TBR) of a probe of the  
CC invention. The probe of the invention contains a TBR, a booster binding  
CC region (BBR), and an optional support or attachment (OSA). The target  
CC binding assembly (TBA) recognised by the probe, contains at least one  
CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an  
CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see  
CC AAR95998-R96006), a nuclear localisation signal sequence (see AAR96007),  
CC and an OSA. The assembly sequence and asymmetry sequences are responsible  
CC for the folding and association of the NARs. The NARs (see AAR95965-

CC R95993) are selected from NF-kappa-B, SPI, TATA, human papillomavirus  
CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding  
CC units. The linker sequence is an oligopeptide, which does not interfere  
CC with NAR function, but provides stability and control over the spacing of  
CC the NAR from the rest of the TBA. The OSA is an attached support or  
CC indicator, or other means of localisation of the probe. The probe can be  
CC used in a method for detecting or localising a specific target nucleic  
CC acid sequence (TNA). The method is highly sensitive, and has a high  
CC degree of specificity. The method can be used for detecting specific  
CC nucleic acid sequences, including those found in human cells, in HIV,  
CC HPV, and other nucleic acid containing systems, including bacteria and  
CC viruses

XX  
SQ Sequence 45 BP; 9 A; 11 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 72.6%; Score 27.6; DB 2; Length 45;  
Best Local Similarity 88.2%; Pred. No. 0.27;  
Matches 30; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACAGGGGACTT 35  
|||||  
DB 7 GGGACTTTCGGCTGGGACTTTCACAGAGGGCGT 40

## RESULT 46

AAA99616/C  
ID AAA99616 standard; DNA; 35 BP.

XX  
AC AAA99616;

XX  
DT 22-JAN-2001 (first entry)

DE NF-kB oligonucleotide #2.

XX NF-kB; alpha-melanocyte stimulating hormone; alpha-MSH; antibacterial;  
KW fungicide; virucide; antiinflammatory; vaginitis; cystitis; urethritis;  
KW balanoposthitis; toxic shock syndrome; sexually transmitted disease;  
KW probe; ss.

XX Homo sapiens.

OS WO200056353-A2.

XX 28-SEP-2000.

XX 23-MAR-2000; 2000WO-US007846.

XX 24-MAR-1999; 99US-0126233P.

XX (ZENG-) ZENGEN INC.

XX Lipton J, Catania A;

XX WPI; 2000-628219/60.

XX Treating uro-genital conditions, such as vaginitis, cystitis, urethritis,  
PT or balanoposthitis comprises using alpha-melanocyte stimulating hormone  
PT or a derivative of it.

XX Example 9; Page 15; 37pp; English.

XX The present sequence is an oligonucleotide used to determine the level of  
CC NF-kB activity in human U1 cells treated with alpha-melanocyte  
CC stimulating hormone (alpha-MSH). Alpha-MSH and its derivatives were shown  
CC to inhibit TNF-alpha induced NF-kB activation and binding. Alpha-MSH and  
CC its derivatives have potent antipyretic and antiinflammatory properties,  
CC yet they have extremely low toxicity. A uro-genital condition treatment  
CC system has been developed that comprises a carrier and a polypeptide  
CC including a sequence derived from alpha-MSH. The system may be used to  
CC treat a uro-genital condition such as vaginitis, cystitis, urethritis, or  
CC balanoposthitis. It may also be used to prevent toxic shock syndrome and  
CC infection from sexually transmitted diseases, and to treat an antibiotic  
CC resistant microorganism. The polypeptides used in the treatment system

CC can reduce the viability of microbes, reduce the germination of yeast,  
CC kill microbes, treat inflammation associated with microbial infection,  
CC increase the accumulation of cAMP in microbes and inhibit replication and  
CC expression of viral pathogens  
XX  
SQ Sequence 35 BP; 9 A; 11 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 72.1%; Score 27.4; DB 3; Length 35;  
Best Local Similarity 96.6%; Pred. No. 0.32;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGG 29  
|||  
DB 32 GGGGACTTTCGGCTGGGGACTTTCACATGG 4

## RESULT 47

ACC47366/c  
ID ACC47366 standard; DNA; 35 BP.

XX  
AC ACC47366;

DT 11-AUG-2003 (first entry)

XX NF-kappaB DNA binding site negative strand.

DE MSH; alpha-melanocyte stimulating hormone; alpha-MSH; cancer; cytostatic;  
KW NF-kappaB; ss.

XX Synthetic.

XX WO2003020223-A2.

PN 13-MAR-2003.

XX 05-SEP-2002; 2002WO-US028257.

XX 05-SEP-2001; 2001US-0317514P.

XX (LIPT/) LIPTON J.  
XX (CATA/) CATANIA A P.

XX Lipton J, Catania AP;

XX WPI; 2003-290144/28.

XX Use of alpha-melanocyte stimulating hormone to combat cancer and in  
XX inhibiting cancer cell proliferation.

XX Example 4; Page 14; 27pp; English.

XX The invention relates to the use of alpha-melanocyte stimulating hormone  
CC (MSH), its derivative, or both, to combat cancer and in inhibiting cancer  
CC cell proliferation by administering the above alpha-MSH to a patient with  
CC cancer. The alpha-MSH is useful for combating cancer and for inhibiting  
CC cancer cell proliferation, where the cancer is mesothelioma, and is  
CC selected from Hodgkin lymphoma, non-Hodgkin lymphoma, squamous cell  
CC carcinoma, breast cancer and colorectal cancer. Sequences ACC47365-366  
CC represent positive and negative strands of NF-kappaB DNA binding site,  
CC used in DNA binding assays for determining alpha-MSH inhibition of NF-  
CC kappaB in cancer cells

SQ Sequence 35 BP; 9 A; 11 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 72.1%; Score 27.4; DB 10; Length 35;  
Best Local Similarity 96.6%; Pred. No. 0.32;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGG 29  
|||  
DB 32 GGGGACTTTCGGCTGGGGACTTTCACATGG 4

## RESULT 48

AAT30604  
ID AAT30604 standard; DNA; 44 BP.

XX  
AC AAT30604;

XX 19-FEB-1997 (first entry)

DT Target binding region #24.

XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;  
XX TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
KW virus; ss.

XX Synthetic.

XX WO9617956-A2.

XX 13-JUN-1996.

XX 07-DEC-1995; 95WO-US015944.

XX 09-DEC-1994; 94US-00353476.

XX (GENE-) GENE POOL INC.

XX Weininger S, Weininger AM;

XX WPI; 1996-287199/29.

XX Probe nucleic acids, target binding assemblies, etc - for detection and  
XX localisation of specific nucleic acid sequences, esp. HIV and HPV.

XX Disclosure; Page 71; 172pp; English.

XX AAT30581-T30614 represent target binding regions (TBR) of a probe of the  
CC invention. The probe of the invention contains a TBR, a booster binding  
CC region (BBR), and an optional support or attachment (OSA). The target  
CC binding assembly (TBA) recognised by the probe, contains at least one  
CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an  
CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see  
CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),  
CC and an OSA. The assembly sequence and asymmetry sequences are responsible  
CC for the folding and association of the NARs. The NARs (see AAR95965-  
CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus  
CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding  
CC units. The linker sequence is an oligopeptide, which does not interfere  
CC with NAR function, but provides stability and control over the spacing of  
CC the NAR from the rest of the TBA. The OSA is an attached support or  
CC indicator, or other means of localisation of the probe. The probe can be  
CC used in a method for detecting or localising a specific target nucleic  
CC acid sequence (TNA). The method is highly sensitive, and has a high  
CC degree of specificity. The method can be used for detecting specific  
CC nucleic acid sequences, including those found in human cells, in HIV,  
CC HPV, and other nucleic acid containing systems, including bacteria and  
CC viruses

XX Sequence 44 BP; 6 A; 12 C; 16 G; 10 T; 0 U; 0 Other;

Query Match 72.1%; Score 27.4; DB 2; Length 44;  
Best Local Similarity 83.8%; Pred. No. 0.33;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGACTTTCACGGGGACTTTC 38  
|||  
DB 7 GGGACTTTCGGCTGGGGACTTTCGGGGAGCGTGCC 43

## RESULT 49

AAT30605  
ID AAT30605 standard; DNA; 44 BP.



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:56:18 ; Search time 85.4215 Seconds  
(without alignments)  
790.754 Million cell updates/sec

Title: US-09-669-187A-148

Perfect score: 38

Sequence: 1 999gactttccgtgggactttccaggggactttcc 38

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Issued Patents NA:\*

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2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*

8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*

9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 38    | 100.0       | 38     | 2  | US-08-607-519-2   |
| 2          | 30.8  | 81.1        | 43     | 2  | US-08-353-476-29  |
| 3          | 30.2  | 79.5        | 46     | 2  | US-08-353-476-28  |
| 4          | 30    | 78.9        | 39     | 2  | US-08-450-257-43  |
| C 5        | 30    | 78.9        | 39     | 2  | US-08-450-257-44  |
| 6          | 30    | 78.9        | 39     | 2  | US-08-450-246-43  |
| C 7        | 30    | 78.9        | 39     | 2  | US-08-450-246-44  |
| 8          | 30    | 78.9        | 39     | 2  | US-08-450-098-43  |
| C 9        | 30    | 78.9        | 39     | 2  | US-08-450-098-44  |
| 10         | 30    | 78.9        | 39     | 2  | US-08-451-233-43  |
| C 11       | 30    | 78.9        | 39     | 2  | US-08-451-233-44  |
| 12         | 30    | 78.9        | 39     | 2  | US-08-450-236-43  |
| C 13       | 30    | 78.9        | 39     | 2  | US-08-450-236-44  |
| 14         | 30    | 78.9        | 39     | 3  | US-08-235-403-43  |
| C 15       | 30    | 78.9        | 39     | 3  | US-08-235-403-44  |
| 16         | 29.8  | 78.4        | 44     | 3  | US-09-314-691-9   |
| 17         | 29.8  | 78.4        | 44     | 3  | US-09-999-495-9   |
| 18         | 29.8  | 78.4        | 44     | 3  | US-09-992-837-9   |
| 19         | 29.8  | 78.4        | 44     | 3  | US-10-000-720-9   |
| 20         | 29.2  | 76.8        | 45     | 2  | US-08-580-988A-12 |
| 21         | 29.2  | 76.8        | 45     | 2  | US-08-353-476-19  |
| 22         | 29.2  | 76.8        | 45     | 2  | US-08-353-476-23  |
| 23         | 29    | 76.3        | 46     | 2  | US-08-353-476-20  |
| 24         | 29    | 76.3        | 46     | 2  | US-08-353-476-21  |

|       |      |      |    |   |                       |                    |       |      |      |    |   |                       |                    |
|-------|------|------|----|---|-----------------------|--------------------|-------|------|------|----|---|-----------------------|--------------------|
| C 98  | 16.6 | 43.7 | 47 | 3 | US-09-641-638-1046    | Sequence 1046, Ap  | C 171 | 14   | 36.8 | 30 | 3 | US-09-052-689-1       | Sequence 1, Appl   |
| C 99  | 16.6 | 43.7 | 47 | 3 | US-10-170-097-1046    | Sequence 1046, Ap  | C 172 | 14   | 36.8 | 32 | 2 | US-08-174-672D-49     | Sequence 49, Appl  |
| C 100 | 16.4 | 43.2 | 38 | 2 | US-08-120-607A-12     | Sequence 12, Appl  | C 173 | 14   | 36.8 | 33 | 2 | US-08-741-881-47      | Sequence 47, Appl  |
| C 101 | 16.4 | 43.2 | 38 | 2 | US-08-453-848-27      | Sequence 27, Appl  | C 174 | 14   | 36.8 | 33 | 2 | US-08-739-158-47      | Sequence 47, Appl  |
| C 102 | 16.4 | 43.2 | 38 | 2 | US-09-169-027-27      | Sequence 27, Appl  | C 175 | 14   | 36.8 | 33 | 2 | US-08-739-167-47      | Sequence 47, Appl  |
| C 103 | 16.2 | 42.6 | 40 | 2 | US-08-682-021-23      | Sequence 23, Appl  | C 176 | 14   | 36.8 | 33 | 3 | US-08-404-796-47      | Sequence 47, Appl  |
| C 104 | 16.2 | 42.6 | 46 | 2 | US-08-734-925-5       | Sequence 5, Appl   | C 177 | 14   | 36.8 | 33 | 3 | US-08-931-869-47      | Sequence 47, Appl  |
| C 105 | 15.8 | 41.6 | 47 | 3 | US-09-386-642-36      | Sequence 36, Appl  | C 178 | 14   | 36.8 | 33 | 3 | US-09-350-399-47      | Sequence 47, Appl  |
| C 106 | 15.4 | 40.5 | 25 | 3 | US-09-388-349-4       | Sequence 4, Appl   | C 179 | 14   | 36.8 | 33 | 3 | US-09-236-140A-47     | Sequence 47, Appl  |
| C 107 | 15.4 | 40.5 | 25 | 3 | US-09-396-196G-74122  | Sequence 74122, A  | C 180 | 14   | 36.8 | 34 | 3 | US-08-646-789A-35     | Sequence 35, Appl  |
| C 108 | 15.4 | 40.5 | 25 | 3 | US-09-396-196G-110222 | Sequence 110222, A | C 181 | 14   | 36.8 | 34 | 3 | US-08-646-789A-93     | Sequence 93, Appl  |
| C 109 | 15.2 | 40.0 | 23 | 6 | PCT-US92-10770-9      | Sequence 9, Appl   | C 182 | 14   | 36.8 | 38 | 2 | US-08-663-769-5       | Sequence 5, Appl   |
| C 110 | 15.2 | 40.0 | 23 | 6 | PCT-US92-10770-9      | Sequence 9, Appl   | C 183 | 14   | 36.8 | 38 | 2 | US-08-663-769-5       | Sequence 5, Appl   |
| C 111 | 15.2 | 40.0 | 50 | 3 | US-08-131-827-5964    | Sequence 5964, Ap  | C 184 | 14   | 36.8 | 40 | 2 | US-08-425-684-92      | Sequence 92, Appl  |
| C 112 | 15   | 39.5 | 15 | 2 | US-08-353-476-4       | Sequence 4, Appl   | C 185 | 14   | 36.8 | 40 | 2 | US-08-675-502-92      | Sequence 92, Appl  |
| C 113 | 15   | 39.5 | 33 | 2 | US-08-435-350-30      | Sequence 30, Appl  | C 186 | 14   | 36.8 | 40 | 9 | 5281520-28            | Patent No. 5281520 |
| C 114 | 15   | 39.5 | 45 | 2 | US-08-528-057-17      | Sequence 17, Appl  | C 187 | 14   | 36.8 | 45 | 2 | US-08-882-756-1       | Sequence 1, Appl   |
| C 115 | 14.8 | 38.9 | 31 | 2 | US-08-390-850-254     | Sequence 254, App  | C 188 | 14   | 36.8 | 45 | 2 | US-08-882-756-2       | Sequence 2, Appl   |
| C 116 | 14.8 | 38.9 | 31 | 2 | US-08-390-850-255     | Sequence 255, App  | C 189 | 14   | 36.8 | 45 | 2 | US-08-882-756-5       | Sequence 5, Appl   |
| C 117 | 14.8 | 38.9 | 31 | 2 | US-08-390-850-256     | Sequence 256, App  | C 190 | 14   | 36.8 | 45 | 3 | US-09-301-153-1       | Sequence 1, Appl   |
| C 118 | 14.8 | 38.9 | 31 | 2 | US-08-435-634-254     | Sequence 254, App  | C 191 | 14   | 36.8 | 45 | 3 | US-09-301-153-2       | Sequence 2, Appl   |
| C 119 | 14.8 | 38.9 | 31 | 2 | US-08-435-634-255     | Sequence 255, App  | C 192 | 14   | 36.8 | 47 | 3 | US-09-422-978-114     | Sequence 114, App  |
| C 120 | 14.8 | 38.9 | 31 | 2 | US-08-435-634-256     | Sequence 256, App  | C 193 | 14   | 36.8 | 47 | 3 | US-09-422-978-1280    | Sequence 1280, Ap  |
| C 121 | 14.6 | 38.4 | 25 | 3 | US-09-396-196G-50814  | Sequence 50814, A  | C 194 | 14   | 36.8 | 47 | 3 | US-09-422-978-2397    | Sequence 2397, Ap  |
| C 122 | 14.6 | 38.4 | 25 | 3 | US-09-396-196G-89802  | Sequence 89802, A  | C 195 | 14   | 36.8 | 50 | 3 | US-09-380-190A-40     | Sequence 40, Appl  |
| C 123 | 14.6 | 38.4 | 25 | 3 | US-09-671-317-664     | Sequence 664, App  | C 196 | 14   | 36.8 | 50 | 3 | US-09-554-929-99      | Sequence 99, Appl  |
| C 124 | 14.6 | 38.4 | 47 | 3 | US-09-396-196G-124375 | Sequence 124375, A | C 197 | 14   | 36.8 | 50 | 3 | US-10-131-827-6644    | Sequence 6644, Ap  |
| C 125 | 14.6 | 38.4 | 50 | 3 | US-08-832-571-5       | Sequence 5, Appl   | C 198 | 14   | 36.8 | 50 | 3 | US-10-131-827-7034    | Sequence 7034, Ap  |
| C 126 | 14.4 | 37.9 | 25 | 3 | US-09-396-196G-18395  | Sequence 18395, A  | C 199 | 13.8 | 36.3 | 20 | 3 | US-09-198-452A-5896   | Sequence 5896, Ap  |
| C 127 | 14.4 | 37.9 | 25 | 3 | US-09-396-196G-50815  | Sequence 50815, A  | C 200 | 13.8 | 36.3 | 25 | 3 | US-09-396-196G-45915  | Sequence 45915, A  |
| C 128 | 14.4 | 37.9 | 37 | 2 | US-08-426-236-8       | Sequence 8, Appl   | C 201 | 13.8 | 36.3 | 25 | 3 | US-09-396-196G-89803  | Sequence 89803, A  |
| C 129 | 14.4 | 37.9 | 38 | 3 | US-09-770-158-11      | Sequence 11, Appl  | C 202 | 13.8 | 36.3 | 25 | 3 | US-09-396-196G-122080 | Sequence 122080, A |
| C 130 | 14.4 | 37.9 | 46 | 3 | US-09-372-934-25      | Sequence 25, Appl  | C 203 | 13.8 | 36.3 | 26 | 3 | US-09-538-709-903     | Sequence 903, App  |
| C 131 | 14.4 | 37.9 | 46 | 3 | US-09-766-916-25      | Sequence 25, Appl  | C 204 | 13.8 | 36.3 | 27 | 2 | US-08-859-998-1252    | Sequence 1252, Ap  |
| C 132 | 14.4 | 37.9 | 46 | 3 | US-09-766-916-25      | Sequence 25, Appl  | C 205 | 13.8 | 36.3 | 27 | 3 | US-09-225-928-1252    | Sequence 1252, Ap  |
| C 133 | 14.4 | 37.9 | 46 | 3 | US-09-637-040C-25     | Sequence 25, Appl  | C 206 | 13.8 | 36.3 | 27 | 3 | US-09-225-928-1252    | Sequence 1252, Ap  |
| C 134 | 14.4 | 37.9 | 46 | 3 | US-10-306-249-25      | Sequence 25, Appl  | C 207 | 13.8 | 36.3 | 33 | 2 | US-08-634-060-48      | Sequence 48, Appl  |
| C 135 | 14.4 | 37.9 | 50 | 3 | US-10-131-827-434     | Sequence 434, App  | C 208 | 13.8 | 36.3 | 36 | 2 | US-08-221-816B-5      | Sequence 5, Appl   |
| C 136 | 14.4 | 37.9 | 50 | 3 | US-10-131-827-2647    | Sequence 2647, App | C 209 | 13.8 | 36.3 | 36 | 3 | US-10-112-547-5       | Sequence 5, Appl   |
| C 137 | 14.2 | 37.4 | 25 | 3 | US-09-396-196G-2950   | Sequence 2950, Ap  | C 210 | 13.8 | 36.3 | 36 | 3 | US-10-112-241-5       | Sequence 5, Appl   |
| C 138 | 14.2 | 37.4 | 25 | 3 | US-09-396-196G-67905  | Sequence 67905, A  | C 211 | 13.8 | 36.3 | 36 | 3 | US-10-104-611-5       | Sequence 5, Appl   |
| C 139 | 14.2 | 37.4 | 40 | 2 | US-08-503-964-3       | Sequence 3, Appl   | C 212 | 13.8 | 36.3 | 36 | 3 | US-10-109-368-5       | Sequence 5, Appl   |
| C 140 | 14.2 | 37.4 | 40 | 2 | US-08-766-014-19      | Sequence 19, Appl  | C 213 | 13.8 | 36.3 | 36 | 3 | US-09-724-380-5       | Sequence 8, Appl   |
| C 141 | 14.2 | 37.4 | 40 | 2 | US-08-640-378-19      | Sequence 19, Appl  | C 214 | 13.8 | 36.3 | 38 | 2 | US-08-616-398-8       | Sequence 8, Appl   |
| C 142 | 14.2 | 37.4 | 40 | 2 | US-08-679-522D-8      | Sequence 8, Appl   | C 215 | 13.8 | 36.3 | 38 | 2 | US-09-963-946-22      | Sequence 22, Appl  |
| C 143 | 14.2 | 37.4 | 40 | 2 | US-08-664-863B-12     | Sequence 12, Appl  | C 216 | 13.8 | 36.3 | 38 | 3 | US-09-474-432B-1400   | Sequence 1400, Ap  |
| C 144 | 14.2 | 37.4 | 40 | 3 | US-09-141-401-8       | Sequence 8, Appl   | C 217 | 13.8 | 36.3 | 38 | 3 | US-09-476-387-1399    | Sequence 1399, Ap  |
| C 145 | 14.2 | 37.4 | 40 | 3 | US-09-290-577-40      | Sequence 40, Appl  | C 218 | 13.8 | 36.3 | 38 | 3 | US-09-685-664B-5689   | Sequence 5689, Ap  |
| C 146 | 14.2 | 37.4 | 40 | 3 | US-09-061-757B-7      | Sequence 7, Appl   | C 219 | 13.8 | 36.3 | 39 | 2 | US-08-634-060-55      | Sequence 55, Appl  |
| C 147 | 14.2 | 37.4 | 40 | 3 | US-09-290-452-40      | Sequence 40, Appl  | C 220 | 13.8 | 36.3 | 39 | 2 | US-08-634-060-56      | Sequence 56, Appl  |
| C 148 | 14.2 | 37.4 | 40 | 3 | US-09-290-338-40      | Sequence 40, Appl  | C 221 | 13.8 | 36.3 | 41 | 3 | US-08-327-874A-32     | Sequence 32, Appl  |
| C 149 | 14.2 | 37.4 | 40 | 3 | US-09-686-179A-7      | Sequence 7, Appl   | C 222 | 13.8 | 36.3 | 41 | 3 | US-10-008-960-32      | Sequence 32, Appl  |
| C 150 | 14.2 | 37.4 | 40 | 3 | US-09-290-000-40      | Sequence 40, Appl  | C 223 | 13.8 | 36.3 | 41 | 6 | PCT-US94-09700-32     | Sequence 32, Appl  |
| C 151 | 14.2 | 37.4 | 40 | 3 | US-09-354-594A-40     | Sequence 40, Appl  | C 224 | 13.8 | 36.3 | 42 | 2 | US-08-634-060-43      | Sequence 43, Appl  |
| C 152 | 14.2 | 37.4 | 40 | 3 | US-09-981-621-7       | Sequence 7, Appl   | C 225 | 13.8 | 36.3 | 42 | 2 | US-08-634-060-44      | Sequence 44, Appl  |
| C 153 | 14.2 | 37.4 | 40 | 3 | US-09-705-043A-8      | Sequence 8, Appl   | C 226 | 13.8 | 36.3 | 47 | 3 | US-09-422-978-3517    | Sequence 3517, Ap  |
| C 154 | 14.2 | 37.4 | 40 | 3 | US-09-865-807-40      | Sequence 40, Appl  | C 227 | 13.8 | 36.3 | 50 | 3 | US-10-131-827-3550    | Sequence 3550, Ap  |
| C 155 | 14.2 | 37.4 | 40 | 3 | US-09-944-604-7       | Sequence 7, Appl   | C 228 | 13.8 | 36.3 | 50 | 3 | US-10-131-827-5063    | Sequence 5063, Ap  |
| C 156 | 14.2 | 37.4 | 44 | 3 | US-09-339-913B-100    | Sequence 100, App  | C 229 | 13.6 | 35.8 | 21 | 3 | US-08-755-587-171     | Sequence 171, App  |
| C 157 | 14.2 | 37.4 | 44 | 3 | US-09-339-904A-100    | Sequence 100, App  | C 230 | 13.6 | 35.8 | 25 | 3 | US-09-396-196G-44164  | Sequence 44164, A  |
| C 158 | 14.2 | 37.4 | 44 | 3 | US-08-769-062B-100    | Sequence 100, App  | C 231 | 13.6 | 35.8 | 25 | 3 | US-09-396-196G-50788  | Sequence 50788, A  |
| C 159 | 14.2 | 37.4 | 44 | 3 | US-09-344-002B-100    | Sequence 100, App  | C 232 | 13.6 | 35.8 | 25 | 3 | US-09-396-196G-94631  | Sequence 94631, A  |
| C 160 | 14.2 | 37.4 | 44 | 3 | US-09-559-565C-100    | Sequence 100, App  | C 233 | 13.6 | 35.8 | 25 | 3 | US-09-396-196G-106551 | Sequence 106551, A |
| C 161 | 14.2 | 37.4 | 44 | 3 | US-09-693-350-100     | Sequence 100, App  | C 234 | 13.6 | 35.8 | 25 | 3 | US-09-396-196G-106551 | Sequence 106551, A |
| C 162 | 14.2 | 37.4 | 44 | 3 | US-08-693-389-100     | Sequence 100, App  | C 235 | 13.6 | 35.8 | 29 | 3 | US-09-810-506-5       | Sequence 5, Appl   |
| C 163 | 14.2 | 37.4 | 44 | 3 | US-09-559-671A-100    | Sequence 100, App  | C 236 | 13.6 | 35.8 | 37 | 2 | US-08-468-700-17      | Sequence 17, Appl  |
| C 164 | 14.2 | 37.4 | 44 | 3 | US-09-339-926A-100    | Sequence 100, App  | C 237 | 13.6 | 35.8 | 37 | 2 | US-08-704-706A-17     | Sequence 17, Appl  |
| C 165 | 14.2 | 37.4 | 44 | 3 | US-09-954-692-100     | Sequence 100, App  | C 238 | 13.6 | 35.8 | 37 | 2 | US-08-985-659-17      | Sequence 17, Appl  |
| C 166 | 14.2 | 37.4 | 47 | 3 | US-09-422-978-1819    | Sequence 1819, Ap  | C 239 | 13.6 | 35.8 | 40 | 3 | US-09-626-354-2       | Sequence 2, Appl   |
| C 167 | 14.2 | 37.4 | 50 | 2 | US-08-832-468-5       | Sequence 5, Appl   | C 240 | 13.6 | 35.8 | 47 | 3 | US-09-422-978-2935    | Sequence 2935, Ap  |
| C 168 | 14   | 36.8 | 21 | 3 | US-09-021-247-6       | Sequence 6, Appl   | C 241 | 13.6 | 35.8 | 49 | 3 | US-10-012-231A-82     | Sequence 82, Appl  |
| C 169 | 14   | 36.8 | 21 | 3 | US-09-810-863-6       | Sequence 6, Appl   | C 242 | 13.6 | 35.8 | 49 | 3 | US-10-015-389A-82     | Sequence 82, Appl  |
| C 170 | 14   | 36.8 | 25 | 3 | US-09-396-196G-108554 | Sequence 108554, A | C 243 | 13.6 | 35.8 | 49 | 3 | US-10-006-768A-82     | Sequence 82, Appl  |



244 13.6 35.8 49 3 US-10-015-671A-82 Sequence 82, Appl  
245 13.6 35.8 49 3 US-10-015-393A-82 Sequence 82, Appl  
246 13.6 35.8 49 3 US-10-011-833A-82 Sequence 82, Appl  
247 13.6 35.8 49 3 US-10-006-041A-82 Sequence 82, Appl  
248 13.6 35.8 49 3 US-10-012-064A-82 Sequence 82, Appl  
249 13.6 35.8 50 3 US-10-131-827-3363 Sequence 3363, Ap  
250 13.4 35.3 25 3 US-09-396-196G-4564 Sequence 4564, Ap  
251 13.4 35.3 25 3 US-09-396-196G-63468 Sequence 63468, A  
252 13.4 35.3 25 3 US-09-396-196G-72208, A Sequence 72208, A  
253 13.4 35.3 25 3 US-09-396-196G-90859, A Sequence 90859, A  
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256 13.4 35.3 25 3 US-09-396-196G-106418 Sequence 106418, A  
257 13.4 35.3 25 3 US-09-396-196G-112751 Sequence 112751, A  
258 13.4 35.3 27 2 US-08-758-306-348 Sequence 348, App  
259 13.4 35.3 27 2 US-09-253-396A-7 Sequence 7, Appl  
260 13.4 35.3 29 2 US-07-642-734C-19 Sequence 19, Appl  
261 13.4 35.3 29 2 US-08-439-009A-19 Sequence 19, Appl  
262 13.4 35.3 30 3 US-09-341-007B-30 Sequence 30, Appl  
263 13.4 35.3 32 2 US-08-942-423-59 Sequence 59, Appl  
264 13.4 35.3 32 2 US-08-942-423-62 Sequence 62, Appl  
265 13.4 35.3 32 2 US-09-595-684B-65 Sequence 65, Appl  
266 13.4 35.3 35 9 5171670-3 Patent No. 5171670  
267 13.4 35.3 37 2 US-08-616-398-7 Sequence 7, Appl  
268 13.4 35.3 37 2 US-09-600-747-4 Sequence 4, Appl  
269 13.4 35.3 38 2 US-08-963-946-33 Sequence 33, Appl  
270 13.4 35.3 40 3 US-08-327-874A-33 Sequence 33, Appl  
271 13.4 35.3 40 3 US-10-008-960-33 Sequence 33, Appl  
272 13.4 35.3 40 6 PCT-US94-09700-33 Sequence 33, Appl  
273 13.4 35.3 42 3 US-09-425-804-18 Sequence 18, Appl  
274 13.4 35.3 42 6 PCT-US95-13975-36 Sequence 36, Appl  
275 13.4 35.3 45 2 US-08-661-507-5 Sequence 5, Appl  
276 13.2 34.7 25 3 US-09-396-196G-96047 Sequence 96047, A  
277 13.2 34.7 25 3 US-09-396-196G-96048 Sequence 96048, A  
278 13.2 34.7 25 3 US-09-396-196G-96049 Sequence 96049, A  
279 13.2 34.7 25 3 US-09-396-196G-106466 Sequence 106466, A  
280 13.2 34.7 25 3 US-09-396-196G-108555 Sequence 108555, A  
281 13.2 34.7 25 3 US-09-396-196G-119899 Sequence 119899, A  
282 13.2 34.7 25 3 US-09-396-196G-119900 Sequence 119900, A  
283 13.2 34.7 25 3 US-09-396-196G-119901 Sequence 119901, A  
284 13.2 34.7 25 3 US-09-396-196G-119902 Sequence 119902, A  
285 13.2 34.7 28 2 US-08-859-998-924 Sequence 924, App  
286 13.2 34.7 28 3 US-09-225-928-924 Sequence 924, App  
287 13.2 34.7 28 3 US-09-225-201B-924 Sequence 924, App  
288 13.2 34.7 29 2 US-08-846-012A-13 Sequence 13, Appl  
289 13.2 34.7 29 2 US-09-100-297-13 Sequence 13, Appl  
290 13.2 34.7 29 3 US-09-084-120-6 Sequence 6, Appl  
291 13.2 34.7 33 3 US-09-724-678D-10 Sequence 10, Appl  
292 13.2 34.7 34 3 US-09-277-431A-19 Sequence 19, Appl  
293 13.2 34.7 38 2 US-08-663-769-3 Sequence 3, Appl  
294 13.2 34.7 41 3 US-08-813-507-76 Sequence 76, Appl  
295 13.2 34.7 41 3 US-09-351-814-55 Sequence 55, Appl  
296 13.2 34.7 41 3 US-09-464-453-76 Sequence 76, Appl  
297 13.2 34.7 41 3 US-09-573-377-6 Sequence 6, Appl  
298 13.2 34.7 42 3 US-09-461-697-276 Sequence 276, App  
299 13.2 34.7 45 3 US-09-356-575B-22 Sequence 22, Appl  
300 13.2 34.7 45 3 US-09-912-552-22 Sequence 22, Appl

## ALIGNMENTS

RESULT 1  
US-08-607-519-2  
; Sequence 2, Application US/08607519  
; Patent No. 5990090  
; GENERAL INFORMATION:  
; APPLICANT: Nabel, Gary J.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATMENT  
; OF DISEASES  
; TITLE OF INVENTION: OF DISEASES  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/607,519  
FILING DATE: 27-FEB-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/123,188  
FILING DATE: 20-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, NO. 5990090man P.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 6042-001-68  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid;  
DESCRIPTION: SYNTHETIC DNA  
FEATURE:  
NAME/KEY: misc difference  
LOCATION: replace(1..38, "n")  
OTHER INFORMATION: /note= "ANY OF THE PHOSPHATE GROUPS  
LINKING ANY OF THE NUCLEOSIDES MAY BE REPLACED  
WITH PHOSPHOROTHIATE GROUPS, METHYL ESTER  
US-08-607-519-2  
Query Match 100.0%; Score 38; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38  
Db 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38  
RESULT 2  
US-08-353-476-29  
; Sequence 29, Application US/08353476  
; Patent No. 5871902  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A  
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25



Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 38  
 |||||  
 Db 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTTC 38  
 |||||

RESULT 5  
 US-08-450-257-44/c  
 ; Sequence 44, Application US/08450257  
 ; Patent No. 5652122  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANKEL, Alan  
 ; APPLICANT: PABO, Carl  
 ; APPLICANT: BARSOUM, James G.  
 ; APPLICANT: FAWELL, Stephen E.  
 ; APPLICANT: PEPINSKY, R. B.  
 ; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FISH & NEAVE  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10020  
 ; COMPUTER READABLE FORM:  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/08/450,257  
 ; FILING DATE: 25-MAY-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/235,403  
 ; FILING DATE: 28-APR-1994  
 ; APPLICATION NUMBER: US 07/934,375  
 ; FILING DATE: 21-AUG-1992  
 ; APPLICATION NUMBER: US 07/098,766  
 ; FILING DATE: 28-JUL-1993  
 ; APPLICATION NUMBER: PCT/US93/07833  
 ; FILING DATE: 19-AUG-1993  
 ; APPLICATION NUMBER: US 07/454,450  
 ; FILING DATE: 21-DEC-1989  
 ; APPLICATION NUMBER: US 07/636,662  
 ; FILING DATE: 02-JAN-1991  
 ; APPLICATION NUMBER: US 08/158,015  
 ; FILING DATE: 24-NOV-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Haley Jr., James F.  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: B170 CIP 2  
 ; TELEPHONE: (212) 596-9000  
 ; TELEFAX: (212) 596-9090  
 ; TELEX: 14-8367  
 ; INFORMATION FOR SEQ ID NO: 44:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 39 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-450-257-44

Query Match 78.9%; Score 30; DB 2; Length 39;  
 Best Local Similarity 86.8%; Pred. No. 0.0052;  
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 38  
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Db 39 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTTC 2

RESULT 6  
 US-08-450-246-43  
 ; Sequence 43, Application US/08450246  
 ; Patent No. 5670617  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANKEL, Alan  
 ; APPLICANT: PABO, Carl  
 ; APPLICANT: BARSOUM, James G.  
 ; APPLICANT: FAWELL, Stephen E.  
 ; APPLICANT: PEPINSKY, R. B.  
 ; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FISH & NEAVE  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10020  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/08/450,246  
 ; FILING DATE: 25-MAY-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/235,403  
 ; FILING DATE: 28-APR-1994  
 ; APPLICATION NUMBER: US 07/934,375  
 ; FILING DATE: 21-AUG-1992  
 ; APPLICATION NUMBER: US 07/098,766  
 ; FILING DATE: 28-JUL-1993  
 ; APPLICATION NUMBER: PCT/US93/07833  
 ; FILING DATE: 19-AUG-1993  
 ; APPLICATION NUMBER: US 07/454,450  
 ; FILING DATE: 21-DEC-1989  
 ; APPLICATION NUMBER: US 07/636,662  
 ; FILING DATE: 02-JAN-1991  
 ; APPLICATION NUMBER: US 08/158,015  
 ; FILING DATE: 24-NOV-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Haley Jr., James F.  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: B170 CIP 2  
 ; TELEPHONE: (212) 596-9000  
 ; TELEFAX: (212) 596-9090  
 ; TELEX: 14-8367  
 ; INFORMATION FOR SEQ ID NO: 43:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 39 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-450-246-43

Query Match 78.9%; Score 30; DB 2; Length 39;  
 Best Local Similarity 86.8%; Pred. No. 0.0052;  
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTTC 38  
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 Db 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTTC 38  
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RESULT 7

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US-08-450-246-.44/c
; Sequence 44, Application US/08450246
; Patent No. 5670617
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPIŒSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,246
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-450-246-.44

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Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%;  
Matches 33; Conservative 0; Mismatches 5; Indels  
Pred. No. 0.0052;

**Qy** 1 GGGGACTTTCGCTGGGGACTTTCCAGGGGAC TTTC 38  
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**Db** 39 GGGGACTTTCGCTGGGGACTTTCCAGGGGAC TTTC 2  
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|||||

RESULT 8  
US-08-450-098-43  
; Sequence 43, Application US/08450098  
; Patent No. 567980  
; GENERAL INFORMATION:

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1 APPLICANT: FRANKEL, Alan
2 APPLICANT: PABO, Carl
3 APPLICANT: BARSOUM, James G.
4 APPLICANT: FAWELL, Stephen E.
5 APPLICANT: PEPINSKY, R. B.
6 TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
7 NUMBER OF SEQUENCES: 69
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: FISH & NEAVE
10 STREET: 1251 Avenue of the Americas
11 CITY: New York
12 STATE: New York
13 COUNTRY: USA
14 ZIP: 10020
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/450,098
22 FILING DATE: 25-MAY-1995
23 CLASSIFICATION: 514
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/235,403
26 FILING DATE: 28-APR-1994
27 APPLICATION NUMBER: US 07/934,375
28 FILING DATE: 21-AUG-1992
29 APPLICATION NUMBER: US 07/098,766
30 FILING DATE: 28-JUL-1993
31 APPLICATION NUMBER: PCT/US93/07833
32 FILING DATE: 19-AUG-1993
33 APPLICATION NUMBER: US 07/454,450
34 FILING DATE: 21-DEC-1989
35 APPLICATION NUMBER: US 07/636,662
36 FILING DATE: 02-JAN-1991
37 APPLICATION NUMBER: US 08/158,015
38 FILING DATE: 24-NOV-1993
39 ATTORNEY/AGENT INFORMATION:
40 NAME: Haley Jr., James F.
41 REGISTRATION NUMBER: 27,794
42 REFERENCE/DOCKET NUMBER: B170 CIP 2
43 TELECOMMUNICATION INFORMATION:
44 TELEPHONE: (212) 596-9000
45 TELEFAX: (212) 596-9090
46 TELEX: 14-8367
47 INFORMATION FOR SEQ ID NO: 43:
48 SEQUENCE CHARACTERISTICS:
49 LENGTH: 39 base pairs
50 TYPE: nucleic acid
51 STRANDEDNESS: single
52 TOPOLOGY: linear
53 MOLECULE TYPE: DNA (genomic)
54 US-08-450-098-43

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Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33: Conservative 0; Mismatches 5; Indels

Qy 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTC 38  
|||||

Db 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||

RESULT 9  
US-08-450-098-44/c  
; Sequence 44, Application US/08450098  
; Patent No. 5674980  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOOM, James G.  
; APPLICANT: FAWELL, Stephen E.



/ COUNTRY: USA  
/ ZIP: 10020  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/451,233  
/ FILING DATE: 25-MAY-1995  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION NUMBER: US 08/235,403  
/ FILING DATE: 28-APR-1994  
/ APPLICATION NUMBER: US 07/934,375  
/ FILING DATE: 21-AUG-1992  
/ APPLICATION NUMBER: US 07/098,766  
/ FILING DATE: 28-JUL-1993  
/ APPLICATION NUMBER: PCT/US93/07833  
/ FILING DATE: 19-AUG-1993  
/ APPLICATION NUMBER: US 07/454,450  
/ FILING DATE: 21-DEC-1989  
/ APPLICATION NUMBER: US 07/636,662  
/ FILING DATE: 02-JAN-1991  
/ APPLICATION NUMBER: US 08/158,015  
/ FILING DATE: 24-NOV-1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Haley Jr., James F.  
/ REGISTRATION NUMBER: 27,794  
/ REFERENCE/DOCKET NUMBER: B170 CIP 2  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 596-9000  
/ TELEFAX: (212) 596-9090  
/ TELEX: 14-8367  
/ INFORMATION FOR SEQ ID NO: 44:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 39 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ US-08-451-233-44

Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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|||||  
Db 39 GGGGACTTTCCTGGGGACTTTCAGGGGGACTTTC 2

RESULT 12  
US-08-450-236-43  
/ Sequence 43, Application US/08450236  
/ Patent No. 5804604  
/ GENERAL INFORMATION:  
/ APPLICANT: FRANKEL, Alan  
/ APPLICANT: PABO, Carl  
/ APPLICANT: BARSOUM, James G.  
/ APPLICANT: FAWELL, Stephen E.  
/ APPLICANT: PEPINSKY, R. B.  
/ TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
/ NUMBER OF SEQUENCES: 69  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: FISH & NEAVE  
/ STREET: 1251 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10020  
/ COMPUTER READABLE FORM: disk  
/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/450,236  
/ FILING DATE: 25-MAY-1995  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION NUMBER: US 08/235,403  
/ FILING DATE: 28-APR-1994  
/ APPLICATION NUMBER: US 07/934,375  
/ FILING DATE: 21-AUG-1992  
/ APPLICATION NUMBER: US 07/098,766  
/ FILING DATE: 28-JUL-1993  
/ APPLICATION NUMBER: PCT/US93/07833  
/ FILING DATE: 19-AUG-1993  
/ APPLICATION NUMBER: US 07/454,450  
/ FILING DATE: 21-DEC-1989  
/ APPLICATION NUMBER: US 07/636,662  
/ FILING DATE: 02-JAN-1991  
/ APPLICATION NUMBER: US 08/158,015  
/ FILING DATE: 24-NOV-1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Haley Jr., James F.  
/ REGISTRATION NUMBER: 27,794  
/ REFERENCE/DOCKET NUMBER: B170 CIP 2  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 596-9000  
/ TELEFAX: (212) 596-9090  
/ TELEX: 14-8367  
/ INFORMATION FOR SEQ ID NO: 43:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 39 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ US-08-450-236-43

Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCTGGGGACTTTCAGGGGGACTTTC 38  
|||||  
Db 1 GGGGACTTTCCTGGGGACTTTCAGGGGGACTTTC 38

RESULT 13  
US-08-450-236-44/c  
/ Sequence 44, Application US/08450236  
/ Patent No. 5804604  
/ GENERAL INFORMATION:  
/ APPLICANT: FRANKEL, Alan  
/ APPLICANT: PABO, Carl  
/ APPLICANT: BARSOUM, James G.  
/ APPLICANT: FAWELL, Stephen E.  
/ APPLICANT: PEPINSKY, R. B.  
/ TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
/ NUMBER OF SEQUENCES: 69  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: FISH & NEAVE  
/ STREET: 1251 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10020  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/450,236  
/ FILING DATE: 25-MAY-1995  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/235,403  
/ FILING DATE: 28-APR-1994  
/ APPLICATION NUMBER: US 07/934,375  
/ FILING DATE: 21-AUG-1992  
/ APPLICATION NUMBER: US 07/098,766  
/ FILING DATE: 28-JUL-1993  
/ APPLICATION NUMBER: PCT/US93/07833  
/ FILING DATE: 19-AUG-1993  
/ APPLICATION NUMBER: US 07/454,450  
/ FILING DATE: 21-DEC-1989  
/ APPLICATION NUMBER: US 07/636,662  
/ FILING DATE: 02-JAN-1991  
/ APPLICATION NUMBER: US 08/158,015  
/ FILING DATE: 24-NOV-1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Haley Jr., James F.  
/ REGISTRATION NUMBER: 27,794  
/ REFERENCE/DOCKET NUMBER: B170 CIP 2  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 596-9000  
/ TELEFAX: (212) 596-9090  
/ TELEX: 14-8367  
/ INFORMATION FOR SEQ ID NO: 44:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 39 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ US-08-450-236-44

Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGACTTTCACAGGGGACTTTC 38  
Db 39 GGGGACTTTCGCTGGGACTTTCACAGGGGACTTTC 2

RESULT 14  
US-08-235-403-43  
/ Sequence 43, Application US/08235403  
/ Patent No. 6316003  
/ GENERAL INFORMATION:  
/ APPLICANT: FRANKEL, Alan  
/ APPLICANT: PABO, Carl  
/ APPLICANT: BARSOUM, James G.  
/ APPLICANT: FAWELL, Stephen E.  
/ APPLICANT: PEPINSKY, R. B.  
/ TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
/ NUMBER OF SEQUENCES: 69  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: FISH & NEAVE  
/ STREET: 1251 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10020  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/235,403  
/ FILING DATE:  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 07/934,375  
/ FILING DATE: 21-AUG-1992  
/ APPLICATION NUMBER: US 07/098,766  
/ FILING DATE: 28-JUL-1993  
/ APPLICATION NUMBER: PCT/US93/07833  
/ FILING DATE: 19-AUG-1993  
/ APPLICATION NUMBER: US 07/454,450  
/ FILING DATE: 21-DEC-1989  
/ APPLICATION NUMBER: US 07/636,662  
/ FILING DATE: 02-JAN-1991  
/ APPLICATION NUMBER: US 08/158,015  
/ FILING DATE: 24-NOV-1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Haley Jr., James F.  
/ REGISTRATION NUMBER: 27,794  
/ REFERENCE/DOCKET NUMBER: B170 CIP 2  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 596-9000  
/ TELEFAX: (212) 596-9090  
/ TELEX: 14-8367  
/ INFORMATION FOR SEQ ID NO: 43:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 39 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ US-08-235-403-43

Query Match 78.9%; Score 30; DB 3; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGACTTTCACAGGGGACTTTC 38  
Db 1 GGGGACTTTCGCTGGGACTTTCACAGGGGACTTTC 38

RESULT 15  
US-08-235-403-44/c  
/ Sequence 44, Application US/08235403  
/ Patent No. 6316003  
/ GENERAL INFORMATION:  
/ APPLICANT: FRANKEL, Alan  
/ APPLICANT: PABO, Carl  
/ APPLICANT: BARSOUM, James G.  
/ APPLICANT: FAWELL, Stephen E.  
/ APPLICANT: PEPINSKY, R. B.  
/ TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
/ NUMBER OF SEQUENCES: 69  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: FISH & NEAVE  
/ STREET: 1251 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10020  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/235,403  
/ FILING DATE:  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 07/934,375  
/ FILING DATE: 21-AUG-1992  
/ APPLICATION NUMBER: US 07/098,766  
/ FILING DATE: 28-JUL-1993  
/ APPLICATION NUMBER: PCT/US93/07833  
/ FILING DATE: 19-AUG-1993

; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US 08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B170 CIP 2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-235-403-44

Query Match 78.9%; Score 30; DB 3; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGACTTTCGCTGGGACTTTCAGGGGACTTTC 38  
Db 39 GGGGACTTTCCTGGGACTTTCACGGGGGACTTTC 2

## RESULT 16

US-09-314-691-9

; Sequence 9, Application US/09314691  
; Patent No. 6444233  
; GENERAL INFORMATION:  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: BLAKE, MARY E.  
; APPLICANT: GUTTERMAN, JORDAN U.  
; APPLICANT: HOFFMANN, JOSEPH J.  
; APPLICANT: BAILEY, DAVID T.  
; APPLICANT: JAYATILAKE, GAMINI S.  
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: CLFR:006  
; CURRENT APPLICATION NUMBER: US/09/314,691  
; CURRENT FILING DATE: 1999-05-19  
; EARLIER APPLICATION NUMBER: 60/099,066  
; EARLIER FILING DATE: 1998-09-03  
; EARLIER APPLICATION NUMBER: 60/085,997  
; EARLIER FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
; US-09-314-691-9

Query Match 78.4%; Score 29.8; DB 3; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.0065;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGCTGGGACTTTCAGGGGACT 34  
Db 10 GGGACTTTCGCTGGGACTTTCAGGGGAGCT 42

## RESULT 17

US-09-999-495-9

; Sequence 9, Application US/09999495  
; Patent No. 6889398  
; GENERAL INFORMATION:  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: BLAKE, MARY E.  
; APPLICANT: GUTTERMAN, JORDAN U.  
; APPLICANT: HOFFMANN, JOSEPH J.  
; APPLICANT: BAILEY, DAVID T.  
; APPLICANT: JAYATILAKE, GAMINI S.  
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: CLFR:006  
; CURRENT APPLICATION NUMBER: US/09/999,495  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 09/314,691  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/099,066  
; PRIOR FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: 60/085,997  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
; US-09-999-495-9

Query Match 78.4%; Score 29.8; DB 3; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.0065;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGCTGGGACTTTCAGGGGACT 34  
Db 10 GGGACTTTCGCTGGGACTTTCAGGGGAGCT 42

## RESULT 18

US-09-992-837-9

; Sequence 9, Application US/09992837  
; Patent No. 6746696  
; GENERAL INFORMATION:  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: BLAKE, MARY E.  
; APPLICANT: GUTTERMAN, JORDAN U.  
; APPLICANT: HOFFMANN, JOSEPH J.  
; APPLICANT: BAILEY, DAVID T.  
; APPLICANT: JAYATILAKE, GAMINI S.  
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: CLFR:006  
; CURRENT APPLICATION NUMBER: US/09/992,837  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/314,691  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/085,997  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
; US-09-992-837-9

Query Match 78.4%; Score 29.8; DB 3; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.0065;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



```
Qy 2 GGGACTTCCGCTGGGAGCTTTCAGGGGACT 34
Db 10 GGGACTTCCGCTGGGAGCTTTCAGGGGACT 42

RESULT 19
US-10-000-720-9
; Sequence 9, Application US/10000720
; Patent No. 6962720
; GENERAL INFORMATION:
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: BLAKE, MARY E.
; APPLICANT: GUTTERMAN, JORDAN U.
; APPLICANT: HOFFMANN, JOSEPH J.
; APPLICANT: BAILEY, DAVID T.
; APPLICANT: JAYATILAKE, GAMINI S.
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: CLFR:006
; CURRENT APPLICATION NUMBER: US/10/000,720
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/314,691
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,066
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/085,997
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-000-720-9

Query Match 78.4%; Score 29.8; DB 3; Length 44;
Best Local Similarity 93.9%; Pred. No. 0.0065;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGACTTCCGCTGGGAGCTTTCAGGGGACT 34
Db 10 GGGACTTCCGCTGGGAGCTTTCAGGGGACT 42

RESULT 20
US-08-580-988A-12
; Sequence 12, Application US/08580988A
; Patent No. 5856161
; GENERAL INFORMATION:
; APPLICANT: Aggarwal et al.
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
; TITLE OF INVENTION: For Its Use
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,988A
; FILING DATE: January 3, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D., J.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5721CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 bp
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; US-08-580-988A-12

Query Match 76.8%; Score 29.2; DB 2; Length 45;
Best Local Similarity 91.2%; Pred. No. 0.011;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGCTGGGAGCTTTCAGGGGACTT 35
Db 10 GGGACTTTCGCTGGGAGCTTTCAGGGGACTT 43

RESULT 21
US-08-353-476-19
; Sequence 19, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
```

US-08-353-476-19

Query Match 76.8%; Score 29.2; DB 2; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.011;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGACTTTCAGGGGACTT 35  
|||||  
Db 7 GGGACTTCCGCTGGGACTTTCAGGGGAGCGT 40

RESULT 22

US-08-353-476-23

; Sequence 23, Application US/08353476

; Patent No. 5871902

; GENERAL INFORMATION:

; APPLICANT: Weininger, Susan

; APPLICANT: Weininger, Arthur M

; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A

; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

; NUMBER OF SEQUENCES: 117

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik &amp; Saliwanchik

; STREET: 2421 N.W. 41st St., Suite A-1

; CITY: Gainesville

; STATE: Florida

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/353,476

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Bencen, Gerard H

; REGISTRATION NUMBER: 35,746

; REFERENCE/DOCKET NUMBER: GP-100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (904) 375-8100

; TELEFAX: (904) 372-5800

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 45 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-353-476-23

Query Match 76.8%; Score 29.2; DB 2; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.011;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGACTTTCAGGGGACTT 35  
|||||  
Db 7 GGGACTTCCGCTGGGACTTTCAGGGGAGCGT 40

RESULT 23

US-08-353-476-20

; Sequence 20, Application US/08353476

; Patent No. 5871902

; GENERAL INFORMATION:

; APPLICANT: Weininger, Susan

; APPLICANT: Weininger, Arthur M

; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A

; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,476  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bencen, Gerard H  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-353-476-20

Query Match 76.3%; Score 29; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGACTTTCAGGGG 30  
|||||  
Db 7 GGGACTTCCGCTGGGACTTTCAGGGG 35

RESULT 24

US-08-353-476-21

; Sequence 21, Application US/08353476

; Patent No. 5871902

; GENERAL INFORMATION:

; APPLICANT: Weininger, Susan

; APPLICANT: Weininger, Arthur M

; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A

; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

; NUMBER OF SEQUENCES: 117

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik &amp; Saliwanchik

; STREET: 2421 N.W. 41st St., Suite A-1

; CITY: Gainesville

; STATE: Florida

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/353,476

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Bencen, Gerard H

; REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-353-476-21

Query Match 76.3%; Score 29; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGG 30  
|||||  
DB 7 GGGACTTTCGCTGGGACTTTCAGGGG 35

RESULT 25  
US-08-353-476-22  
Sequence 22, Application US/08353476  
Patent No. 5871902  
GENERAL INFORMATION:  
APPLICANT: Weininger, Susan  
APPLICANT: Weininger, Arthur M  
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A  
REFERENCE/DOCKET NUMBER: GP-100  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,476  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bencen, Gerard H  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-353-476-22

Query Match 76.3%; Score 29; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGG 30

Db 7 GGGACTTTCGCTGGGACTTTCAGGGG 35  
|||||

RESULT 26  
US-08-353-476-27  
Sequence 27, Application US/08353476  
Patent No. 5871902  
GENERAL INFORMATION:  
APPLICANT: Weininger, Susan  
APPLICANT: Weininger, Arthur M  
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A  
REFERENCE/DOCKET NUMBER: GP-100  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,476  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bencen, Gerard H  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-353-476-27

Query Match 76.3%; Score 29; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGG 30  
|||||  
DB 7 GGGACTTTCGCTGGGACTTTCAGGGG 35

RESULT 27  
US-08-465-590-142  
Sequence 142, Application US/08465590  
Patent No. 5824770  
GENERAL INFORMATION:  
APPLICANT: Georgopoulos, Katia A.  
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, Suite 510  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII (text)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/465,590
/ FILING DATE: 05-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/238,212
/ FILING DATE: 02-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/121,438
/ FILING DATE: 14-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/946,233
/ FILING DATE: 14-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Myers, Paul L.
/ REGISTRATION NUMBER: 35,695
/ REFERENCE/DOCKET NUMBER: MPG-006C2DV
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)227-5941
/ INFORMATION FOR SEQ ID NO: 142:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ US-08-465-590-142

Query Match 75.8%; Score 28.8; DB 2; Length 36;
Best Local Similarity 93.8%; Pred. No. 0.016;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGGACTTTCAGGGGAC 33
Db 4 GGGACTTTCGGCTGGGGACTTTCAGGGAGGC 35

RESULT 28
US-08-711-417C-142
/ Sequence 142, Application US/08711417C
/ Patent No. 6228611
/ GENERAL INFORMATION:
/ APPLICANT: Georgopoulos, Katia A.
/ TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
/ NUMBER OF SEQUENCES: 202
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows 95
/ SOFTWARE: FastSeq for Windows Version 2.0b
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/711,417C
/ FILING DATE: 05-SEP-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/238,212
/ FILING DATE: 02-MAY-1994
/ APPLICATION NUMBER: 08/121,438
/ FILING DATE: 14-SEP-1993
/ APPLICATION NUMBER: 07/946,233
/ FILING DATE: 14-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Myers, Louis P.
/ REGISTRATION NUMBER: 35,965
/ REFERENCE/DOCKET NUMBER: 10287/007001
/ TELEPHONE: 617/542-5070
/ TELEFAX: 617/542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 142:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 142:
```

```
/ REGISTRATION NUMBER: 35,965
/ REFERENCE/DOCKET NUMBER: 10287/007001
/ TELEPHONE: 617/542-5070
/ TELEFAX: 617/542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 142:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-08-711-417C-142

Query Match 75.8%; Score 28.8; DB 3; Length 36;
Best Local Similarity 93.8%; Pred. No. 0.016;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGGACTTTCAGGGGAC 33
Db 4 GGGACTTTCGGCTGGGGACTTTCAGGGAGGC 35

RESULT 29
US-09-723-909-142
/ Sequence 142, Application US/09723909
/ Patent No. 6630141
/ GENERAL INFORMATION:
/ APPLICANT: Georgopoulos, Katia A.
/ TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
/ NUMBER OF SEQUENCES: 202
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows 95
/ SOFTWARE: FastSeq for Windows Version 2.0b
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/723,909
/ FILING DATE: 28-NOV-2000
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/711,417
/ FILING DATE: 05-SEP-1996
/ APPLICATION NUMBER: 08/238,212
/ FILING DATE: 02-MAY-1994
/ APPLICATION NUMBER: 08/121,438
/ FILING DATE: 14-SEP-1993
/ APPLICATION NUMBER: 07/946,233
/ FILING DATE: 14-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Myers, Louis P.
/ REGISTRATION NUMBER: 35,965
/ REFERENCE/DOCKET NUMBER: 10287/007001
/ TELEPHONE: 617/542-5070
/ TELEFAX: 617/542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 142:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ SEQUENCE DESCRIPTION: SEQ ID NO: 142:
```

## US-09-723-909-142

Query Match 75.8%; Score 28.8; DB 3; Length 36;  
Best Local Similarity 93.8%; Pred. No. 0.016;  
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGGAC 33  
|||||  
Db 4 GGGACTTTCGCTGGGACTTTCAGGGAGGC 35

## RESULT 30

PCT-US93-08743-142  
; Sequence 142, Application PC/TUS9308743  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
; NUMBER OF SEQUENCES: 152  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08743  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 946,233  
; FILING DATE: 14-SEP-1992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 142:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
PCT-US93-08743-142

Query Match 75.8%; Score 28.8; DB 6; Length 36;  
Best Local Similarity 93.8%; Pred. No. 0.016;  
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGGAC 33  
|||||  
Db 4 GGGACTTTCGCTGGGACTTTCAGGGAGGC 35

## RESULT 31

US-08-353-476-38  
; Sequence 38, Application US/08353476  
; Patent No. 5871902  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A  
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/353,476

; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bencen, Gerard H  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-353-476-38

Query Match 74.7%; Score 28.4; DB 2; Length 37;  
Best Local Similarity 96.7%; Pred. No. 0.023;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGGG 31  
|||||  
Db 7 GGGACTTTCGCTGGGACTTTCAGGGAG 36

## RESULT 32

US-09-522-775A-9  
; Sequence 9, Application US/09522775A  
; Patent No. 6660906  
; GENERAL INFORMATION:  
; APPLICANT: Tsichlis, Philip N.  
; TITLE OF INVENTION: Inhibition of Tpl2 To Treat inflammatory Diseases  
; FILE REFERENCE: OTT-3202  
; CURRENT APPLICATION NUMBER: US/09/522,775A  
; CURRENT FILING DATE: 2000-03-08  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-09-522-775A-9

Query Match 73.7%; Score 28; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGG 29  
|||||  
Db 5 GGGACTTTCGCTGGGACTTTCAGGG 32

## RESULT 33

US-09-522-775A-11  
; Sequence 11, Application US/09522775A  
; Patent No. 6660906  
; GENERAL INFORMATION:  
; APPLICANT: Tsichlis, Philip N.  
; TITLE OF INVENTION: Inhibition of Tpl2 To Treat inflammatory Diseases  
; FILE REFERENCE: OTT-3202  
; CURRENT APPLICATION NUMBER: US/09/522,775A  
; CURRENT FILING DATE: 2000-03-08  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 32  
; TYPE: DNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-522-775A-11

Query Match      73.7%; Score 28; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGACTTTCGCTGGGGACTTTCAGG 29
    |||||
Db   5 GGGACTTTCGCTGGGGACTTTCAGG 32
    |||||

RESULT 34
US-09-440-967-4
; Sequence 4, Application US/09440967
; Patent No. 6730302
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: INTRACELLULAR TARGETED DELIVERY OF COMPOUNDS BY 70 KD HEAT SHOCK
; FILE REFERENCE: DB8
; CURRENT APPLICATION NUMBER: US/09/440,967
; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/109,872
; PRIOR FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-440-967-4

Query Match      73.7%; Score 28; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGACTTTCGCTGGGGACTTTCAGG 28
    |||||
Db   8 GGGACTTTCGCTGGGGACTTTCAGG 35
    |||||

RESULT 35
US-08-353-476-26
; Sequence 26, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bercen, Gerard H.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: Gp-100

; ORGANISM: Artificial Sequence
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-353-476-26

Query Match      72.6%; Score 27.6; DB 2; Length 45;
Best Local Similarity 88.2%; Pred. No. 0.05;
Matches 30; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  2 GGGACTTTCGCTGGGGACTTTCAGGGGACTT 35
    |||||
Db   7 GGGACTTTCGCTGGGGACTTTCAGAGAGGCGT 40
    |||||

RESULT 36
US-09-533-341-6/c
; Sequence 6, Application US/09533341
; Patent No. 6803044
; GENERAL INFORMATION:
; APPLICANT: Zengen, Inc.
; APPLICANT: Lipton, James M.
; APPLICANT: Catania, Anna P.
; TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY PEPTIDES FOR USE IN HUMAN
; FILE REFERENCE: IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 54275.8004.US00
; CURRENT APPLICATION NUMBER: US/09/533,341
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 60/126,233
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-533-341-6

Query Match      72.1%; Score 27.4; DB 3; Length 35;
Best Local Similarity 96.6%; Pred. No. 0.057;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 GGGACTTTCGCTGGGGACTTTCAGGG 29
    |||||
Db   32 GGGACTTTCGCTGGGGACTTTCATGG 4
    |||||

RESULT 37
US-08-353-476-24
; Sequence 24, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
```

; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; APPLICATION NUMBER: US/08/353,476  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bencen, Gerard H  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-353-476-24

Query Match 72.1%; Score 27.4; DB 2; Length 44;  
Best Local Similarity 83.8%; Pred. No. 0.06; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 6;

QY 2 GGGACTTTCCGCTGGGACTTTCAGGGGACTTTC 38  
DB 7 GGGACTTTCGCTGGGACTTTCGGGGAGGTGCC 43

RESULT 38  
US-08-353-476-25  
; Sequence 25, Application US/08353476  
; Patent No. 5871902  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A  
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; APPLICATION NUMBER: US/08/353,476  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bencen, Gerard H  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-353-476-25

Query Match 71.6%; Score 27.2; DB 2; Length 44;  
Best Local Similarity 90.6%; Pred. No. 0.072; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 3;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGGAC 33  
DB 7 GGGACTTTCGCTGGGACTTTCGGGGAGGC 38

RESULT 39  
US-09-535-066F-9  
; Sequence 9, Application US/09535066F  
; Patent No. 6800291  
; GENERAL INFORMATION:  
; APPLICANT: ZENGEN, INC.  
; APPLICANT: Lipton, M.J.  
; APPLICANT: Catania, A.P.  
; TITLE OF INVENTION: A LYS-PRO-VAL DIMER, FORMULATIONS AND APPLICATIONS  
; FILE REFERENCE: 54275.8005.US00  
; CURRENT APPLICATION NUMBER: US/09/535,066F  
; CURRENT FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: US 60/126,233  
; PRIOR FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide probes for NF-kB.  
; US-09-535-066F-9

Query Match 69.5%; Score 26.4; DB 3; Length 35;  
Best Local Similarity 96.4%; Pred. No. 0.14; Indels 0; Gaps 0;  
Matches 27; Conservative 0; Mismatches 1;

QY 1 GGGGACTTTCGCTGGGGACTTTCAGG 28  
DB 8 GGGGACTTTCGCTGGGGACTTTCATG 35

RESULT 40  
US-09-533-341-5  
; Sequence 5, Application US/09533341  
; Patent No. 6803044  
; GENERAL INFORMATION:  
; APPLICANT: Zengen, Inc.  
; APPLICANT: Lipton, James M.  
; APPLICANT: Catania, Anna P.  
; TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY PEPTIDES FOR USE IN HUMAN  
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS  
; FILE REFERENCE: 54275.8004.US00  
; CURRENT APPLICATION NUMBER: US/09/533,341  
; CURRENT FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: US 60/126,233  
; PRIOR FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

## US-09-533-341-5

Query Match 69.5%; Score 26.4; DB 3; Length 35;  
Best Local Similarity 96.4%; Pred. No. 0.14;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCCAGG 28  
|||||  
Db 8 GGGGACTTTCGCTGGGGACTTTCCATG 35

## RESULT 41

US-09-031-629A-5  
; Sequence 5, Application US/09031629A  
; Patent No. 6617171  
; GENERAL INFORMATION:  
; APPLICANT: Faustman  
; APPLICANT: Hayaashi  
; TITLE OF INVENTION: Methods for Treating and Diagnosing Autoimmune Disease  
; FILE REFERENCE: MGH/Faustman 17633/1030  
; CURRENT APPLICATION NUMBER: US/09/031,629A  
; CURRENT FILING DATE: 1998-02-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Probe for  
; OTHER INFORMATION: wild-type kappa B1 sequence  
US-09-031-629A-5

Query Match 68.4%; Score 26; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCCAG 27  
|||||  
Db 7 GGGACTTTCGCTGGGGACTTTCCAG 32

## RESULT 42

US-09-258-682-1  
; Sequence 1, Application US/09258682  
; Patent No. 6773705  
; GENERAL INFORMATION:  
; APPLICANT: Faustman et al., Denise L.  
; TITLE OF INVENTION: Methods for diagnosing and treating autoimmune disease  
; FILE REFERENCE: 17633-1120 Kathleen M. Williams  
; CURRENT APPLICATION NUMBER: US/09/258,682  
; CURRENT FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-258-682-1

Query Match 68.4%; Score 26; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCCAG 27  
|||||  
Db 7 GGGACTTTCGCTGGGGACTTTCCAG 32

## RESULT 43

US-08-484-397A-25  
; Sequence 25, Application US/08484397A  
; Patent No. 5869055

## GENERAL INFORMATION:

; APPLICANT: Juan, Shao-Chieh  
; APPLICANT: Lichenstein, Henri S.  
; APPLICANT: Wright, Samuel D.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMGEN INC  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,397A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Curry, Daniel R.  
; REGISTRATION NUMBER: 32,727  
; REFERENCE/DOCKET NUMBER: A-324A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 805/447-1000  
; TELEFAX: 805/447-1090  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-484-397A-25

Query Match 68.4%; Score 26; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCCAG 27  
|||||  
Db 7 GGGACTTTCGCTGGGGACTTTCCAG 32

## RESULT 44

US-08-484-397A-26/c  
; Sequence 26, Application US/08484397A  
; Patent No. 5869055  
; GENERAL INFORMATION:  
; APPLICANT: Juan, Shao-Chieh  
; APPLICANT: Lichenstein, Henri S.  
; APPLICANT: Wright, Samuel D.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMGEN INC  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,397A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424



```
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-484-397A-26

Query Match 58.4%; Score 26; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGACTTTCAG 27
Db 31 GGGACTTTCGGCTGGGACTTTCAG 6

RESULT 45
US-09-535-066F-10/c
; Sequence 10, Application US/09535066F
; Patent No. 6800291
; GENERAL INFORMATION:
; APPLICANT: ZENGEN, INC.
; APPLICANT: Lipton, M.J.
; APPLICANT: Catania, A.P.
; TITLE OF INVENTION: A LYS-PRO-VAL DIMER, FORMULATIONS AND APPLICATIONS
; FILE REFERENCE: 54275.8005.US00
; CURRENT APPLICATION NUMBER: US/09/535,066F
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 60/126,233
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probes for NF-kB.
US-09-535-066F-10

Query Match 67.9%; Score 25.8; DB 3; Length 35;
Best Local Similarity 93.1%; Pred. No. 0.25;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGACTTTCGGCTGGGACTTTCAGG 29
Db 32 GGGAGTTTCGGCTGGGACTTTCATGG 4

RESULT 46
US-08-353-476-30
; Sequence 30, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; REFERENCE/DOCKET NUMBER: 35,746
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
```

```
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-353-476-30

Query Match 66.3%; Score 25.2; DB 2; Length 48;
Best Local Similarity 90.0%; Pred. No. 0.47;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CTTTCGCTGGGACTTTCAGGGGACTT 35
Db 1 CTTTCGCTGGGACTTTCAGGGGAGCGT 30

RESULT 47
US-08-353-476-7
; Sequence 7, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
```

```
/ LENGTH: 27 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
US-08-353-476-7

Query Match          65.8%; Score 25; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGACTTTCGCTGGGACTTTCCA 26
Db   3 GGGACTTTCGCTGGGACTTTCCA 27

RESULT 48
US-09-844-915-1
/ Sequence 1, Application US/09844915
/ Patent No. 6936468
/ GENERAL INFORMATION:
/ APPLICANT: Robbins, Paul D.
/ APPLICANT: Lu, Lina
/ APPLICANT: Giannoukakis, Nick
/ TITLE OF INVENTION: THE USE OF TOLEROGENIC DENDRITIC CELLS
/ TITLE OF INVENTION: FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
/ TITLE OF INVENTION: MAKING THE SAME
/ FILE REFERENCE: AP32737 / 072396.0225
/ CURRENT APPLICATION NUMBER: US/09/844,915
/ CURRENT FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: 60/200,479
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-1

Query Match          63.2%; Score 24; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGACTTTCGCTGGGACTTTCC 25
Db   2 GGGACTTTCGCTGGGACTTTCC 25

RESULT 49
US-09-844-915-2/c
/ Sequence 2, Application US/09844915
/ Patent No. 6936468
/ GENERAL INFORMATION:
/ APPLICANT: Robbins, Paul D.
/ APPLICANT: Lu, Lina
/ APPLICANT: Giannoukakis, Nick
/ TITLE OF INVENTION: THE USE OF TOLEROGENIC DENDRITIC CELLS
/ TITLE OF INVENTION: FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
/ TITLE OF INVENTION: MAKING THE SAME
/ FILE REFERENCE: AP32737 / 072396.0225
/ CURRENT APPLICATION NUMBER: US/09/844,915
/ CURRENT FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: 60/200,479
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 25

/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-2

Query Match          63.2%; Score 24; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGACTTTCGCTGGGACTTTCC 25
Db   4 GGGACTTTCGCTGGGACTTTCC 27

RESULT 50
US-08-479-852-44
/ Sequence 44, Application US/08479852
/ Patent No. 5712385
/ GENERAL INFORMATION:
/ APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
/ APPLICANT: Yeasing Yang
/ TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
/ TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
/ TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
/ NUMBER OF SEQUENCES: 139
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 611 West Sixth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90017
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
/ COMPUTER: IBM PS/2 Model 50Z or 55SX
/ OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
/ SOFTWARE: WordPerfect (Version 5.0)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/479,852
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/040,745
/ FILING DATE:
/ APPLICATION NUMBER: U.S. Serial No. 5712385 07/550,837
/ FILING DATE: 7/10/90
/ APPLICATION NUMBER: U.S. Serial No. 5712385 07/379,501
/ FILING DATE: 7/11/89
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 196/189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 27
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-479-852-44

Query Match          63.2%; Score 24; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGACTTTCGCTGGGACTTTCC 25
Db   4 GGGACTTTCGCTGGGACTTTCC 27
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Search completed: February 15, 2006, 21:14:22  
Job time : 89.4215 secs

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OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 01:43:22 ; Search time 551.471 Seconds  
(without alignments)  
569.815 Million cell updates/sec

Title: US-09-669-187A-148

Perfect score: 38

Sequence: 1 ggggacttcctcggtgggactttccagggggactttcc 38

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA\_Main:\*

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2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description                         |
|------------|-------|---------------|--------|----|-------------------------------------|
| 1          | 38    | 100.0         | 38     | 3  | US-09-888-326-417 Sequence 417, App |
| 2          | 38    | 100.0         | 38     | 3  | US-09-776-479-148 Sequence 148, App |
| 3          | 38    | 100.0         | 38     | 3  | US-09-776-479-148 Sequence 148, App |
| 4          | 38    | 100.0         | 38     | 5  | US-10-112-653-141 Sequence 141, App |
| 5          | 38    | 100.0         | 38     | 5  | US-10-017-995-148 Sequence 148, App |
| 6          | 38    | 100.0         | 38     | 6  | US-10-314-578-148 Sequence 148, App |
| 7          | 38    | 100.0         | 38     | 8  | US-10-831-778-148 Sequence 148, App |
| 8          | 30.8  | 81.1          | 43     | 2  | US-08-860-844-29 Sequence 29, Appl  |
| 9          | 30.8  | 81.1          | 43     | 6  | US-10-407-543-29 Sequence 29, Appl  |
| 10         | 30.2  | 79.5          | 46     | 2  | US-08-860-844-28 Sequence 28, Appl  |
| 11         | 30.2  | 79.5          | 46     | 6  | US-10-407-543-28 Sequence 28, Appl  |
| 12         | 29.8  | 78.4          | 44     | 3  | US-09-992-837-9 Sequence 9, Appl    |
| 13         | 29.8  | 78.4          | 44     | 3  | US-09-999-495-9 Sequence 9, Appl    |
| 14         | 29.8  | 78.4          | 44     | 5  | US-10-000-720-9 Sequence 9, Appl    |
| 15         | 29.8  | 78.4          | 44     | 6  | US-10-238-647-9 Sequence 9, Appl    |
| 16         | 29.2  | 76.8          | 45     | 2  | US-08-860-844-19 Sequence 19, Appl  |
| 17         | 29.2  | 76.8          | 45     | 6  | US-10-407-543-19 Sequence 19, Appl  |
| 18         | 29.2  | 76.8          | 45     | 6  | US-10-407-543-19 Sequence 19, Appl  |
| 19         | 29.2  | 76.8          | 45     | 6  | US-10-407-543-23 Sequence 23, Appl  |
| 20         | 29.2  | 76.8          | 45     | 7  | US-10-602-303-4 Sequence 4, Appl    |
| 21         | 29.2  | 76.8          | 45     | 9  | US-10-925-608-1 Sequence 1, Appl    |
| 22         | 29.2  | 76.8          | 45     | 9  | US-10-981-082-1 Sequence 1, Appl    |
| 23         | 29    | 76.3          | 46     | 2  | US-08-860-844-20 Sequence 20, Appl  |

|    |      |      |    |   |                                      |
|----|------|------|----|---|--------------------------------------|
| 24 | 29   | 76.3 | 46 | 2 | US-08-860-844-21 Sequence 21, Appl   |
| 25 | 29   | 76.3 | 46 | 2 | US-08-860-844-22 Sequence 22, Appl   |
| 26 | 29   | 76.3 | 46 | 2 | US-08-860-844-27 Sequence 27, Appl   |
| 27 | 29   | 76.3 | 46 | 6 | US-10-407-543-20 Sequence 20, Appl   |
| 28 | 29   | 76.3 | 46 | 6 | US-10-407-543-21 Sequence 21, Appl   |
| 29 | 29   | 76.3 | 46 | 6 | US-10-407-543-22 Sequence 22, Appl   |
| 30 | 29   | 76.3 | 46 | 6 | US-10-407-543-27 Sequence 27, Appl   |
| 31 | 28.4 | 74.7 | 37 | 6 | US-08-860-844-38 Sequence 38, Appl   |
| 32 | 28.4 | 74.7 | 37 | 6 | US-10-407-543-38 Sequence 38, Appl   |
| 33 | 28   | 73.7 | 34 | 6 | US-10-037-341-53 Sequence 53, Appl   |
| 34 | 27.6 | 72.6 | 45 | 2 | US-08-860-844-26 Sequence 26, Appl   |
| 35 | 27.6 | 72.6 | 45 | 6 | US-10-407-543-26 Sequence 26, Appl   |
| 36 | 27.4 | 72.1 | 44 | 5 | US-10-235-682-9 Sequence 9, Appl     |
| 37 | 27.4 | 72.1 | 44 | 6 | US-08-860-844-24 Sequence 24, Appl   |
| 38 | 27.2 | 71.6 | 44 | 6 | US-10-407-543-24 Sequence 24, Appl   |
| 39 | 27.2 | 71.6 | 44 | 6 | US-08-860-844-25 Sequence 25, Appl   |
| 40 | 27.2 | 71.6 | 44 | 6 | US-10-407-543-25 Sequence 25, Appl   |
| 41 | 26.4 | 69.5 | 35 | 5 | US-10-235-682-8 Sequence 8, Appl     |
| 42 | 26.4 | 69.5 | 35 | 8 | US-10-659-053-11 Sequence 11, Appl   |
| 43 | 26   | 68.4 | 32 | 3 | US-09-031-629A-5 Sequence 5, Appl    |
| 44 | 26   | 68.4 | 32 | 9 | US-10-775-487A-1 Sequence 1, Appl    |
| 45 | 25.8 | 67.9 | 35 | 8 | US-10-659-053-12 Sequence 12, Appl   |
| 46 | 25.2 | 66.3 | 48 | 2 | US-08-860-844-30 Sequence 30, Appl   |
| 47 | 25.2 | 66.3 | 48 | 6 | US-10-407-543-30 Sequence 30, Appl   |
| 48 | 25   | 65.8 | 27 | 2 | US-08-860-844-7 Sequence 7, Appl     |
| 49 | 25   | 65.8 | 27 | 6 | US-10-407-543-7 Sequence 7, Appl     |
| 50 | 24   | 63.2 | 25 | 3 | US-09-844-915-1 Sequence 1, Appl     |
| 51 | 24   | 63.2 | 25 | 3 | US-09-844-915-2 Sequence 2, Appl     |
| 52 | 24   | 63.2 | 27 | 3 | US-08-860-844-8 Sequence 8, Appl     |
| 53 | 24   | 63.2 | 27 | 3 | US-09-766-095-44 Sequence 44, Appl   |
| 54 | 24   | 63.2 | 27 | 3 | US-09-766-095-124 Sequence 124, App  |
| 55 | 24   | 63.2 | 27 | 6 | US-10-244-490-17 Sequence 17, Appl   |
| 56 | 24   | 63.2 | 27 | 6 | US-10-407-543-8 Sequence 8, Appl     |
| 57 | 24   | 63.2 | 29 | 3 | US-09-747-552-1 Sequence 1, Appl     |
| 58 | 24   | 63.2 | 29 | 3 | US-09-747-552-2 Sequence 2, Appl     |
| 59 | 24   | 63.2 | 29 | 3 | US-09-887-879-12 Sequence 12, Appl   |
| 60 | 24   | 63.2 | 29 | 3 | US-09-993-234-10 Sequence 10, Appl   |
| 61 | 24   | 63.2 | 29 | 3 | US-09-992-964-12 Sequence 12, Appl   |
| 62 | 24   | 63.2 | 29 | 5 | US-10-080-455-6 Sequence 6, Appl     |
| 63 | 24   | 63.2 | 29 | 5 | US-10-052-798-4 Sequence 4, Appl     |
| 64 | 24   | 63.2 | 29 | 5 | US-10-081-280-10 Sequence 10, Appl   |
| 65 | 24   | 63.2 | 29 | 5 | US-10-112-793-10 Sequence 10, Appl   |
| 66 | 24   | 63.2 | 29 | 5 | US-10-112-193-14 Sequence 14, Appl   |
| 67 | 24   | 63.2 | 29 | 5 | US-10-207-295-4 Sequence 4, Appl     |
| 68 | 24   | 63.2 | 29 | 6 | US-10-242-383-12 Sequence 12, Appl   |
| 69 | 24   | 63.2 | 29 | 6 | US-10-288-917-4 Sequence 4, Appl     |
| 70 | 24   | 63.2 | 29 | 6 | US-10-423-448-4 Sequence 4, Appl     |
| 71 | 24   | 63.2 | 29 | 8 | US-10-713-391-6 Sequence 6, Appl     |
| 72 | 23   | 60.5 | 23 | 3 | US-09-888-938-3 Sequence 3, Appl     |
| 73 | 23   | 60.5 | 23 | 3 | US-09-852-238A-3 Sequence 3, Appl    |
| 74 | 22   | 57.9 | 22 | 8 | US-10-862-363-60 Sequence 60, Appl   |
| 75 | 21.4 | 56.3 | 29 | 6 | US-10-383-773-1 Sequence 1, Appl     |
| 76 | 21.4 | 56.3 | 45 | 9 | US-10-981-082-2 Sequence 2, Appl     |
| 77 | 20.2 | 53.2 | 31 | 7 | US-10-673-882-3 Sequence 3, Appl     |
| 78 | 20.2 | 53.2 | 31 | 9 | US-10-926-749-3 Sequence 3, Appl     |
| 79 | 19.8 | 52.1 | 26 | 2 | US-08-860-844-16 Sequence 16, Appl   |
| 80 | 19.8 | 52.1 | 26 | 6 | US-10-407-543-16 Sequence 16, Appl   |
| 81 | 19.2 | 50.5 | 26 | 2 | US-08-860-844-9 Sequence 9, Appl     |
| 82 | 19.2 | 50.5 | 26 | 2 | US-08-860-844-15 Sequence 15, Appl   |
| 83 | 19.2 | 50.5 | 26 | 6 | US-10-407-543-9 Sequence 9, Appl     |
| 84 | 19.2 | 50.5 | 26 | 6 | US-10-407-543-15 Sequence 15, Appl   |
| 85 | 19   | 50.0 | 19 | 6 | US-10-225-023-556 Sequence 556, App  |
| 86 | 19   | 50.0 | 19 | 6 | US-10-225-023-576 Sequence 576, App  |
| 87 | 19   | 50.0 | 19 | 6 | US-10-225-023-606 Sequence 606, App  |
| 88 | 19   | 50.0 | 19 | 6 | US-10-225-023-617 Sequence 617, App  |
| 89 | 19   | 50.0 | 19 | 6 | US-10-225-023-622 Sequence 622, App  |
| 90 | 19   | 50.0 | 19 | 6 | US-10-225-023-661 Sequence 661, App  |
| 91 | 19   | 50.0 | 19 | 6 | US-10-225-023-689 Sequence 689, App  |
| 92 | 19   | 50.0 | 19 | 6 | US-10-225-023-1294 Sequence 1294, Ap |
| 93 | 19   | 50.0 | 19 | 6 | US-10-225-023-1314 Sequence 1314, Ap |
| 94 | 19   | 50.0 | 19 | 6 | US-10-225-023-1344 Sequence 1344, Ap |
| 95 | 19   | 50.0 | 19 | 6 | US-10-225-023-1355 Sequence 1355, Ap |
| 96 | 19   | 50.0 | 19 | 6 | US-10-225-023-1360 Sequence 1360, Ap |

|       |      |      |    |      |                      |                   |                    |                   |       |      |      |    |                      |                      |                   |
|-------|------|------|----|------|----------------------|-------------------|--------------------|-------------------|-------|------|------|----|----------------------|----------------------|-------------------|
| C 97  | 19   | 50.0 | 19 | 50.0 | 19                   | 6                 | US-10-225-023-1399 | Sequence 1399, Ap | 170   | 15.4 | 40.5 | 25 | 7                    | US-10-719-956-467968 | Sequence 467968,  |
| C 98  | 19   | 50.0 | 19 | 50.0 | 19                   | 6                 | US-10-225-023-1427 | Sequence 1427, Ap | 171   | 15.4 | 40.5 | 25 | 8                    | US-10-719-900-424043 | Sequence 424043,  |
| 99    | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-556  | Sequence 556, App | C 172 | 15.4 | 40.5 | 25 | 8                    | US-10-719-900-877620 | Sequence 877620,  |
| 100   | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-576  | Sequence 576, App | C 173 | 15.4 | 40.5 | 25 | 8                    | US-10-719-900-967003 | Sequence 967003,  |
| 101   | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-606  | Sequence 606, App | C 174 | 15.4 | 40.5 | 25 | 9                    | US-10-809-189-74122  | Sequence 74122, A |
| 102   | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-617  | Sequence 617, App | C 175 | 15.4 | 40.5 | 25 | 9                    | US-10-809-189-110222 | Sequence 110222,  |
| 103   | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-622  | Sequence 622, App | C 176 | 15.4 | 40.5 | 25 | 9                    | US-10-661-378-4      | Sequence 4, Appli |
| 104   | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-661  | Sequence 661, App | C 177 | 15.4 | 40.5 | 25 | 10                   | US-11-036-317-107187 | Sequence 107187,  |
| 105   | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-689  | Sequence 689, App | C 178 | 15.4 | 40.5 | 25 | 10                   | US-11-036-317-330597 | Sequence 330597,  |
| C 106 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-1294 | Sequence 1294, Ap | C 179 | 15.4 | 40.5 | 25 | 10                   | US-11-060-756-279032 | Sequence 279032,  |
| C 107 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-1344 | Sequence 1314, Ap | C 180 | 15.2 | 40.0 | 25 | 7                    | US-10-681-773-62807  | Sequence 62807, A |
| C 108 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-1344 | Sequence 1344, Ap | C 181 | 15.2 | 40.0 | 25 | 7                    | US-10-681-773-62809  | Sequence 62809, A |
| C 109 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-1355 | Sequence 1355, Ap | C 182 | 15.2 | 40.0 | 25 | 7                    | US-10-681-773-114771 | Sequence 114771,  |
| C 110 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-1355 | Sequence 1360, Ap | C 183 | 15.2 | 40.0 | 25 | 7                    | US-10-681-773-114772 | Sequence 114772,  |
| C 111 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-1360 | Sequence 1360, Ap | C 184 | 15.2 | 40.0 | 25 | 8                    | US-10-719-900-147015 | Sequence 147015,  |
| C 112 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-1399 | Sequence 1399, Ap | C 185 | 15.2 | 40.0 | 25 | 8                    | US-10-719-900-749313 | Sequence 749313,  |
| C 113 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-923-473-1427 | Sequence 1427, Ap | C 186 | 15.2 | 40.0 | 25 | 8                    | US-10-719-900-834294 | Sequence 834294,  |
| C 114 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-08-860-844-10   | Sequence 10, Appl | C 187 | 15.2 | 40.0 | 25 | 10                   | US-11-036-317-100981 | Sequence 100981,  |
| C 115 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-08-860-844-10   | Sequence 14, Appl | C 188 | 15.2 | 40.0 | 32 | 7                    | US-10-296-085A-72    | Sequence 72, Appl |
| C 116 | 19   | 50.0 | 19 | 50.0 | 19                   | 9                 | US-10-407-543-10   | Sequence 10, Appl | C 189 | 15.2 | 40.0 | 48 | 3                    | US-09-877-478-5923   | Sequence 5923, Ap |
| C 117 | 17.6 | 46.3 | 26 | 6    | US-10-407-543-14     | Sequence 14, Appl | Sequence 14, Appl  | C 190             | 15.2  | 40.0 | 48   | 7  | US-10-342-903-5923   | Sequence 5923, Ap    |                   |
| C 118 | 17.6 | 46.3 | 26 | 6    | US-08-860-844-13     | Sequence 13, Appl | Sequence 13, Appl  | C 191             | 15.2  | 40.0 | 48   | 7  | US-10-669-841-10814  | Sequence 10814, A    |                   |
| C 119 | 17.6 | 46.3 | 26 | 6    | US-10-407-543-13     | Sequence 13, Appl | Sequence 13, Appl  | C 192             | 15.2  | 40.0 | 50   | 6  | US-10-131-827-5964   | Sequence 5964, Ap    |                   |
| C 120 | 17.6 | 46.3 | 30 | 6    | US-10-407-543-11     | Sequence 80, Appl | Sequence 80, Appl  | C 193             | 15    | 39.5 | 15   | 2  | US-08-860-844-4      | Sequence 4, Appli    |                   |
| C 121 | 17.6 | 46.3 | 41 | 6    | US-10-224-683-6      | Sequence 6, Appli | Sequence 6, Appli  | C 194             | 15    | 39.5 | 15   | 6  | US-10-407-543-4      | Sequence 4, Appli    |                   |
| C 122 | 17.6 | 46.3 | 41 | 6    | US-10-942-561A-6     | Sequence 12, Appl | Sequence 12, Appl  | C 195             | 15    | 39.5 | 25   | 5  | US-10-098-263B-89477 | Sequence 89477, A    |                   |
| C 123 | 17.2 | 45.3 | 26 | 6    | US-08-860-844-12     | Sequence 12, Appl | Sequence 12, Appl  | C 196             | 15    | 39.5 | 25   | 5  | US-10-098-263B-89478 | Sequence 89478, A    |                   |
| C 124 | 16.8 | 44.2 | 26 | 2    | US-10-407-543-11     | Sequence 11, Appl | Sequence 11, Appl  | C 197             | 15    | 39.5 | 25   | 7  | US-10-719-956-18936  | Sequence 18936, A    |                   |
| C 125 | 16.8 | 44.2 | 26 | 6    | US-10-407-543-11     | Sequence 11, Appl | Sequence 11, Appl  | C 198             | 15    | 39.5 | 25   | 7  | US-10-719-956-11676  | Sequence 11676,      |                   |
| C 126 | 16.8 | 44.2 | 30 | 6    | US-10-383-773-2      | Sequence 2, Appli | Sequence 2, Appli  | C 199             | 15    | 39.5 | 25   | 7  | US-10-719-956-154856 | Sequence 154856,     |                   |
| C 127 | 16.8 | 44.2 | 41 | 6    | US-10-224-683-18     | Sequence 18, Appl | Sequence 18, Appl  | C 200             | 15    | 39.5 | 25   | 7  | US-10-719-956-162253 | Sequence 162253,     |                   |
| C 128 | 16.8 | 44.2 | 41 | 6    | US-10-942-561A-18    | Sequence 18, Appl | Sequence 18, Appl  | C 201             | 15    | 39.5 | 25   | 7  | US-10-719-956-162255 | Sequence 162255,     |                   |
| C 129 | 16.6 | 43.7 | 25 | 8    | US-10-719-900-687511 | Sequence 687511,  | Sequence 687511,   | C 202             | 15    | 39.5 | 25   | 7  | US-10-719-956-395203 | Sequence 395203,     |                   |
| C 130 | 16.6 | 43.7 | 25 | 8    | US-10-719-900-907199 | Sequence 907199,  | Sequence 907199,   | C 203             | 15    | 39.5 | 25   | 8  | US-10-719-900-410035 | Sequence 410035,     |                   |
| C 131 | 16.6 | 43.7 | 47 | 6    | US-10-170-097-1046   | Sequence 1046, Ap | Sequence 1046, Ap  | C 204             | 15    | 39.5 | 25   | 8  | US-10-719-900-427817 | Sequence 427817,     |                   |
| C 132 | 16.6 | 43.7 | 47 | 8    | US-10-926-684-1046   | Sequence 1046, Ap | Sequence 1046, Ap  | C 205             | 15    | 39.5 | 25   | 8  | US-10-719-900-595944 | Sequence 595944,     |                   |
| C 133 | 16.4 | 43.2 | 25 | 7    | US-10-719-956-46282  | Sequence 46282, A | Sequence 46282, A  | C 206             | 15    | 39.5 | 25   | 8  | US-10-719-900-687512 | Sequence 687512,     |                   |
| C 134 | 16.4 | 43.2 | 41 | 7    | US-10-035-833A-410   | Sequence 410, App | Sequence 410, App  | C 207             | 15    | 39.5 | 25   | 10 | US-10-719-900-907200 | Sequence 907200,     |                   |
| C 135 | 16.4 | 43.2 | 41 | 7    | US-10-035-833A-6556  | Sequence 6556, Ap | Sequence 6556, Ap  | C 208             | 15    | 39.5 | 25   | 10 | US-11-036-317-98328  | Sequence 98328, A    |                   |
| C 136 | 16.2 | 42.6 | 25 | 7    | US-10-681-773-42889  | Sequence 42889, A | Sequence 42889, A  | C 209             | 15    | 39.5 | 25   | 10 | US-11-036-317-167249 | Sequence 167249,     |                   |
| C 137 | 16.2 | 42.6 | 25 | 7    | US-10-681-773-42890  | Sequence 42890, A | Sequence 42890, A  | C 210             | 15    | 39.5 | 25   | 10 | US-11-036-317-219733 | Sequence 219733,     |                   |
| C 138 | 16.2 | 42.6 | 25 | 7    | US-10-681-773-96774  | Sequence 96774, A | Sequence 96774, A  | C 211             | 15    | 39.5 | 25   | 10 | US-11-036-317-345805 | Sequence 345805,     |                   |
| C 139 | 16.2 | 42.6 | 25 | 7    | US-10-681-773-96775  | Sequence 96775, A | Sequence 96775, A  | C 212             | 15    | 39.5 | 25   | 10 | US-11-036-317-354890 | Sequence 354890,     |                   |
| C 140 | 16.2 | 42.6 | 41 | 7    | US-10-035-833A-1001  | Sequence 1001, Ap | Sequence 1001, Ap  | C 213             | 15    | 39.5 | 25   | 10 | US-11-036-317-426282 | Sequence 426282,     |                   |
| C 141 | 16.2 | 42.6 | 41 | 7    | US-10-035-833A-6896  | Sequence 6896, Ap | Sequence 6896, Ap  | C 214             | 15    | 39.5 | 25   | 10 | US-11-036-317-474393 | Sequence 474393,     |                   |
| C 142 | 16   | 42.1 | 25 | 7    | US-10-719-956-140710 | Sequence 140710,  | Sequence 140710,   | C 215             | 15    | 39.5 | 25   | 10 | US-11-036-317-705651 | Sequence 705651,     |                   |
| C 143 | 16   | 42.1 | 25 | 8    | US-10-719-900-180328 | Sequence 180328,  | Sequence 180328,   | C 216             | 15    | 39.5 | 25   | 10 | US-11-036-317-777918 | Sequence 777918,     |                   |
| C 144 | 16   | 42.1 | 25 | 8    | US-10-719-900-594649 | Sequence 594649,  | Sequence 594649,   | C 217             | 15    | 39.5 | 25   | 10 | US-11-036-317-777919 | Sequence 777919,     |                   |
| C 145 | 16   | 42.1 | 25 | 8    | US-11-036-317-261860 | Sequence 261860,  | Sequence 261860,   | C 218             | 15    | 39.5 | 25   | 10 | US-11-036-317-777919 | Sequence 777919,     |                   |
| C 146 | 16   | 42.1 | 25 | 10   | US-11-036-317-332512 | Sequence 332512,  | Sequence 332512,   | C 219             | 15    | 39.5 | 25   | 10 | US-11-060-756-274270 | Sequence 274270,     |                   |
| C 147 | 16   | 42.1 | 25 | 10   | US-11-036-317-394706 | Sequence 394706,  | Sequence 394706,   | C 220             | 15    | 39.5 | 31   | 3  | US-09-801-274-11427  | Sequence 1127, Ap    |                   |
| C 148 | 15.8 | 41.6 | 21 | 8    | US-10-751-736-10156  | Sequence 10156, A | Sequence 10156, A  | C 221             | 15    | 39.5 | 31   | 3  | US-10-187-975-1137   | Sequence 130, App    |                   |
| C 149 | 15.8 | 41.6 | 21 | 8    | US-10-751-736-10157  | Sequence 10157, A | Sequence 10157, A  | C 222             | 15    | 39.5 | 31   | 3  | US-10-214-417A-75    | Sequence 75, Appl    |                   |
| C 150 | 15.8 | 41.6 | 25 | 8    | US-10-719-900-211217 | Sequence 211217,  | Sequence 211217,   | C 223             | 14.8  | 38.9 | 22   | 6  | US-10-098-263B-74178 | Sequence 74178, A    |                   |
| C 151 | 15.8 | 41.6 | 28 | 7    | US-10-416-914A-70    | Sequence 70, Appl | Sequence 70, Appl  | C 224             | 14.8  | 38.9 | 25   | 7  | US-10-681-773-1648   | Sequence 1648, Ap    |                   |
| C 152 | 15.8 | 41.6 | 47 | 8    | US-10-015-989A-36    | Sequence 36, Appl | Sequence 36, Appl  | C 225             | 14.8  | 38.9 | 25   | 7  | US-10-681-773-37265  | Sequence 37265, A    |                   |
| C 153 | 15.6 | 41.1 | 25 | 5    | US-10-098-263B-53836 | Sequence 53836, A | Sequence 53836, A  | C 226             | 14.8  | 38.9 | 25   | 7  | US-10-681-773-40488  | Sequence 40488, A    |                   |
| C 154 | 15.6 | 41.1 | 25 | 7    | US-10-719-956-287898 | Sequence 287898,  | Sequence 287898,   | C 227             | 14.8  | 38.9 | 25   | 7  | US-10-681-773-46450  | Sequence 46450, A    |                   |
| C 155 | 15.6 | 41.1 | 25 | 7    | US-10-719-956-629690 | Sequence 629690,  | Sequence 629690,   | C 228             | 14.8  | 38.9 | 25   | 7  | US-10-719-956-46281  | Sequence 46281, A    |                   |
| C 156 | 15.6 | 41.1 | 25 | 9    | US-10-956-157-319640 | Sequence 319640,  | Sequence 319640,   | C 229             | 14.8  | 38.9 | 25   | 7  | US-10-719-956-406592 | Sequence 406592,     |                   |
| C 157 | 15.6 | 41.1 | 25 | 10   | US-11-036-317-248960 | Sequence 248960,  | Sequence 248960,   | C 230             | 14.8  | 38.9 | 25   | 7  | US-10-719-956-654896 | Sequence 654896,     |                   |
| C 158 | 15.6 | 41.1 | 25 | 10   | US-11-036-317-309493 | Sequence 309493,  | Sequence 309493,   | C 231             | 14.8  | 38.9 | 25   | 7  | US-10-719-900-776952 | Sequence 776952,     |                   |
| C 159 | 15.6 | 41.1 | 25 | 10   | US-11-036-317-457857 | Sequence 457857,  | Sequence 457857,   | C 232             | 14.8  | 38.9 | 25   | 10 | US-11-060-756-190043 | Sequence 190043,     |                   |
| C 160 | 15.6 | 41.1 | 25 | 10   | US-11-036-317-555463 | Sequence 555463,  | Sequence 555463,   | C 233             | 14.8  | 38.9 | 34   | 6  | US-10-292-896-85     | Sequence 85, Appl    |                   |
| C 161 | 15.4 | 40.5 | 21 | 8    | US-10-751-736-10039  | Sequence 10039, A | Sequence 10039, A  | C 234             | 14.8  | 38.9 | 34   | 6  | US-10-705-401-82     | Sequence 82, Appl    |                   |
| C 162 | 15.4 | 40.5 | 21 | 8    | US-10-751-736-10040  | Sequence 10040, A | Sequence 10040, A  | C 235             | 14.8  | 38.9 | 37   | 3  | US-09-864-785-1772   | Sequence 1772, Ap    |                   |
| C 163 | 15.4 | 40.5 | 25 | 3    | US-09-955-524-4      | Sequence 4, Appli | Sequence 4, Appli  | C 236             | 14.8  | 38.9 | 39   | 7  | US-10-423-688A-37    | Sequence 37, Appl    |                   |
| C 164 | 15.4 | 40.5 | 25 | 5    | US-10-098-263B-95686 | Sequence 95686, A | Sequence 95686, A  | C 237             | 14.8  | 38.9 | 45   | 6  | US-10-400-670-3      | Sequence 3, Appli    |                   |
| C 165 | 15.4 | 40.5 | 25 | 7    | US-10-719-956-255572 | Sequence 255572,  | Sequence 255572,   | C 238             | 14.8  | 38.9 | 45   | 6  | US-10-400-670-3      | Sequence 3, Appli    |                   |
| C 166 | 15.4 | 40.5 | 25 | 7    | US-10-719-956-330869 | Sequence 330869,  | Sequence 330869,   | C 239             | 14.8  | 38.9 | 49   | 9  | US-10-973-783-182    | Sequence 182, App    |                   |
| C 167 | 15.4 | 40.5 | 25 | 7    | US-10-719-956-358894 | Sequence 358894,  | Sequence 358894,   | C 240             | 14.6  | 38.4 | 24   | 3  | US-09-940-185-403    | Sequence 403, App    |                   |
| C 168 | 15.4 | 40.5 | 25 | 7    | US-10-719-956-358895 | Sequence 358895,  | Sequence 358895,   | C 241             | 14.6  | 38.4 | 25   | 3  | US-09-940-185-4378   | Sequence 4378, Ap    |                   |
| C 169 | 15.4 | 40.5 | 25 | 7    | US-10-719-956-419087 | Sequence 419087,  | Sequence 419087,   | C 242             | 14.6  | 38.4 | 25   | 7  | US-10-681-773-71138  | Sequence 71138, A    |                   |

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290 14.6 38.4 25 9 US-10-809-189-50814
291 14.6 38.4 25 9 US-10-809-189-50814
292 14.6 38.4 25 9 US-10-809-189-50814
293 14.6 38.4 25 9 US-10-809-189-50814
294 14.6 38.4 25 9 US-10-809-189-50814
295 14.6 38.4 25 9 US-10-809-189-50814
296 14.6 38.4 25 9 US-10-809-189-50814
297 14.6 38.4 25 9 US-10-809-189-50814
298 14.6 38.4 25 9 US-10-809-189-50814
299 14.6 38.4 25 9 US-10-809-189-50814
300 14.6 38.4 25 9 US-10-809-189-50814
```

## ALIGNMENTS

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RESULT 1
US-09-888-326-417
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 417
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-417
```

```
Query Match 100.0%; Score 38; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
```

```
RESULT 2
US-09-776-479-148
; Sequence 148, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-148
```

```
Query Match 100.0%; Score 38; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
```

```
RESULT 3
US-09-776-479-148
; Sequence 148, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
```

```
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-148

Query Match      100.0%; Score 38; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38
      |||||||
Db      1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38

RESULT 4
US-10-112-653-141
; Sequence 141, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060 (AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 141
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-141

Query Match      100.0%; Score 38; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38
      |||||||
Db      1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38

RESULT 5
US-10-017-995-148
; Sequence 148, Application US/10017995
; Publication No. US2003005014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; FILE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-148

Query Match      100.0%; Score 38; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38
      |||||||
Db      1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38

RESULT 6
US-10-314-578-148
; Sequence 148, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-148

Query Match      100.0%; Score 38; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38
      |||||||
Db      1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38

RESULT 7
US-10-831-778-148
; Sequence 148, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourton, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-148
```



## US-10-831-778-148

Query Match 100.0%; Score 38; DB 8; Length 38;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACTTCC 38  
|||||  
Db 1 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACTTCC 38

## RESULT 8

US-08-860-844-29  
; Sequence 29, Application US/08860844  
; Publication No. US20030104361A1  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,844  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/353,476  
; FILING DATE: 09-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-860-844-29

Query Match 81.1%; Score 30.8; DB 2; Length 43;  
Best Local Similarity 94.1%; Pred. No. 0.019;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACT 34  
|||||  
Db 6 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACT 39

## RESULT 9

US-10-407-543-29  
; Sequence 29, Application US/10407543  
; Publication No. US20030175789A1  
; GENERAL INFORMATION:

APPLICANT: Weininger, Susan  
Weininger, Arthur M  
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
SPECIFIC SEQUENCE COMPOSITION  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/407,543  
FILING DATE: 03-Apr-2003  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,844  
FILING DATE: 09-JUN-1997  
APPLICATION NUMBER: 08/353,476  
FILING DATE: 09-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-10-407-543-29

Query Match 81.1%; Score 30.8; DB 6; Length 43;  
Best Local Similarity 94.1%; Pred. No. 0.019;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACT 34  
|||||  
Db 6 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACT 39

## RESULT 10

US-08-860-844-28  
; Sequence 28, Application US/08860844  
; Publication No. US20030104361A1  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-28
;
; Query Match 79.5%; Score 30.2; DB 2; Length 46;
; Best Local Similarity 91.4%; Pred. No. 0.032;
; Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
QY 1 GGGGACTTCCGCTGGGGACTTCCAGGGGGACTT 35
| | | | | | | | | | | | | | | | | | | |
Db 6 GGGGACTTCCGCTGGGGACTTCCAGGGGGGCGT 40
| | | | | | | | | | | | | | | | | | | |

RESULT 11
US-10-407-543-28
; Sequence 28, Application US/10407543
; Publication No. US20030175789A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/407,543
; FILING DATE: 03-APR-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
;
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-992-837-9
;
; Query Match 78.4%; Score 29.8; DB 3; Length 44;
; Best Local Similarity 93.9%; Pred. No. 0.046;
; Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 2 GGGACTTCCGCTGGGGACTTCCAGGGGGACT 34
| | | | | | | | | | | | | | | | | | | |
Db 10 GGGACTTCCGCTGGGGACTTCCAGGGGAGCT 42
| | | | | | | | | | | | | | | | | | | |

RESULT 12
US-09-992-837-9
; Sequence 9, Application US/09992837
; Publication No. US20030039705A1
; GENERAL INFORMATION:
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: BLAKE, MARY E.
; APPLICANT: GUTTERMAN, JORDAN U.
; APPLICANT: HOFFMANN, JOSEPH J.
; APPLICANT: BAILEY, DAVID T.
; APPLICANT: JAYATILAKE, GAMINI S.
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: CLFR:006
; CURRENT APPLICATION NUMBER: US/09/992,837
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/314,691
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/085,997
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; US-09-992-837-9
;
; Query Match 79.5%; Score 30.2; DB 6; Length 46;
; Best Local Similarity 91.4%; Pred. No. 0.032;
; Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
QY 1 GGGGACTTCCGCTGGGGACTTCCAGGGGGACTT 35
| | | | | | | | | | | | | | | | | | | |
Db 6 GGGGACTTCCGCTGGGGACTTCCAGGGGGGCGT 40
| | | | | | | | | | | | | | | | | | | |

RESULT 13
US-09-999-495-9
; Sequence 9, Application US/09999495
; Publication No. US20030054052A1
; GENERAL INFORMATION:
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: BLAKE, MARY E.
; APPLICANT: GUTTERMAN, JORDAN U.
; APPLICANT: HOFFMANN, JOSEPH J.
; APPLICANT: BAILEY, DAVID T.
;
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-10-407-543-28
;
; Query Match 79.5%; Score 30.2; DB 6; Length 46;
; Best Local Similarity 91.4%; Pred. No. 0.032;
; Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
QY 1 GGGGACTTCCGCTGGGGACTTCCAGGGGGACTT 35
| | | | | | | | | | | | | | | | | | | |
Db 6 GGGGACTTCCGCTGGGGACTTCCAGGGGGGCGT 40
| | | | | | | | | | | | | | | | | | | |
```

```

; APPLICANT: JAYATILAKE, GAMINI S.
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: CLFR:006
; CURRENT APPLICATION NUMBER: US/09/999,495
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/314,691
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/099,066
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/085,997
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-999-495-9

Query Match      78.4%; Score 29.8; DB 3; Length 44;
Best Local Similarity 93.9%; Pred. No. 0.046; 2; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 0;

QY      2 GGGACTTTCGCTGGGACTTTCAGGGGACT 34
Db      10 GGGACTTTCGCTGGGACTTTCAGGGGACT 42
|||||
RESULT 14
US-10-000-720-9
; Sequence 9, Application US/10000720
; Publication No. US20030031738A1
; GENERAL INFORMATION:
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: BLAKE, MARY E.
; APPLICANT: GUTTERMAN, JORDAN U.
; APPLICANT: HOFFMANN, JOSEPH J.
; APPLICANT: BAILEY, DAVID T.
; APPLICANT: JAYATILAKE, GAMINI S.
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: CLFR:006
; CURRENT APPLICATION NUMBER: US/10/000,720
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/314,691
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,066
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/085,997
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-000-720-9

Query Match      78.4%; Score 29.8; DB 5; Length 44;
Best Local Similarity 93.9%; Pred. No. 0.046; 2; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 0;

QY      2 GGGACTTTCGCTGGGACTTTCAGGGGACT 34
Db      10 GGGACTTTCGCTGGGACTTTCAGGGGACT 42
|||||
RESULT 15
```

```

US-10-238-647-9
; Sequence 9, Application US/10238647
; Publication No. US20030203049A1
; GENERAL INFORMATION:
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: BLAKE, MARY E.
; APPLICANT: GUTTERMAN, JORDAN U.
; APPLICANT: HOFFMANN, JOSEPH J.
; APPLICANT: BAILEY, DAVID T.
; APPLICANT: JAYATILAKE, GAMINI S.
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: CLFR:006
; CURRENT APPLICATION NUMBER: US/10/238,647
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US/09/314,691
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-238-647-9

Query Match      78.4%; Score 29.8; DB 6; Length 44;
Best Local Similarity 93.9%; Pred. No. 0.046; 2; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 0;

QY      2 GGGACTTTCGCTGGGACTTTCAGGGGACT 34
Db      10 GGGACTTTCGCTGGGACTTTCAGGGGACT 42
|||||
RESULT 16
US-08-860-844-19
; Sequence 19, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
```

INFORMATION FOR SEQ ID NO: 19;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 45 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-860-844-19

Query Match 76.8%; Score 29.2; DB 2; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.08;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTTCACGGGGACTT 35  
 DB 7 GGGACTTCCGCTGGGGACTTTCACGGGGACTT 40

RESULT 17  
 US-08-860-844-23  
 ; Sequence 23, Application US/08860844  
 ; Publication No. US20030104361A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weininger, Susan M  
 ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st St., Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/08/860,844  
 ; FILING DATE: 09-JUN-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/353,476  
 ; FILING DATE: 09-DEC-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 35,746  
 ; REFERENCE/DOCKET NUMBER: GP-100C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (352) 375-8100  
 ; TELEFAX: (352) 372-5800  
 ; INFORMATION FOR SEQ ID NO: 23:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 US-08-860-844-23

Query Match 76.8%; Score 29.2; DB 2; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.08;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTTCACGGGGACTT 35  
 DB 7 GGGACTTCCGCTGGGGACTTTCACGGGGACTT 40

RESULT 18  
 US-10-407-543-19  
 ; Sequence 19, Application US/10407543  
 ; Publication No. US20030175789A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weininger, Susan M  
 ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st St., Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/10/407,543  
 ; FILING DATE: 03-APR-2003  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/860,844  
 ; FILING DATE: 09-JUN-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 35,746  
 ; REFERENCE/DOCKET NUMBER: GP-100C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (352) 375-8100  
 ; TELEFAX: (352) 372-5800  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 US-10-407-543-19

Query Match 76.8%; Score 29.2; DB 6; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.08;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTTCACGGGGACTT 35  
 DB 7 GGGACTTCCGCTGGGGACTTTCACGGGGACTT 40

RESULT 19  
 US-10-407-543-23  
 ; Sequence 23, Application US/10407543  
 ; Publication No. US20030175789A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weininger, Susan M  
 ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 ; NUMBER OF SEQUENCES: 118

Db 7 GGGACTTCCGCTGGGGACTTTCACGGGGACTT 40

RESULT 18  
 US-10-407-543-19  
 ; Sequence 19, Application US/10407543  
 ; Publication No. US20030175789A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weininger, Susan M  
 ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st St., Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/10/407,543  
 ; FILING DATE: 03-APR-2003  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/860,844  
 ; FILING DATE: 09-JUN-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 35,746  
 ; REFERENCE/DOCKET NUMBER: GP-100C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (352) 375-8100  
 ; TELEFAX: (352) 372-5800  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 US-10-407-543-19

QY 2 GGGACTTCCGCTGGGGACTTTCACGGGGACTT 35  
 DB 7 GGGACTTCCGCTGGGGACTTTCACGGGGACTT 40

RESULT 19  
 US-10-407-543-23  
 ; Sequence 23, Application US/10407543  
 ; Publication No. US20030175789A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weininger, Susan M  
 ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 ; NUMBER OF SEQUENCES: 118



```
RESULT 23
US-08-860-844-20
; Sequence 20, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-20

Query Match 76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACGGG 30
| | | | | | | | | | | | | | | | | |
Db 7 GGGACTTTCGGCTGGGACTTTCACGGG 35

RESULT 24
US-08-860-844-21
; Sequence 21, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-20

Query Match 76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACGGG 30
| | | | | | | | | | | | | | | | | |
Db 7 GGGACTTTCGGCTGGGACTTTCACGGG 35

RESULT 25
US-08-860-844-22
; Sequence 22, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
```

```
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-21

Query Match 76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACGGG 30
| | | | | | | | | | | | | | | | | |
Db 7 GGGACTTTCGGCTGGGACTTTCACGGG 35

RESULT 25
US-08-860-844-22
; Sequence 22, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
```

|   |   |                                     |
|---|---|-------------------------------------|
| Query Match   |   | 76.3%; Score 29; DB 2; Length 46;   |
| Best Local Similarity   |   | 100.0%; Pred. No. 0.096;            |
| Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;       |   |                                     |
| <br>  |   |                                     |
| QY  | 2 | GCGACTTTCGCTGGGGAGCTTTCCAGGG 30<br> |
| Db  | 7 | GCGACTTTCGCTGGGGAGCTTTCCAGGG 35<br> |
| <br>  |   |                                     |
| RESULT 27   |   |                                     |
| US-10-407-543-20  |   |                                     |
| ; Sequence 20, Application US/10407543                            |   |                                     |
| ; Publication No. US20030175789A1                                 |   |                                     |
| ; GENERAL INFORMATION:  |   |                                     |
| ; APPLICANT: Weininger, Susan                                     |   |                                     |
| ; Weininger, Arthur M   |   |                                     |
| ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A |   |                                     |
| ; SPECIFIC SEQUENCE COMPOSITION                                   |   |                                     |
| ; NUMBER OF SEQUENCES: 118  |   |                                     |
| ; CORRESPONDENCE ADDRESS:   |   |                                     |
| ; ADDRESSEE: Saliwanchik & Saliwanchik                            |   |                                     |
| ; STREET: 2421 N.W. 41st St., Suite A-1                           |   |                                     |
| ; CITY: Gainesville   |   |                                     |
| ; STATE: Florida  |   |                                     |
| ; COUNTRY: USA  |   |                                     |
| ; ZIP: 32606  |   |                                     |
| ; COMPUTER READABLE FORM:   |   |                                     |
| ; MEDIUM TYPE: Floppy disk  |   |                                     |
| ; COMPUTER: IBM PC compatible                                     |   |                                     |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS                                 |   |                                     |
| ; SOFTWARE: PatentIn Release #1.0, Version #1.25                  |   |                                     |
| ; CURRENT APPLICATION DATA:                                       |   |                                     |
| ; FILING DATE: 03-Apr-2003  |   |                                     |
| ; APPLICATION NUMBER: US/10/407,543                               |   |                                     |
| ; CLASSIFICATION: 435   |   |                                     |
| ; PRIOR APPLICATION DATA:   |   |                                     |
| ; APPLICATION NUMBER: US/08/860,844                               |   |                                     |
| ; FILING DATE: 09-JUN-1997  |   |                                     |
| ; APPLICATION NUMBER: 08/353,476                                  |   |                                     |
| ; FILING DATE: 09-DEC-1994  |   |                                     |
| ; ATTORNEY/AGENT INFORMATION:                                     |   |                                     |
| ; NAME: Saliwanchik, David R.                                     |   |                                     |
| ; REGISTRATION NUMBER: 35,746                                     |   |                                     |
| ; REFERENCE/DOCKET NUMBER: GP-100C1                               |   |                                     |
| ; TELECOMMUNICATION INFORMATION:                                  |   |                                     |
| ; TELEPHONE: (352) 375-8100                                       |   |                                     |
| ; TELEFAX: (352) 372-5800   |   |                                     |
| ; INFORMATION FOR SEQ ID NO: 20:                                  |   |                                     |
| ; SEQUENCE CHARACTERISTICS:                                       |   |                                     |
| ; LENGTH: 46 base pairs   |   |                                     |
| ; TYPE: nucleic acid  |   |                                     |
| ; STRANDEDNESS: both  |   |                                     |
| ; TOPOLOGY: linear  |   |                                     |
| ; MOLECULE TYPE: cDNA   |   |                                     |
| ; HYPOTHETICAL: NO  |   |                                     |
| ; ANTI-SENSE: NO  |   |                                     |
| ; SEQUENCE DESCRIPTION: SEQ ID NO: 20:                            |   |                                     |
| US-10-407-543-20  |   |                                     |
| <br>  |   |                                     |
| Query Match   |   | 76.3%; Score 29; DB 6; Length 46;   |
| Best Local Similarity   |   | 100.0%; Pred. No. 0.096;            |
| Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;       |   |                                     |
| <br>  |   |                                     |
| QY  | 2 | GCGACTTTCGCTGGGGAGCTTTCCAGGG 30<br> |
| Db  | 7 | GCGACTTTCGCTGGGGAGCTTTCCAGGG 35<br> |
| <br>  |   |                                     |
| RESULT 28   |   |                                     |
| US-10-407-543-21  |   |                                     |
| ; Sequence 21, Application US/10407543                            |   |                                     |
| ; Publication No. US20030175789A1                                 |   |                                     |
| ; GENERAL INFORMATION:  |   |                                     |





|   |        |                             |       |               |           |         |        |                 |       |               |           |         |
|---|--------|-----------------------------|-------|---------------|-----------|---------|--------|-----------------|-------|---------------|-----------|---------|
| Query Match   | 74.7%; | Score 28.4;                 | DB 2; | Length 37;    |           |         |        |                 |       |               |           |         |
| Best Local Similarity   | 96.7%; | Pred. No. 0.17;             |       |               |           |         |        |                 |       |               |           |         |
| Matches   | 29;    | Conservative                | 0;    | Mismatches 1; | Indels 0; | Gaps 0; |        |                 |       |               |           |         |
| Qy  | 2      | GGGACTTTCGCTGGGGACTTTCAGGGG | 31    |               |           |         |        |                 |       |               |           |         |
| Db  | 7      | GGGACTTTCGCTGGGGACTTTCAGGGG | 36    |               |           |         |        |                 |       |               |           |         |
| RESULT 32   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| US-10-407-543-38  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; Sequence 38, Application US/10407543                            |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; Publication No. US20030175789A1                                 |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; GENERAL INFORMATION:  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; APPLICANT: Weininger, Susan                                     |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; SPECIFIC SEQUENCE COMPOSITION                                   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; NUMBER OF SEQUENCES: 118  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; CORRESPONDENCE ADDRESS:   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; ADDRESSEE: Saliwanchik & Saliwanchik                            |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; STREET: 2421 N.W. 41st St., Suite A-1                           |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; CITY: Gainesville   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; STATE: Florida  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; COUNTRY: USA  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; ZIP: 32606  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; COMPUTER READABLE FORM:   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; MEDIUM TYPE: Floppy disk  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; COMPUTER: IBM PC compatible                                     |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS                                 |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; SOFTWARE: Patent In Release #1.0, Version #1.25                 |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; CURRENT APPLICATION DATA:                                       |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; APPLICATION NUMBER: US/10/407,543                               |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; FILING DATE: 03-Apr-2003  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; CLASSIFICATION: 435   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; PRIOR APPLICATION DATA:   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; APPLICATION NUMBER: US/08/860,844                               |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; FILING DATE: 09-JUN-1997  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; APPLICATION NUMBER: 08/353,476                                  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; FILING DATE: 09-DEC-1994  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; ATTORNEY/AGENT INFORMATION:                                     |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; NAME: Saliwanchik, David R.                                     |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; REGISTRATION NUMBER: 35,746                                     |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; REFERENCE/DOCKET NUMBER: GP-100C1                               |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; TELECOMMUNICATION INFORMATION:                                  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; TELEPHONE: (352) 375-8100                                       |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; TELEFAX: (352) 372-5800   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; INFORMATION FOR SEQ ID NO: 38:                                  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; SEQUENCE CHARACTERISTICS:                                       |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; LENGTH: 37 base pairs   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; TYPE: nucleic acid  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; STRANDEDNESS: both  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; TOPOLOGY: linear  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; MOLECULE TYPE: cdna   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; HYPOTHETICAL: NO  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; ANTI-SENSE: NO  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; SEQUENCE DESCRIPTION: SEQ ID NO: 38:                            |        |                             |       |               |           |         |        |                 |       |               |           |         |
| US-10-407-543-38  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| Query Match   |        |                             |       |               |           |         | 74.7%; | Score 28.4;     | DB 6; | Length 37;    |           |         |
| Best Local Similarity   |        |                             |       |               |           |         | 96.7%; | Pred. No. 0.17; |       |               |           |         |
| Matches   |        |                             |       |               |           |         | 29;    | Conservative    | 0;    | Mismatches 1; | Indels 0; | Gaps 0; |
| Qy  | 2      | GGGACTTTCGCTGGGGACTTTCAGGGG | 31    |               |           |         |        |                 |       |               |           |         |
| Db  | 7      | GGGACTTTCGCTGGGGACTTTCAGGGG | 36    |               |           |         |        |                 |       |               |           |         |
| RESULT 33   |        |                             |       |               |           |         |        |                 |       |               |           |         |
| US-10-037-341-53  |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; Sequence 53, Application US/10037341                            |        |                             |       |               |           |         |        |                 |       |               |           |         |
| ; Publication No. US20040214757A1                                 |        |                             |       |               |           |         |        |                 |       |               |           |         |

```

Query Match          72.6%; Score 27.6; DB 2; Length 45;
Best Local Similarity 88.2%; Pred. No. 0.34;
Matches 30; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 GGGACTTTCCGCTGGGGACTTTCCAGGGGGACTT 35
          |||||
Db       7 GGGACTTTCCGCTGGGGACTTTCCAGAGAGCGCT 40

RESULT 35
US-10-407-543-26
; Sequence 26, Application US/10407543
; Publication No. US20030175789A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
;

```

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 SPECIFIC SEQUENCE COMPOSITION  
 NUMBER OF SEQUENCES: 118

ADDRESS: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville

```

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,543
FILING DATE: 03-Apr-2003
CLASSIFICATION: 435
PRIORITY INFORMATION:
APPLICATION NUMBER: US/08/860,844
FILING DATE: 09-JUN-1997
APPLICATION NUMBER: 08/353,476
FILING DATE: 03-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.

```

REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs

```

; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-407-543-26

Query Match 72.6%; Score 27.6; DB 6; Length 45;
Best Local Similarity 88.2%; Pred. No. 0.34;
Matches 30; Conservative 0; Mismatches 4; Indels

```

RESULT 36  
US-10-235-682-9/c  
; Sequence 9, Application US/10235682  
; Publication No. US20030108523A1  
; GENERAL INFORMATION:

APPLICANT: Lipton, James  
APPLICANT: Catania, Anna P.  
TITLE OF INVENTION: A CANCER TREATMENT SYSTEM  
FILE REFERENCE: 8022 US01  
CURRENT APPLICATION NUMBER: US/10/235,682  
CURRENT FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/317,514  
PRIOR FILING DATE: 2002-09-05  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 35  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: NF-kappa B DNA binding site, negative strand  
US-10-235-682-9

Query Match 72.1%; Score 27.4; DB 5; Length 35;  
Best Local Similarity 96.6%; Pred. No. 0.41;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACTTTCGGCTGGGACTTCCAGGG 29  
Db 32 GGGACTTTCGGCTGGGACTTTCATGG 4

RESULT 37  
US-08-860-844-24  
; Sequence 24, Application US/08860844  
; Publication No. US20030104361A1  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,844  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/353,476  
; FILING DATE: 09-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100C1  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

US-08-860-844-24  
Query Match 72.1%; Score 27.4; DB 2; Length 44;  
Best Local Similarity 83.8%; Pred. No. 0.41;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGACTTTCAGGGGACTTTC 38  
Db 7 GGGACTTTCGGCTGGGACTTTCAGGGGAGCGTGGCC 43

RESULT 38  
US-10-407-543-24  
; Sequence 24, Application US/10407543  
; Publication No. US20030175789A1  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/407,543  
; FILING DATE: 03-Apr-2003  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,844  
; FILING DATE: 09-JUN-1997  
; APPLICATION NUMBER: 08/353,476  
; FILING DATE: 09-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100C1  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-10-407-543-24

Query Match 72.1%; Score 27.4; DB 6; Length 44;  
Best Local Similarity 83.8%; Pred. No. 0.41;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGACTTTCAGGGGACTTTC 38  
Db 7 GGGACTTTCGGCTGGGACTTTCAGGGGAGCGTGGCC 43

RESULT 39  
US-08-860-844-25  
; Sequence 25, Application US/08860844

```

; Publication No. US20030104361A1
;
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; NUMBER OF SEQUENCES: 118
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
;
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
; US-08-860-844-25
;
; Query Match 71.6%; Score 27.2; DB 2; Length 44;
; Best Local Similarity 90.6%; Pred No. 0, 49;
; Matches 29; Conservative 0; Mismatches 3; Indels 0;
;
; QY 2 GGGACTTCCGCTGGGGACTTTCACAGGGGAC 33
; | | | | | | | | | | | | | | | | | |
; Db 7 GGGACTTCCGCTGGGGACTTTCGCGGGAGGC 38
; | | | | | | | | | | | | | | | | | |
;
; RESULT 40
; US-10-407-543-25
; Sequence 25, Application US/10407543
; Publication No. US20030175789A1
;
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/407,543
; FILING DATE: 03-APR-2003
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
;
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
;
; US-10-407-543-25
;
; Query Match 71.6%; Score 27.2; DB 6; Length 44;
; Best Local Similarity 90.6%; Pred. No. 0.49;
; Matches 29; Conservative 0; Mismatches 3; Indels 0;
;
; Qy 2 GGGACTTTCGCTGGGGACTTTCAGGGGAC 33
; Db 7 GGGACTTTCGCTGGGGACTTTCGGGGAGGC 38
;
; RESULT 41
; US-10-235-682-8
; Sequence 8, Application US/10235682
; Publication No. US20030108523A1
; GENERAL INFORMATION:
; APPLICANT: Lipton, James
; APPLICANT: Catania, Anna P.
; TITLE OF INVENTION: A CANCER TREATMENT SYSTEM
; FILE REFERENCE: 8022.US01
; CURRENT APPLICATION NUMBER: US/10/235,682
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/317,514
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NF-kappa B DNA binding site, positive strand
;
; US-10-235-682-8
;
; Query Match 69.5%; Score 26.4; DB 5; Length 35;
; Best Local Similarity 96.4%; Pred. No. 1;
; Matches 27; Conservative 0; Mismatches 1; Indels 0;
;
; Qy 1 GGGGACTTTCGGCTGGGGACTTTCACGG 28
; Db 8 GGGGACTTTCGGCTGGGGACTTTCATG 35
;
; RESULT 42

```

US-10-659-053-11  
; Sequence 11, Application US/10659053  
; Publication No. US20050037032A1  
; GENERAL INFORMATION:  
; APPLICANT: ZENGEN, INC.  
; APPLICANT: Catania, Anna P.  
; APPLICANT: Lipton, James M.  
; TITLE OF INVENTION: A COMPOSITION AND METHOD OF TREATMENT FOR UROGENITAL CONDITIONS  
; FILE REFERENCE: 54275.8005.US03  
; CURRENT APPLICATION NUMBER: US/10/659,053  
; CURRENT FILING DATE: 2003-09-08  
; PRIOR APPLICATION NUMBER: US 09/535,066  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: US 60/126,233  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: US 10/442,683  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/382,887  
; PRIOR FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide probes for NF-KB.  
US-10-659-053-11

Query Match 69.5%; Score 26.4; DB 8; Length 35;  
Best Local Similarity 96.4%; Pred. No. 1;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGACTTTCGGCTGGGGACTTTCACG 28  
Db 8 GGGGACTTTCGGCTGGGGACTTTCACG 35

RESULT 43  
US-09-031-629A-5  
; Sequence 5, Application US/09031629A  
; Patent No. US20020106889A1  
; GENERAL INFORMATION:  
; APPLICANT: Faustman  
; APPLICANT: Havashi  
; TITLE OF INVENTION: Methods for Treating and Diagnosing Autoimmune Disease  
; FILE REFERENCE: MGH/Faustman 17633/1030  
; CURRENT APPLICATION NUMBER: US/09/031,629A  
; CURRENT FILING DATE: 1998-02-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Probe for  
; OTHER INFORMATION: wild-type kappa B1 sequence  
US-09-031-629A-5

Query Match 68.4%; Score 26; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGGACTTTCACG 27  
Db 7 GGGACTTTCGGCTGGGGACTTTCACG 32

RESULT 44  
US-10-775-487A-1  
; Sequence 1, Application US/10775487A  
; Publication No. US20050158302A1

; GENERAL INFORMATION:  
; APPLICANT: Faustman, Denise L.  
; APPLICANT: Havashi, Takuma  
; TITLE OF INVENTION: Methods For Diagnosing Autoimmune  
; TITLE OF INVENTION: Disease  
; FILE REFERENCE: 00786/457003  
; CURRENT APPLICATION NUMBER: US/10/775,487A  
; CURRENT FILING DATE: 2004-02-10  
; PRIOR APPLICATION NUMBER: 09/358,682  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 09/031,629  
; PRIOR FILING DATE: 1998-02-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-775-487A-1

Query Match 68.4%; Score 26; DB 9; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGGACTTTCACG 27  
Db 7 GGGACTTTCGGCTGGGGACTTTCACG 32

RESULT 45  
US-10-659-053-12/c  
; Sequence 12, Application US/10659053  
; Publication No. US20050037032A1  
; GENERAL INFORMATION:  
; APPLICANT: ZENGEN, INC.  
; APPLICANT: Catania, Anna P.  
; APPLICANT: Lipton, James M.  
; TITLE OF INVENTION: A COMPOSITION AND METHOD OF TREATMENT FOR UROGENITAL CONDITIONS  
; FILE REFERENCE: 54275.8005.US03  
; CURRENT APPLICATION NUMBER: US/10/659,053  
; CURRENT FILING DATE: 2003-09-08  
; PRIOR APPLICATION NUMBER: US 09/535,066  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: US 60/126,233  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: US 10/442,683  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/382,887  
; PRIOR FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide probes for NF-KB.  
US-10-659-053-12

Query Match 67.9%; Score 25.8; DB 8; Length 35;  
Best Local Similarity 93.1%; Pred. No. 1.8;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGACTTTCGGCTGGGGACTTTCACGG 29  
Db 32 GGGGAGTTTCGGCTGGGGACTTTCATGG 4

RESULT 46  
US-08-860-844-30  
; Sequence 30, Application US/08860844

```
/ Publication No. US20030104361A1
/ GENERAL INFORMATION:
/ APPLICANT: Weininger, Susan
/ APPLICANT: Weininger, Arthur M
/ TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
/ TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
/ NUMBER OF SEQUENCES: 118
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st St., Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM: disk
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US/08/860,844
/ FILING DATE: 09-JUN-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/353,476
/ FILING DATE: 09-DEC-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 35,746
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-08-860-844-30

Query Match 66.3%; Score 25.2; DB 2; Length 48;
Best Local Similarity 90.0%; Pred. No. 3;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTTTCGCTGGGACATTCACGGGGACTT 35
Db 1 CTTTCGCTGGGACATTCACGGGGAGCGT 30

RESULT 47
US-10-407-543-30
/ Sequence 30, Application US/10407543
/ Publication No. US20030175789A1
/ GENERAL INFORMATION:
/ APPLICANT: Weininger, Susan
/ APPLICANT: Weininger, Arthur M
/ TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
/ TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
/ NUMBER OF SEQUENCES: 118
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st St., Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US/08/860,844
/ FILING DATE: 09-JUN-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/353,476
/ FILING DATE: 09-DEC-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 35,746
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-407-543-30
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US/10/407,543
/ FILING DATE: 03-APR-2003
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/860,844
/ FILING DATE: 09-JUN-1997
/ APPLICATION NUMBER: 08/353,476
/ FILING DATE: 09-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 35,746
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-407-543-30

Query Match 66.3%; Score 25.2; DB 6; Length 48;
Best Local Similarity 90.0%; Pred. No. 3;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTTTCGCTGGGACATTCACGGGGACTT 35
Db 1 CTTTCGCTGGGACATTCACGGGGAGCGT 30

RESULT 48
US-08-860-844-7
/ Sequence 7, Application US/08860844
/ Publication No. US20030104361A1
/ GENERAL INFORMATION:
/ APPLICANT: Weininger, Susan
/ APPLICANT: Weininger, Arthur M
/ TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
/ TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
/ NUMBER OF SEQUENCES: 118
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st St., Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US/08/860,844
/ FILING DATE: 09-JUN-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/353,476
/ FILING DATE: 09-DEC-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 35,746
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; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-7

Query Match 65.8%; Score 25; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCCA 26
Db 3 GGGACTTTCGCTGGGACTTTCCA 27

RESULT 49
US-10-407-543-7
; Sequence 7, Application US/10407543
; Publication No. US20030175789A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/407,543
; FILING DATE: 03-Apr-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-407-543-7

; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-407-543-7

Query Match 65.8%; Score 25; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCCA 26
Db 3 GGGACTTTCGCTGGGACTTTCCA 27

RESULT 50
US-09-844-915-1
; Sequence 1, Application US/09844915
; Patent No. US20020048564A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Lu, Lina
; APPLICANT: Giannoukakis, Nick
; TITLE OF INVENTION: THE USE OF TOLEROGENIC DENDRITIC CELLS
; FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
; MAKING THE SAME
; FILE REFERENCE: AP32737 / 072396.0225
; CURRENT APPLICATION NUMBER: US/09/844,915
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,479
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleotide sequence
; US-09-844-915-1

Query Match 63.2%; Score 24; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 GGGACTTTCGCTGGGACTTTCC 25

Search completed: February 16, 2006, 02:34:12
Job time : 555.471 secs
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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 02:03:53 ; Search time 354.248 Seconds  
(without alignments)  
98.157 Million cell updates/sec

Title: US-09-669-187A-148

Perfect score: 38

Sequence: 1 ggggactttccgtgggactttccaggggactttccc 38

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 11812030

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA New:\*

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12: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description          |
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| 1          | 38    | 100.0         | 38     | 11 | US-11-127-654-141    |
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| 4          | 24    | 63.2          | 29     | 11 | US-11-116-746-12     |
| 5          | 23    | 60.5          | 23     | 8  | US-11-175-815-3      |
| 6          | 21.4  | 56.3          | 45     | 11 | US-11-179-321-2      |
| 7          | 21.4  | 56.3          | 45     | 11 | US-11-179-321-6      |
| 8          | 18    | 45.3          | 50     | 11 | US-11-175-859-100529 |
| 9          | 17.2  | 45.3          | 25     | 11 | US-11-136-527-200528 |
| C 10       | 17.2  | 45.3          | 50     | 11 | US-11-175-859-32817  |
| C 11       | 16.4  | 43.2          | 50     | 11 | US-11-175-859-66382  |
| C 12       | 16    | 42.1          | 25     | 11 | US-11-121-849-3916   |
| C 13       | 16    | 42.1          | 25     | 11 | US-11-121-849-43102  |
| C 14       | 15.6  | 41.1          | 25     | 11 | US-11-121-849-565799 |
| C 15       | 15.6  | 41.1          | 25     | 11 | US-11-136-527-273210 |
| C 16       | 15.6  | 41.1          | 25     | 11 | US-11-136-527-273212 |
| C 17       | 15.6  | 41.1          | 50     | 11 | US-11-175-859-21940  |
| C 18       | 15.4  | 40.5          | 25     | 11 | US-11-121-849-103498 |
| C 19       | 15.4  | 40.5          | 25     | 11 | US-11-121-849-260545 |
| C 20       | 15.4  | 40.5          | 25     | 11 | US-11-121-849-507340 |
| C 21       | 15.4  | 40.5          | 25     | 11 | US-11-121-849-528104 |
|            |       |               |        |    | Sequence 141, App    |
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|            |       |               |        |    | Sequence 5, Appli    |
|            |       |               |        |    | Sequence 12, Appl    |
|            |       |               |        |    | Sequence 3, Appli    |
|            |       |               |        |    | Sequence 2, Appli    |
|            |       |               |        |    | Sequence 6, Appli    |
|            |       |               |        |    | Sequence 100529,     |
|            |       |               |        |    | Sequence 200528,     |
|            |       |               |        |    | Sequence 32817, A    |
|            |       |               |        |    | Sequence 66382, A    |
|            |       |               |        |    | Sequence 3916, Ap    |
|            |       |               |        |    | Sequence 43102, A    |
|            |       |               |        |    | Sequence 565799,     |
|            |       |               |        |    | Sequence 273210,     |
|            |       |               |        |    | Sequence 273212,     |
|            |       |               |        |    | Sequence 21940, A    |
|            |       |               |        |    | Sequence 103498,     |
|            |       |               |        |    | Sequence 260545,     |
|            |       |               |        |    | Sequence 507340,     |
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| Sequence 2, Appli | US-11-032-236-2        | 41 | 11 | 40.5 | 15.4 |
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| Sequence 298241,  | US-10-310-914A-298241  | 23 | 7  | 40.0 | 15.2 |
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| Sequence 1226668, | US-10-310-914A-1226668 | 26 | 7  | 40.0 | 15.2 |
| Sequence 1383495, | US-10-310-914A-1383495 | 27 | 7  | 40.0 | 15.2 |
| Sequence 43456, A | US-11-175-859-43456    | 50 | 11 | 40.0 | 15.2 |
| Sequence 66764, A | US-11-175-859-66764    | 50 | 11 | 40.0 | 15.2 |
| Sequence 815249,  | US-10-310-914A-815249  | 24 | 7  | 39.5 | 15   |
| Sequence 196232,  | US-11-121-849-196232   | 25 | 11 | 39.5 | 15   |
| Sequence 378884,  | US-11-121-849-378884   | 25 | 11 | 39.5 | 15   |
| Sequence 510666,  | US-11-121-849-510666   | 25 | 11 | 39.5 | 15   |
| Sequence 280766,  | US-11-136-527-280766   | 25 | 11 | 39.5 | 15   |
| Sequence 314081,  | US-11-136-527-314081   | 25 | 11 | 39.5 | 15   |
| Sequence 318283,  | US-11-136-527-318283   | 25 | 11 | 39.5 | 15   |
| Sequence 358480,  | US-11-136-527-358480   | 25 | 11 | 39.5 | 15   |
| Sequence 11173, A | US-11-175-859-11173    | 50 | 11 | 39.5 | 15   |
| Sequence 74560, A | US-11-175-859-74560    | 50 | 11 | 39.5 | 15   |
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| Sequence 571272,  | US-11-121-849-571272   | 25 | 11 | 38.9 | 14.8 |
| Sequence 1145, Ap | US-11-175-859-1145     | 50 | 11 | 38.9 | 14.8 |
| Sequence 5345, Ap | US-11-175-859-5345     | 50 | 11 | 38.9 | 14.8 |
| Sequence 5396, Ap | US-11-175-859-5396     | 50 | 11 | 38.9 | 14.8 |
| Sequence 27611, A | US-11-175-859-27611    | 50 | 11 | 38.9 | 14.8 |
| Sequence 68699, A | US-11-175-859-68699    | 50 | 11 | 38.9 | 14.8 |
| Sequence 86367, A | US-11-175-859-86367    | 50 | 11 | 38.9 | 14.8 |
| Sequence 279653,  | US-10-310-914A-279653  | 21 | 7  | 38.4 | 14.6 |
| Sequence 905240,  | US-10-310-914A-905240  | 21 | 7  | 38.4 | 14.6 |
| Sequence 1244998, | US-10-310-914A-1244998 | 21 | 7  | 38.4 | 14.6 |
| Sequence 815248,  | US-10-310-914A-815248  | 22 | 7  | 38.4 | 14.6 |
| Sequence 400363,  | US-10-310-914A-400363  | 22 | 7  | 38.4 | 14.6 |
| Sequence 819776,  | US-10-310-914A-819776  | 24 | 7  | 38.4 | 14.6 |
| Sequence 915881,  | US-10-310-914A-915881  | 24 | 7  | 38.4 | 14.6 |
| Sequence 369219,  | US-11-121-849-369219   | 25 | 11 | 38.4 | 14.6 |
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| Sequence 577777,  | US-11-121-849-577777   | 25 | 11 | 38.4 | 14.6 |
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| Sequence 300956,  | US-10-310-914A-300956  | 23 | 7  | 37.9 | 14.4 |
| Sequence 856110,  | US-10-310-914A-856110  | 23 | 7  | 37.9 | 14.4 |
| Sequence 767653,  | US-10-310-914A-767653  | 24 | 7  | 37.9 | 14.4 |
| Sequence 860553,  | US-10-310-914A-860553  | 25 | 11 | 37.9 | 14.4 |
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| Sequence 454205,  | US-11-121-849-454205   | 25 | 11 | 37.9 | 14.4 |
| Sequence 139879,  | US-11-136-527-139879   | 25 | 11 | 37.9 | 14.4 |
| Sequence 139984,  | US-11-136-527-139984   | 25 | 11 | 37.9 | 14.4 |
| Sequence 213033,  | US-11-136-527-213033   | 25 | 11 | 37.9 | 14.4 |
| Sequence 213054,  | US-11-136-527-213054   | 25 | 11 | 37.9 | 14.4 |
| Sequence 255943,  | US-11-136-527-255943   | 25 | 11 | 37.9 | 14.4 |
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| Sequence 264938,  | US-11-136-527-264938   | 25 | 11 | 37.9 | 14.4 |
| Sequence 295909,  | US-11-136-527-295909   | 25 | 11 | 37.9 | 14.4 |
| Sequence 318422,  | US-11-136-527-318422   | 25 | 11 | 37.9 | 14.4 |
| Sequence 323032,  | US-11-136-527-323032   | 25 | 11 | 37.9 | 14.4 |
| Sequence 337618,  | US-11-136-527-337618   | 25 | 11 | 37.9 | 14.4 |
| Sequence 1042809, | US-10-310-914A-1042809 | 27 | 7  | 37.9 | 14.4 |
| Sequence 860573,  | US-10-310-914A-860573  | 28 | 7  | 37.9 | 14.4 |

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|   | 97  | 14.4 | 37.9 | 50 | 11 | US-11-175-859-78404    | Sequence 78404, A   | C 170 | 13.8 | 36.3 | 19 | 7  | US-10-310-914A-603980  | Sequence 603980,  |
|   | 98  | 14.4 | 37.9 | 50 | 11 | US-11-175-859-108242   | Sequence 108242, A  | C 171 | 13.8 | 36.3 | 19 | 7  | US-10-310-914A-1286243 | Sequence 1286243, |
|   | 99  | 14.4 | 37.9 | 50 | 11 | US-11-175-859-111846   | Sequence 111846,    | C 172 | 13.8 | 36.3 | 19 | 9  | US-11-101-244-662609   | Sequence 662609,  |
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|   | 103 | 14.2 | 37.4 | 19 | 9  | US-11-101-244-1342196  | Sequence 1342196,   | C 176 | 13.8 | 36.3 | 20 | 7  | US-10-310-914A-197603  | Sequence 197603,  |
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|   | 105 | 14.2 | 37.4 | 20 | 7  | US-10-310-914A-400362  | Sequence 400362, A  | C 178 | 13.8 | 36.3 | 20 | 7  | US-10-310-914A-1084298 | Sequence 1084298, |
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|   | 107 | 14.2 | 37.4 | 20 | 7  | US-10-310-914A-983911  | Sequence 983911, A  | C 180 | 13.8 | 36.3 | 20 | 7  | US-10-310-914A-1216378 | Sequence 1216378, |
|   | 108 | 14.2 | 37.4 | 21 | 7  | US-10-770-726-1531     | Sequence 1531, Ap   | C 181 | 13.8 | 36.3 | 21 | 7  | US-10-310-914A-1216655 | Sequence 1216655, |
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|   | 112 | 14.2 | 37.4 | 22 | 7  | US-10-310-914A-1229664 | Sequence 1229664, A | C 185 | 13.8 | 36.3 | 24 | 7  | US-10-310-914A-38730   | Sequence 38730, A |
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|   | 114 | 14.2 | 37.4 | 23 | 7  | US-10-310-914A-920517  | Sequence 920517, A  | C 187 | 13.8 | 36.3 | 25 | 7  | US-10-310-914A-257305  | Sequence 257305,  |
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|   | 116 | 14.2 | 37.4 | 25 | 11 | US-11-121-849-92973    | Sequence 92973, A   | C 189 | 13.8 | 36.3 | 25 | 7  | US-10-310-914A-1334567 | Sequence 1334567, |
|   | 117 | 14.2 | 37.4 | 25 | 11 | US-11-121-849-123890   | Sequence 123890, A  | C 190 | 13.8 | 36.3 | 25 | 11 | US-11-121-849-2166     | Sequence 2166, Ap |
|   | 118 | 14.2 | 37.4 | 25 | 11 | US-11-121-849-245310   | Sequence 245310, A  | C 191 | 13.8 | 36.3 | 25 | 11 | US-11-121-849-56581    | Sequence 56581, A |
|   | 119 | 14.2 | 37.4 | 25 | 11 | US-11-121-849-351482   | Sequence 351482, A  | C 192 | 13.8 | 36.3 | 25 | 11 | US-11-121-849-63156    | Sequence 63156, A |
|   | 120 | 14.2 | 37.4 | 25 | 11 | US-11-121-849-392406   | Sequence 392406, A  | C 193 | 13.8 | 36.3 | 25 | 11 | US-11-121-849-76904    | Sequence 76904, A |
|   | 121 | 14.2 | 37.4 | 25 | 11 | US-11-121-849-480753   | Sequence 480753, A  | C 194 | 13.8 | 36.3 | 25 | 11 | US-11-121-849-87010    | Sequence 87010, A |
|   | 122 | 14.2 | 37.4 | 25 | 11 | US-11-121-849-514563   | Sequence 514563, A  | C 195 | 13.8 | 36.3 | 25 | 11 | US-11-121-849-150850   | Sequence 150850,  |
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|   | 124 | 14.2 | 37.4 | 25 | 11 | US-11-121-849-514900   | Sequence 514900, A  | C 197 | 13.8 | 36.3 | 25 | 11 | US-11-121-849-232914   | Sequence 232914,  |
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|   | 126 | 14.2 | 37.4 | 25 | 11 | US-11-136-527-53210    | Sequence 574901, A  | C 199 | 13.8 | 36.3 | 25 | 11 | US-11-121-849-236300   | Sequence 236300,  |
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|   | 128 | 14.2 | 37.4 | 25 | 11 | US-11-136-527-53220    | Sequence 52220, A   | C 201 | 13.8 | 36.3 | 25 | 11 | US-11-121-849-509586   | Sequence 509586,  |
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|   | 130 | 14.2 | 37.4 | 50 | 11 | US-11-175-859-241      | Sequence 241, App   | C 203 | 13.8 | 36.3 | 25 | 11 | US-11-121-849-585617   | Sequence 585617,  |
|   | 131 | 14.2 | 37.4 | 50 | 11 | US-11-175-859-24603    | Sequence 24603, A   | C 204 | 13.8 | 36.3 | 25 | 11 | US-11-136-527-139988   | Sequence 139988,  |
|   | 132 | 14.2 | 37.4 | 50 | 11 | US-11-175-859-62229    | Sequence 62229, A   | C 205 | 13.8 | 36.3 | 25 | 11 | US-11-136-527-139994   | Sequence 139994,  |
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|   | 134 | 14.2 | 37.4 | 50 | 11 | US-11-175-859-94754    | Sequence 94754, A   | C 207 | 13.8 | 36.3 | 25 | 11 | US-11-136-527-216717   | Sequence 216717,  |
|   | 135 | 14.2 | 37.4 | 50 | 11 | US-11-175-859-114859   | Sequence 114859, A  | C 208 | 13.8 | 36.3 | 25 | 11 | US-11-136-527-218537   | Sequence 218537,  |
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|   | 138 | 14   | 36.8 | 23 | 7  | US-10-310-914A-1017158 | Sequence 1017158, A | C 211 | 13.8 | 36.3 | 25 | 11 | US-11-136-527-264917   | Sequence 264917,  |
|   | 139 | 14   | 36.8 | 23 | 7  | US-10-310-914A-1020590 | Sequence 1020590, A | C 212 | 13.8 | 36.3 | 25 | 11 | US-11-136-527-344781   | Sequence 344781,  |
|   | 140 | 14   | 36.8 | 24 | 7  | US-10-310-914A-24012   | Sequence 24012, A   | C 213 | 13.8 | 36.3 | 25 | 11 | US-11-136-527-344817   | Sequence 344817,  |
|   | 141 | 14   | 36.8 | 24 | 7  | US-10-310-914A-1090819 | Sequence 1090819, A | C 214 | 13.8 | 36.3 | 25 | 11 | US-11-136-527-348675   | Sequence 348675,  |
|   | 142 | 14   | 36.8 | 24 | 7  | US-10-310-914A-1242049 | Sequence 1242049, A | C 215 | 13.8 | 36.3 | 26 | 7  | US-10-310-914A-758648  | Sequence 758648,  |
|   | 143 | 14   | 36.8 | 24 | 7  | US-10-310-914A-1298143 | Sequence 1298143, A | C 216 | 13.8 | 36.3 | 36 | 11 | US-11-195-109-5        | Sequence 5, Appli |
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|   | 154 | 14   | 36.8 | 25 | 11 | US-11-121-849-423422   | Sequence 423422, A  | C 227 | 13.8 | 36.3 | 50 | 11 | US-11-175-859-78145    | Sequence 78145, A |
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|   | 156 | 14   | 36.8 | 25 | 11 | US-11-136-527-2255946  | Sequence 2255946, A | C 229 | 13.8 | 36.3 | 50 | 11 | US-11-175-859-92135    | Sequence 92135, A |
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|   | 159 | 14   | 36.8 | 28 | 7  | US-10-310-914A-637718  | Sequence 637718, A  | C 232 | 13.6 | 35.8 | 20 | 7  | US-10-310-914A-394854  | Sequence 394854,  |
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|   | 162 | 14   | 36.8 | 50 | 11 | US-11-175-859-34114    | Sequence 34114, A   | C 235 | 13.6 | 35.8 | 20 | 7  | US-10-310-914A-982390  | Sequence 982390,  |
|   | 163 | 14   | 36.8 | 50 | 11 | US-11-175-859-44652    | Sequence 44652, A   | C 236 | 13.6 | 35.8 | 21 | 7  | US-10-310-914A-67829   | Sequence 67829, A |
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|   | 166 | 14   | 36.8 | 50 | 11 | US-11-175-859-73803    | Sequence 73803, A   | C 239 | 13.6 | 35.8 | 21 | 7  | US-10-310-914A-1011495 | Sequence 1011495, |
|   | 167 | 14   | 36.8 | 50 | 11 | US-11-175-859-86934    | Sequence 86934, A   | C 240 | 13.6 | 35.8 | 21 | 7  | US-10-310-914A-1020589 | Sequence 1020589, |
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; CURRENT APPLICATION NUMBER: US/11/179,321
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: 60/587,187
; PRIOR FILING DATE: 2004-07-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-179-321-5

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Db 10 GGGACTTCCGCTGGGACTTCCAGGGGCGT 43

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US-11-116-746-12
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; Publication No. US20060020114A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P1110
; CURRENT APPLICATION NUMBER: US/11/116,746
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 12
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-116-746-12

Query Match
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RESULT 5
US-11-175-815-3
; Sequence 3, Application US/11/175815
; Publication No. US20060029932A1
; GENERAL INFORMATION:
; APPLICANT: Graham P. Allaway et al.
; TITLE OF INVENTION: A METHOD FOR PREVENTING HIV-1 INFECTION OF CD4 CELLS
; FILE REFERENCE: 2048/50875-DA/JPW/AJD
; CURRENT APPLICATION NUMBER: US/11/175,815
; CURRENT FILING DATE: 2005-07-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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US-11-175-815-3

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RESULT 6
US-11-179-321-2
; Sequence 2, Application US/11/179321
; Publication No. US20060019907A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL, BHARAT
; APPLICANT: SHISHODIA, SHISHIR
; TITLE OF INVENTION: GUGGULSTERONE: AN INHIBITOR OF NUCLEAR FACTOR- B AND
; TITLE OF INVENTION: I B KINASE
; TITLE OF INVENTION: ACTIVATION AND USES THEREOF
; FILE REFERENCE: CLFR:255US
; CURRENT APPLICATION NUMBER: US/11/179,321
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: 60/587,187
; PRIOR FILING DATE: 2004-07-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-179-321-2

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Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 ACTTCCGCTGGGACTTCCAGGGGACTT 35
Db 13 ACTTCCGCTGCTCACTTCCAGGGAGCGT 43

RESULT 7
US-11-179-321-6
; Sequence 6, Application US/11/179321
; Publication No. US20060019907A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL, BHARAT
; APPLICANT: SHISHODIA, SHISHIR
; TITLE OF INVENTION: GUGGULSTERONE: AN INHIBITOR OF NUCLEAR FACTOR- B AND
; TITLE OF INVENTION: I B KINASE
; TITLE OF INVENTION: ACTIVATION AND USES THEREOF
; FILE REFERENCE: CLFR:255US
; CURRENT APPLICATION NUMBER: US/11/179,321
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: 60/587,187
; PRIOR FILING DATE: 2004-07-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-179-321-6

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Db 13 ACTTCCGCTGCTCACTTCCAGGGAGCGT 43
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Best Local Similarity 80.6%; Pred. No. 17;  
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Db 13 ACTTTCGCTGCTCACTTTCAGGGAGGCT 43

RESULT 8

US-11-175-859-100529  
; Sequence 100529, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 100529  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-100529

Query Match 47.4%; Score 18; DB 11; Length 50;  
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Db 1 GGACAGTTTGGGTTGGGACTTACCRGGGTGATGT 36

RESULT 9

US-11-136-527-200528  
; Sequence 200528, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 200528  
; LENGTH: 25  
; TYPE: DNA  
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; OTHER INFORMATION: Probe  
US-11-136-527-200528

Query Match 45.1%; Score 17.2; DB 11; Length 25;  
Best Local Similarity 86.4%; Pred. No. 6.4e+02;  
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QY 8 TTCCGCTGGGACTTTCCAGG 29  
Db 1 TTCTCTGGGACTTTCTGGG 22

RESULT 10

US-11-175-859-32817/c  
; Sequence 32817, Application US/11175859

Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; APPLICANT: Liu, Guoying et al.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 32817  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-32817

Query Match 45.3%; Score 17.2; DB 11; Length 50;  
Best Local Similarity 68.8%; Pred. No. 7e+02;  
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Db 42 ACTTTCGATAGCTACWTTCAAGGCACATT 11

RESULT 11

US-11-175-859-66382/c  
; Sequence 66382, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; APPLICANT: Liu, Guoying et al.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 66382  
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; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-66382

Query Match 43.2%; Score 16.4; DB 11; Length 50;  
Best Local Similarity 71.4%; Pred. No. 1.4e+03;  
Matches 20; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGACTTTCCAGG 28  
Db 48 GGGACATTCACTTGGGACTTCTATG 21

RESULT 12

US-11-121-849-3916/c  
; Sequence 3916, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 3916

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-3916

Query Match      42.1%; Score 16; DB 11; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 10 CCCTGGGGACTTTCAGGGGAC 33
Db 24 CCCTGAAGACCTTTCAGTGGAC 1

RESULT 13
US-11-121-849-43102
; Sequence 43102, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-43102

Query Match      42.1%; Score 16; DB 11; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 GCTGGGGACTTTCAGGGGACTT 35
Db 1 GCTGAGGCAATCCAGGGGACCT 24

RESULT 14
US-11-121-849-565799/c
; Sequence 565799, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 565799
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-565799

Query Match      41.1%; Score 15.6; DB 11; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 TTTCCGCTGGGGACTTTCAGG 28
Db 25 TTTCAGCTTGAACCTTCCAGG 4

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-136-527-273210/c
; Sequence 273210, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 273210
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-273210

Query Match      41.1%; Score 15.6; DB 11; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 16 GGGACTTTCAGGGGACTTTC 37
Db 23 GGTACTTTCAGGCGGCTTC 2

RESULT 16
US-11-136-527-273212/c
; Sequence 273212, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 273212
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-273212

Query Match      41.1%; Score 15.6; DB 11; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 16 GGGACTTTCAGGGGACTTTC 37
Db 22 GGTACTTTCAGGCGGCTTC 1

RESULT 17
US-11-175-859-21940/c
; Sequence 21940, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
```

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; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21940
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-21940

```

```
Query Match      41.1%; Score 15.6; DB 11; Length 50;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 1; Mismatches 5; Indels
```

Qy 4 GACTTTCGCTGGGGACTTTCCAG 27  
||||||| : ||| ||  
Db 37 GACTTTCCTCTRTGGATTTGTAG 14

RESULT 18  
US-11-121-849-103498/c  
; Sequence 103498, Application US/11121849  
; Publication No. US20050272080A1

```

; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of G
; TITLE OF INVENTION: Microarrays

```

```

, FILE REFERENCE: 3684.I
, CURRENT APPLICATION NUMBER: US/11/121,849
, CURRENT FILING DATE: 2005-05-03
, PRIOR APPLICATION NUMBER: 60/567,949
, PRIOR FILING DATE: 2004-05-03
, NUMBER OF SEQ ID NOS: 673904
, SOFTWARE: Microarray Probe Sequence List1
, SEQ ID NO 103498

```

Query Match 40.5%; Score 15.4; DB 11; Length 25;  
Best Local Similarity 76.0%; Pred. No. 3.2e+03;  
Matches 19: Conservative 0; Mismatches 6; Indels

QY 13 CTGGGACTTTCAGGGGACTTC 37  
||| | ||||| |||||  
Db 25 CTAGGGCCGCTCCAGTGGGACTTCC 1

RESULT 19  
US-11-121-849-260545/c  
; Sequence 260545, Application US/11121849  
; Publication No. US20050272080A1

; GENERAL INFORMATION:  
 ; APPLICANT: John Palma  
 ; TITLE OF INVENTION: Methods of G  
 ; TITLE OF INVENTION: Microarrays

```

, FILE REFERENCE: 3884.1
, CURRENT APPLICATION NUMBER: US/11/121,849
, CURRENT FILING DATE: 2005-05-03
, PRIOR APPLICATION NUMBER: 60/567,949
, PRIOR FILING DATE: 2004-05-03
, NUMBER OF SEQ ID NOS: 673904
, SOFTWARE: Microarray Probe Sequence Listi.
, SEQ ID NO: 260545

```

Query Match 40.5%; Score 15.4; DB 11; Length 25;  
Best Local Similarity 76.0%; Pred. No. 3.2e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels

Qy 11 CGCTGGGGACTTTCAGGGGACTT 35  
Db 25 CGCTGGGGTCTTACCAGTGGTGTTT 1

RESULT 20  
US-11-121-849-507340  
; Sequence 507340, Application US/11121849  
; Publication No. US20050272080A1

; GENERAL INFORMATION:  
 ; APPLICANT: John Palma  
 ; TITLE OF INVENTION: Methods of Genetic An  
 ; TITLE OF INVENTION: Microarrays

```

, FILE REFERENCE: 3684.I
, CURRENT APPLICATION NUMBER: US/11/121,849
, CURRENT FILING DATE: 2005-03-03
, PRIOR APPLICATION NUMBER: 60/567,949
, PRIOR FILING DATE: 2004-05-03
, NUMBER OF SEQ ID NOS: 673904
, SOFTWARE: Microarray Probe Sequence List
, SEQ ID NO 507340

```

Query Match 40.5%; Score 15.4; DB 11; Length 25;  
Best Local Similarity 76.0%; Pred. NO. 3.2e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels

QY 14 TGGGGACTTTCCAGGGGGACTTTCC 38  
||| ||| ||| ||| ||| ||| ||| |||  
Db 1 TGCGGGCTTACCAGGAGGCCTGTCC 25

RESULT 21  
US-11-121-849-528104/c  
; Sequence 528104, Application US/11121849  
; Publication No. US20050272080A1

; GENERAL INFORMATION:  
 ; APPLICANT: John Palma  
 ; TITLE OF INVENTION: Methods of Genetic An  
 ; TITLE OF INVENTION: Microarrays

```

/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence List
/ SEQ ID NO: 528104

```

|                          |               |                    |        |            |
|--------------------------|---------------|--------------------|--------|------------|
| Query Match              | 40.5%         | Score 15.4;        | DB 11; | Length 25; |
| Best Local Similarity    | 76.0%;        | Pred. No. 3.2e+03; |        |            |
| Matches 19: Conservative | 0: Mismatches | 6: Indels          |        |            |

QY 7 TTTCCGCTGGGACTTTCAGGGG 31  
| | | | |  
Db 25 TCTCAGCTTGGGACTTCTCAGAGG 1

RESULT 22  
US-11-136-527-139991  
; Sequence 139991, Application US/11136527  
; Publication No. US20050287570A1

```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-139991

Query Match          40.5%; Score 15.4; DB 11; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.2e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGGACTTTCC 25
    ||||| ||||| ||||| |||||
Db 1 GGGGACTTTCAGATGTTTATTTC 25

RESULT 23
US-11-136-527-213042/c
; Sequence 213042, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 213042
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-213042

Query Match          40.5%; Score 15.4; DB 11; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.2e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 ACTTTCGCTGGGACTTTCCAGGG 29
    ||||| ||||| ||||| |||||
Db 25 ACTTCAGCTGAGACTTCCGGGG 1

RESULT 24
US-10-310-914A-767705/c
; Sequence 767705, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 767705
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-767705

Query Match          40.5%; Score 15.4; DB 7; Length 26;
Best Local Similarity 76.0%; Pred. No. 3.2e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CTTTCGCTGGGGACTTTCCAGGG 30
    ||||| ||||| ||||| |||||
Db 26 CTCTGGGTGGGGCTTTTCAGGG 2

RESULT 25
US-11-032-236-2/c
; Sequence 2, Application US/11032236
; Publication No. US20050273867A1
; GENERAL INFORMATION:
; APPLICANT: BROULET, PHILIPPE
; APPLICANT: ROGERS, KELLY
; APPLICANT: PICAUD, SANDRINE
; TITLE OF INVENTION: NON-INVASIVE REAL-TIME IN VIVO BIOLUMINESCENCE IMAGING
; TITLE OF INVENTION: OF LOCAL CA2+ DYNAMICS IN LIVING ORGANISMS
; FILE REFERENCE: 03495.0328
; CURRENT APPLICATION NUMBER: US/11/032,236
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/543,659
; PRIOR FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: flexible linker sequence
US-11-032-236-2

Query Match          40.5%; Score 15.4; DB 11; Length 41;
Best Local Similarity 66.7%; Pred. No. 3.4e+03;
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGACTTTCCAGGGGGAC 33
    ||||| ||||| ||||| |||||
Db 39 GGGGACTGGCCGCGATCCGCTCCGCGCGAC 7

RESULT 26
US-11-175-859-66869/c
; Sequence 66869, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66869
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-66869

Query Match          40.5%; Score 15.4; DB 11; Length 50;
```



Best Local Similarity 70.4%; Pred. No. 3.4e+03; Indels 0; Gaps 0; Matches 19; Conservative 1; Mismatches 7;

QY 10 CCCTGGGACTTTCAGGGGACTTT 36  
||||| : ||||| ||||| ||  
Db 35 CCCTGTCCRCCTTCCATYGGGACATT 9

RESULT 27  
US-11-175-859-103464  
; Sequence 103464, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 103464  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-103464

Query Match 40.5%; Score 15.4; DB 11; Length 50;  
Best Local Similarity 70.4%; Pred. No. 3.4e+03; Indels 0; Gaps 0; Matches 19; Conservative 1; Mismatches 7;

QY 3 GGACTTTCGCTGGGACTTTCAGGG 29  
||||| ||||| ||||| : ||||| |||||  
Db 9 GGACTTTCACTGTTCATCTCTGGG 35

RESULT 28  
US-10-310-914A-298241  
; Sequence 298241, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 298241  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-298241

Query Match 40.0%; Score 15.2; DB 7; Length 23;  
Best Local Similarity 70.0%; Pred. No. 3.7e+03; Indels 0; Gaps 0; Matches 14; Conservative 3; Mismatches 3;

QY 10 CCCTGGGACTTTCAGGG 29  
|||:|||||:|||||  
Db 3 CUGCUGGUGACUCUCCAGGG 22

RESULT 29  
US-10-310-914A-663779  
; Sequence 663779, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 663779  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-663779

Query Match 40.0%; Score 15.2; DB 7; Length 23;  
Best Local Similarity 55.0%; Pred. No. 3.7e+03; Indels 0; Gaps 0; Matches 11; Conservative 6; Mismatches 3;

QY 3 GGACTTTCGCTGGGACTT 22  
|||||:|||||:|||||  
Db 1 GGACUUUCCUGGGAACUU 20

RESULT 30  
US-11-121-849-454114/c  
; Sequence 454114, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 454114  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-454114

Query Match 40.0%; Score 15.2; DB 11; Length 25;  
Best Local Similarity 85.0%; Pred. No. 3.8e+03; Indels 0; Gaps 0; Matches 17; Conservative 0; Mismatches 3;

QY 16 GGGACTTTCAGGGGACTT 35  
||||| ||||| ||||| |||||  
Db 23 GGGACTCTCCATGGGAGTT 4

RESULT 31  
US-10-310-914A-1226668  
; Sequence 1226668, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1226668  
; LENGTH: 26  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1226668

```
Query Match          40.0%; Score 15.2; DB 7; Length 26;
Best Local Similarity 65.0%; Pred. No. 3.8e+03;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGAC 20
   |||||:|:|:|||||
Db 7 GAGGACUUGCCUGGGGAC 26

RESULT 32
US-10-310-914A-1383495
; Sequence 1383495, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1383495
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1383495

Query Match          40.0%; Score 15.2; DB 7; Length 27;
Best Local Similarity 60.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACT 21
   |||||:|:|:|:|:|
Db 8 GGGACUUCUCCUGAGGCCU 27

RESULT 33
US-11-175-859-43456/c
; Sequence 43456, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43456
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-43456

Query Match          40.0%; Score 15.2; DB 11; Length 50;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 20; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 TTTCCTCGGGGACTTTCAGGGGGACTTTT 36
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 30 TTGSGATGACTACTTTCAGGAGACTTTT 1

RESULT 34
US-11-175-859-66764
; Sequence 66764, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66764
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-66764

Query Match          40.0%; Score 15.2; DB 11; Length 50;
Best Local Similarity 63.9%; Pred. No. 4.1e+03;
Matches 23; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTT 36
   |||||:|:|:|:|:|:|:|:|:|:|:|:|
Db 7 GGTCACTTACCTTAGAGAGTGTTCAAGAGGGACTGT 42

RESULT 35
US-10-310-914A-815249
; Sequence 815249, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 815249
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-815249

Query Match          39.5%; Score 15; DB 7; Length 24;
Best Local Similarity 65.2%; Pred. No. 4.5e+03;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 15 GGGGACTTTCAGGGGGACTTTC 37
   |||||:|:|:|:|:|:|:|
Db 1 GGGGAGUGUCCAGGGGCACCUGC 23

RESULT 36
US-11-121-849-196232/c
; Sequence 196232, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 196232
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
```

## US-11-121-849-196232

Query Match 39.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACTTTCGCTGGGGA 19  
|||||  
DB 22 ACTTTCGCTGGGGA 8

## RESULT 37

US-11-121-849-378884/c  
; Sequence 378884, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 378884  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-378884

Query Match 39.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 4.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 15 GGGGACTTCCAGGGGACTTC 37  
|||||  
DB 23 GGGGCTTCCAGACTGAGTTTC 1

## RESULT 38

US-11-121-849-510666  
; Sequence 510666, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 510666  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-510666

Query Match 39.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 4.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 GCTGGGCACTTCCAGGGGACT 34  
|||||  
DB 3 GCTGGGCACTTCCGGGAGTCCT 25

## RESULT 39

US-11-136-527-280766/c

; Sequence 280766, Application US/11136527  
; Publication No. US20050287570A1

; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 280766  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe

US-11-136-527-280766

Query Match 39.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 4.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 13 CTGGGCACTTCCAGGGGACTT 35  
|||||  
DB 23 CAGGGCACTCATCTGGGGACTT 1

## RESULT 40

US-11-136-527-314081/c  
; Sequence 314081, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 314081  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe

US-11-136-527-314081

Query Match 39.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 4.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 11 CGCTGGGCACTTCCAGGGGAC 33  
|||||  
DB 23 CGCTGAGAGCTTCCAGGGCGGC 1

## RESULT 41

US-11-136-527-318283  
; Sequence 318283, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25

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; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 318283
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
;
US-11-136--527-318283

Query Match          39.5%; Score 15; DB 11; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGACTTTCGCTGGGACTTTCC 25
    ||||| ||||| ||||| |||||
Db 2 GGACTAGCAGCTGGGGTCTTTAC 24

RESULT 42
US-11-136-527-358480
; Sequence 358480, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 358480
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
;
US-11-136-527-358480

Query Match          39.5%; Score 15; DB 11; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 TTTCCTGGGACTTTCCAGG 29
    ||||| ||||| ||||| |||||
Db 3 TTTCCTGAAGACTTCCCAAG 25

RESULT 43
US-11-175-859-11173
; Sequence 11173, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11173
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
;
US-11-175-859-11173

Query Match          39.5%; Score 15; DB 11; Length 50;
Best Local Similarity 78.3%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGACTTT 23
    ||||| ||||| ||||| |||||
Db 21 GGGGARTTTCCGCAGTGTACTGT 43

RESULT 46
US-10-310-914A-252171/C
; Sequence 252171, Application US/10310914A
```

```

; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 252171
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-252171

Query Match      38.9%; Score 14.8; DB 7; Length 24;
Best Local Similarity 88.9%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      16 GGGACTTTCCAGGGGGGAC 33
        ||||| ||||| |||||
DB       21 GGGACTAGCCAGGGGGAC 4

RESULT 47
US-11-121-849-508663
; Sequence 508663, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508663
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-508663

Query Match      38.9%; Score 14.8; DB 11; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 ACTTTCGCTGGGGGACTT 22
        ||| ||||| ||||| |||||
DB       1 ACTCTCCGCTGGGAAC TT 18

RESULT 48
US-11-121-849-569838
; Sequence 569838, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 569838
; LENGTH: 25

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Search completed: February 16, 2006, 02:53:06  
Job time : 357.248 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:51:58 ; Search time 479.835 Seconds  
(without alignments)  
2369.293 Million cell updates/sec

Title: US-09-669-187A-906

Perfect score: 20  
Sequence: 1 aggggaggggaggggagggg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_sts.\*  
11: gb\_sy.\*  
12: gb\_un.\*  
13: gb\_vl.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 20    | 100.0       | 20     | 6     | AX104714 Sequence  |
| 2          | 20    | 100.0       | 20     | 6     | AX547767 Sequence  |
| 3          | 20    | 100.0       | 50     | 6     | AX058549 Sequence  |
| C 4        | 20    | 100.0       | 50     | 6     | AX058550 Sequence  |
| C 5        | 17.4  | 87.0        | 27     | 6     | AR091424 Sequence  |
| 6          | 17.4  | 87.0        | 27     | 6     | AR091425 Sequence  |
| C 7        | 17.4  | 87.0        | 27     | 6     | AR125629 Sequence  |
| 8          | 17.4  | 87.0        | 27     | 6     | AR125630 Sequence  |
| 9          | 17.4  | 87.0        | 30     | 6     | AX477591 Sequence  |
| 10         | 17.4  | 87.0        | 30     | 6     | AX505011 Sequence  |
| 11         | 17.4  | 87.0        | 39     | 6     | AR091423 Sequence  |
| 12         | 17.4  | 87.0        | 39     | 6     | AR125628 Sequence  |
| C 13       | 16.4  | 82.0        | 50     | 6     | AR356035 Sequence  |
| C 14       | 16.4  | 82.0        | 50     | 6     | AR537591 Sequence  |
| C 15       | 16    | 80.0        | 17     | 6     | BD202728 Method an |
| 16         | 15.8  | 79.0        | 20     | 6     | ES9332             |
| 17         | 15.8  | 79.0        | 26     | 6     | BD078154 Modulator |
| 18         | 15.8  | 79.0        | 42     | 6     | AR362756 Sequence  |

A28677 Oligonucleo  
A28678 Oligonucleo  
A28674 dsRNA with  
A28685 Oligonucleo  
CQ003486 Sequence  
CQ003487 Sequence  
CQ006699 Sequence  
CQ006700 Sequence  
BD202727 Method an  
AR110134 Sequence  
AR110134 Sequence  
I41099 Sequence 2  
A23688 L. monocyto  
A23689 L. monocyto  
AX058552 Sequence  
AX514983 Sequence  
AX519178 Sequence  
BD078171 Modulator  
BD078223 Modulator  
AR121366 Sequence  
AR213275 Sequence  
AR202976 Sequence  
AR643452 Sequence  
AX158892 Sequence  
AR121583 Sequence  
AR630012 Sequence  
AX351114 Sequence  
AR137709 Sequence  
CQ892090 Sequence  
CS130448 Sequence  
CS130449 Sequence  
EI2675 Ant1-HTLV-1  
AR182883 Sequence  
AR607446 Sequence  
AX045778 Sequence  
AX045788 Sequence  
AX045791 Sequence  
AX104065 Sequence  
AX104338 Sequence  
AX104339 Sequence  
AX104619 Sequence  
AX104795 Sequence  
AX105235 Sequence  
AX355140 Sequence  
AX355141 Sequence  
AX355401 Sequence  
AX355402 Sequence  
AX477342 Sequence  
AX547118 Sequence  
AX547391 Sequence  
AX547392 Sequence  
AX547672 Sequence  
AX547848 Sequence  
AX547848 Sequence  
AX664309 Sequence  
AX664310 Sequence  
AX786642 Sequence  
AX786642 Sequence  
AR074234 Sequence  
AR084522 Sequence  
AR084523 Sequence  
I21020 Sequence 3  
AX575156 Sequence  
AX023407 Sequence  
AX032596 Sequence  
AX133266 Sequence  
AX0420 Sequence 47  
AR010036 Sequence  
AR034771 Sequence  
AR152031 Sequence  
BD138633 Soluble M  
I05045 Sequence 8  
I24744 Sequence 7  
AX104236 Sequence  
AX104771 Sequence

|       |      |      |    |   |                   |                    |       |      |      |    |   |                    |
|-------|------|------|----|---|-------------------|--------------------|-------|------|------|----|---|--------------------|
| C 92  | 14.2 | 71.0 | 24 | 6 | AX355142 Sequence | AX355142 Sequence  | C 165 | 13.8 | 69.0 | 37 | 6 | AR080892 Sequence  |
| C 93  | 14.2 | 71.0 | 24 | 6 | AX547289 Sequence | AX547289 Sequence  | C 166 | 13.8 | 69.0 | 37 | 6 | AR173722 Sequence  |
| C 94  | 14.2 | 71.0 | 24 | 6 | AX547824 Sequence | AX547824 Sequence  | C 167 | 13.8 | 69.0 | 38 | 6 | AX033315 Sequence  |
| C 95  | 14.2 | 71.0 | 25 | 6 | BD087484          | BD087484 De novo o | C 168 | 13.8 | 69.0 | 40 | 6 | AX520121 Sequence  |
| C 96  | 14.2 | 71.0 | 25 | 6 | BD105777          | BD105777 Conjgate  | C 169 | 13.8 | 69.0 | 41 | 6 | AX513947 Sequence  |
| C 97  | 14.2 | 71.0 | 25 | 6 | AR182077          | AR182077 Sequence  | C 170 | 13.8 | 69.0 | 41 | 6 | AX515756 Sequence  |
| C 98  | 14.2 | 71.0 | 25 | 6 | AR261501          | AR261501 Sequence  | C 171 | 13.8 | 69.0 | 41 | 6 | AX518351 Sequence  |
| C 99  | 14.2 | 71.0 | 26 | 6 | BD078156          | BD078156 Modulator | C 172 | 13.8 | 69.0 | 41 | 6 | AX519286 Sequence  |
| C 100 | 14.2 | 71.0 | 27 | 6 | E04886            | E04886 DNA sequenc | C 173 | 13.8 | 69.0 | 41 | 6 | AX520120 Sequence  |
| C 101 | 14.2 | 71.0 | 27 | 6 | E04987            | E04987 DNA sequenc | C 174 | 13.8 | 69.0 | 45 | 6 | AR080900 Sequence  |
| C 102 | 14.2 | 71.0 | 28 | 6 | I06458            | I06458 Sequence 1  | C 175 | 13.8 | 69.0 | 45 | 6 | AR173730 Sequence  |
| C 103 | 14.2 | 71.0 | 28 | 6 | AX104578          | AX104578 Sequence  | C 176 | 13.8 | 69.0 | 47 | 6 | AR288550 Sequence  |
| C 104 | 14.2 | 71.0 | 28 | 6 | AX355143          | AX355143 Sequence  | C 177 | 13.8 | 69.0 | 47 | 6 | AR291483 Sequence  |
| C 105 | 14.2 | 71.0 | 28 | 6 | AX547631          | AX547631 Sequence  | C 178 | 13.8 | 69.0 | 47 | 6 | AR582752 Sequence  |
| C 106 | 14.2 | 71.0 | 30 | 6 | A62990            | A62990 Sequence 2  | C 179 | 13.8 | 69.0 | 50 | 6 | AX158894 Sequence  |
| C 107 | 14.2 | 71.0 | 30 | 6 | A62996            | A62996 Sequence 8  | C 180 | 13.8 | 69.0 | 50 | 8 | HSTPE31A4          |
| C 108 | 14.2 | 71.0 | 30 | 6 | AR179065          | AR179065 Sequence  | C 181 | 13.6 | 68.0 | 21 | 6 | AR066855 Sequence  |
| C 109 | 14.2 | 71.0 | 30 | 6 | AR179071          | AR179071 Sequence  | C 182 | 13.6 | 68.0 | 21 | 6 | AR080893 Sequence  |
| C 110 | 14.2 | 71.0 | 30 | 6 | CS130457          | CS130457 Sequence  | C 183 | 13.6 | 68.0 | 21 | 6 | AR173723 Sequence  |
| C 111 | 14.2 | 71.0 | 30 | 6 | AX104904          | AX104904 Sequence  | C 184 | 13.6 | 68.0 | 23 | 6 | AX033314 Sequence  |
| C 112 | 14.2 | 71.0 | 30 | 6 | AX477343          | AX477343 Sequence  | C 185 | 13.6 | 68.0 | 24 | 6 | AR094559 Sequence  |
| C 113 | 14.2 | 71.0 | 31 | 6 | A40435            | A40435 Sequence 62 | C 186 | 13.6 | 68.0 | 24 | 6 | BD138044           |
| C 114 | 14.2 | 71.0 | 31 | 6 | A62992            | A62992 Sequence 4  | C 187 | 13.6 | 68.0 | 24 | 6 | BD237692           |
| C 115 | 14.2 | 71.0 | 31 | 6 | AR179067          | AR179067 Sequence  | C 188 | 13.6 | 68.0 | 24 | 6 | AX278210 Sequence  |
| C 116 | 14.2 | 71.0 | 32 | 6 | A62993            | A62993 Sequence 5  | C 189 | 13.6 | 68.0 | 25 | 6 | AR609154 Sequence  |
| C 117 | 14.2 | 71.0 | 32 | 6 | AR179068          | AR179068 Sequence  | C 190 | 13.6 | 68.0 | 26 | 6 | BD078200 Modulator |
| C 118 | 14.2 | 71.0 | 35 | 6 | AX104579          | AX104579 Sequence  | C 191 | 13.6 | 68.0 | 30 | 6 | AR018187           |
| C 119 | 14.2 | 71.0 | 35 | 6 | AX355144          | AX355144 Sequence  | C 192 | 13.6 | 68.0 | 30 | 6 | AR430823           |
| C 120 | 14.2 | 71.0 | 35 | 6 | AX547632          | AX547632 Sequence  | C 193 | 13.6 | 68.0 | 40 | 6 | I01689             |
| C 121 | 14.2 | 71.0 | 37 | 6 | AR078293          | AR078293 Sequence  | C 194 | 13.6 | 68.0 | 40 | 9 | MUSTRBRI           |
| C 122 | 14.2 | 71.0 | 37 | 6 | BD135456          | BD135456 Fatty aci | C 195 | 13.6 | 68.0 | 44 | 6 | AX157237 Sequence  |
| C 123 | 14.2 | 71.0 | 37 | 6 | BD135459          | BD135459 Fatty aci | C 196 | 13.6 | 68.0 | 44 | 6 | AR284627 Sequence  |
| C 124 | 14.2 | 71.0 | 37 | 6 | AR285611          | AR285611 Sequence  | C 197 | 13.6 | 68.0 | 47 | 6 | AR080903 Sequence  |
| C 125 | 14.2 | 71.0 | 37 | 6 | AR285614          | AR285614 Sequence  | C 198 | 13.6 | 68.0 | 48 | 6 | AR173733 Sequence  |
| C 126 | 14.2 | 71.0 | 38 | 6 | AR054965          | AR054965 Sequence  | C 199 | 13.6 | 68.0 | 48 | 6 | CQ005982           |
| C 127 | 14.2 | 71.0 | 39 | 6 | A23696            | A23696 L. monocyto | C 200 | 13.6 | 68.0 | 50 | 6 | AX190214 Sequence  |
| C 128 | 14.2 | 71.0 | 40 | 6 | AR149456          | AR149456 Sequence  | C 201 | 13.6 | 68.0 | 50 | 9 | MMU41989           |
| C 129 | 14.2 | 71.0 | 40 | 6 | AR149458          | AR149458 Sequence  | C 202 | 13.6 | 68.0 | 50 | 9 | AX737059 Sequence  |
| C 130 | 14.2 | 71.0 | 40 | 6 | CS130458          | CS130458 Sequence  | C 203 | 13.4 | 67.0 | 17 | 6 | AX737059 Sequence  |
| C 131 | 14.2 | 71.0 | 40 | 6 | E05618            | E05618 Primer for  | C 204 | 13.4 | 67.0 | 22 | 6 | AR594206 Sequence  |
| C 132 | 14.2 | 71.0 | 40 | 6 | E49428            | E49428 Method for  | C 205 | 13.4 | 67.0 | 26 | 6 | AX356948 Sequence  |
| C 133 | 14.2 | 71.0 | 40 | 6 | E49430            | E49430 Method for  | C 206 | 13.4 | 67.0 | 36 | 6 | AX513870 Sequence  |
| C 134 | 14.2 | 71.0 | 41 | 6 | AR080642          | AR080642 Sequence  | C 207 | 13.4 | 67.0 | 41 | 6 | AX515849 Sequence  |
| C 135 | 14.2 | 71.0 | 42 | 6 | AX033316          | AX033316 Sequence  | C 208 | 13.4 | 67.0 | 41 | 6 | AX516477 Sequence  |
| C 136 | 14.2 | 71.0 | 45 | 6 | AR071841          | AR071841 Sequence  | C 209 | 13.4 | 67.0 | 41 | 6 | AX519146 Sequence  |
| C 137 | 14.2 | 71.0 | 45 | 6 | AR112581          | AR112581 Sequence  | C 210 | 13.4 | 67.0 | 41 | 6 | AX520098 Sequence  |
| C 138 | 14.2 | 71.0 | 45 | 6 | BD087459          | BD087459 De novo o | C 211 | 13.4 | 67.0 | 41 | 6 | AX521106 Sequence  |
| C 139 | 14.2 | 71.0 | 45 | 6 | AR182052          | AR182052 Sequence  | C 212 | 13.4 | 67.0 | 47 | 6 | AR288788 Sequence  |
| C 140 | 14.2 | 71.0 | 45 | 6 | AR261476          | AR261476 Sequence  | C 213 | 13.4 | 67.0 | 48 | 6 | CS052981           |
| C 141 | 14.2 | 71.0 | 45 | 6 | AX055492          | AX055492 Sequence  | C 214 | 13.4 | 67.0 | 48 | 6 | AX600119 Sequence  |
| C 142 | 14.2 | 71.0 | 47 | 6 | AR071857          | AR071857 Sequence  | C 215 | 13.4 | 67.0 | 50 | 8 | AF057511 Homo sapi |
| C 143 | 14.2 | 71.0 | 47 | 6 | AR112597          | AR112597 Sequence  | C 216 | 13.2 | 66.0 | 18 | 6 | A87890             |
| C 144 | 14.2 | 71.0 | 49 | 6 | A21777            | A21777 oligonucleo | C 217 | 13.2 | 66.0 | 18 | 6 | A89857             |
| C 145 | 14.2 | 71.0 | 49 | 6 | C0758887          | C0758887 Sequence  | C 218 | 13.2 | 66.0 | 18 | 6 | AR034902 Sequence  |
| C 146 | 14.2 | 71.0 | 50 | 6 | AR032910          | AR032910 Sequence  | C 219 | 13.2 | 66.0 | 18 | 6 | AR168816 Sequence  |
| C 147 | 14.2 | 71.0 | 50 | 6 | AR137494          | AR137494 Sequence  | C 220 | 13.2 | 66.0 | 18 | 6 | AR168817 Sequence  |
| C 148 | 14.2 | 71.0 | 50 | 6 | AR137495          | AR137495 Sequence  | C 221 | 13.2 | 66.0 | 18 | 6 | BD065403           |
| C 149 | 14.2 | 71.0 | 50 | 6 | BD087487          | BD087487 De novo o | C 222 | 13.2 | 66.0 | 18 | 6 | BD065403           |
| C 150 | 14.2 | 71.0 | 50 | 6 | I29650            | I29650 Sequence 52 | C 223 | 13.2 | 66.0 | 18 | 6 | I27811             |
| C 151 | 14.2 | 71.0 | 50 | 6 | I91324            | I91324 Sequence 52 | C 224 | 13.2 | 66.0 | 18 | 6 | AR200285 Sequence  |
| C 152 | 14.2 | 71.0 | 50 | 6 | AR182080          | AR182080 Sequence  | C 225 | 13.2 | 66.0 | 18 | 6 | AR200286 Sequence  |
| C 153 | 14.2 | 71.0 | 50 | 6 | AR209574          | AR209574 Sequence  | C 226 | 13.2 | 66.0 | 18 | 6 | AR262417 Sequence  |
| C 154 | 14.2 | 71.0 | 50 | 6 | AR261504          | AR261504 Sequence  | C 227 | 13.2 | 66.0 | 18 | 6 | AR262418 Sequence  |
| C 155 | 14.2 | 71.0 | 50 | 6 | AR646888          | AR646888 Sequence  | C 228 | 13.2 | 66.0 | 18 | 6 | AR612302 Sequence  |
| C 156 | 14.2 | 71.0 | 50 | 6 | AX147411          | AX147411 Sequence  | C 229 | 13.2 | 66.0 | 18 | 6 | AR613539 Sequence  |
| C 157 | 13.8 | 69.0 | 27 | 6 | AR091427          | AR091427 Sequence  | C 230 | 13.2 | 66.0 | 18 | 6 | AR648018 Sequence  |
| C 158 | 13.8 | 69.0 | 27 | 6 | AR125632          | AR125632 Sequence  | C 231 | 13.2 | 66.0 | 18 | 6 | AX047272 Sequence  |
| C 159 | 13.8 | 69.0 | 27 | 6 | AR125635          | AR125635 Sequence  | C 232 | 13.2 | 66.0 | 18 | 6 | AX047274 Sequence  |
| C 160 | 13.8 | 69.0 | 27 | 6 | AX298100          | AX298100 Sequence  | C 233 | 13.2 | 66.0 | 18 | 6 | AX599745 Sequence  |
| C 161 | 13.8 | 69.0 | 29 | 6 | AX655758          | AX655758 Sequence  | C 234 | 13.2 | 66.0 | 18 | 6 | AX599746 Sequence  |
| C 162 | 13.8 | 69.0 | 29 | 6 | AX496099          | AX496099 Sequence  | C 235 | 13.2 | 66.0 | 19 | 6 | AR300315 Sequence  |
| C 163 | 13.8 | 69.0 | 36 | 6 | AR006854          | AR006854 Sequence  | C 236 | 13.2 | 66.0 | 19 | 6 | AX104367 Sequence  |
| C 164 | 13.8 | 69.0 | 37 | 6 |                   |                    | C 237 | 13.2 | 66.0 | 19 | 6 | AX547420 Sequence  |





JOURNAL Patent: WO 0077250-A 1 21-DEC-2000;  
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)  
(FR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

FEATURES  
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Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

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Query Match 100.0%; Score 20; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20  
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Db 16 AGGGAGGGAGGGAGGGG 35

RESULT 4  
AX058550/c  
LOCUS AX058550 50 bp DNA linear PAT 17-JAN-2001  
DEFINITION Sequence 2 from Patent WO0077250.  
ACCESSION AX058550  
VERSION AX058550.1 GI:12310892  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
Escude, C., Garestier, T., Helene, C. and Roulon, T.  
Method for circularizing oligonucleotides around a double stranded  
nucleic acid, resulting structures and uses thereof  
Patent: WO 0077250-A 2 21-DEC-2000;  
JOURNAL INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)  
(FR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

FEATURES  
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Query Match 100.0%; Score 20; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20  
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Db 35 AGGGAGGGAGGGAGGGG 16

RESULT 5  
AR091424/c  
LOCUS AR091424 27 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 14 from patent US 5994109.  
ACCESSION AR091424  
VERSION AR091424.1 GI:10018179  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Woo, S.L.C., Smith, L.C., Cristiano, R.J., Gottchalk, S. and Sparrow, J.  
TITLE Nucleic acid transporter system and methods of use  
JOURNAL Patent: US 5994109-A 14 30-NOV-1999;  
FEATURES  
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1. .27  
/organism="unknown"  
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ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 27;  
Best Local Similarity 94.7%; Pred. No. 8.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 19  
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Db 24 AGGGAGGGAGGGAGGGG 6

RESULT 6  
AR091425  
LOCUS AR091425 27 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 15 from patent US 5994109.  
ACCESSION AR091425  
VERSION AR091425.1 GI:10018180  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Woo, S.L.C., Smith, L.C., Cristiano, R.J., Gottchalk, S. and Sparrow, J.  
TITLE Nucleic acid transporter system and methods of use  
JOURNAL Patent: US 5994109-A 15 30-NOV-1999;  
FEATURES  
source  
Location/Qualifiers  
1. .27  
/organism="unknown"  
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ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 27;  
Best Local Similarity 94.7%; Pred. No. 8.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 19  
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Db 4 AAGGGAGGGAGGGAGGGG 22

RESULT 7  
AR125629/c  
LOCUS AR125629 27 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 14 from patent US 6177554.  
ACCESSION AR125629  
VERSION AR125629.1 GI:14111691  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Woo, S.L.C., Smith, L.C., Cristiano, R.J., Gottchalk, S. and Sparrow, J.  
TITLE Nucleic acid transporter systems  
JOURNAL Patent: US 6177554-A 14 23-JAN-2001;  
FEATURES  
source  
Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 27;  
Best Local Similarity 94.7%; Pred. No. 8.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 19  
|||||  
Db 24 AGGGAGGGAGGGAGGGG 6

RESULT 8  
AR125630  
LOCUS AR125630 27 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 15 from patent US 6177554.  
ACCESSION AR125630

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|---------------------------------|---|----------------------------------|
| VERSION                         | AR125630.1  | GI:14111692                      |
| KEYWORDS                        | Unknown.  |                                  |
| SOURCE                          | Unknown.  |                                  |
| ORGANISM                        | Unclassified.   |                                  |
| REFERENCE                       | 1 (bases 1 to 27)   |                                  |
| AUTHORS                         | Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J. |                                  |
| TITLE                           | Nucleic acid transporter systems                                    |                                  |
| JOURNAL                         | Patent: US 6177554-A 15 23-JAN-2001;                                |                                  |
| FEATURES                        | Location/Qualifiers   |                                  |
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| ORIGIN                          |   |                                  |
| Query Match                     | 87.0%; Score 17.4; DB 6; Length 27;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.8e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 4 AAGGGAGGGAGGGAGGG 22  |                                  |
| RESULT 9                        |   |                                  |
| LOCUS                           | AX477591  | 30 bp DNA linear PAT 12-AUG-2002 |
| DEFINITION                      | Sequence 43 from Patent WO0246433.                                  |                                  |
| ACCESSION                       | AX477591  |                                  |
| VERSION                         | AX477591.1  | GI:22216771                      |
| KEYWORDS                        | synthetic construct   |                                  |
| SOURCE                          | synthetic construct   |                                  |
| ORGANISM                        | other sequences; artificial sequences.                              |                                  |
| REFERENCE                       | 1   |                                  |
| AUTHORS                         | Saus,J.   |                                  |
| TITLE                           | Tnf-inducible promoters and methods for using                       |                                  |
| JOURNAL                         | Patent: WO 0246433-A 43 13-JUN-2002;                                |                                  |
| FEATURES                        | Saus, Juan (ES)   |                                  |
| source                          | Location/Qualifiers   |                                  |
| 1..30                           |   |                                  |
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| /note="Primer ON-TATADel"       |   |                                  |
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| Query Match                     | 87.0%; Score 17.4; DB 6; Length 30;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.7e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 2 AGGGAGGGGAGGGGTGG 20  |                                  |
| RESULT 10                       |   |                                  |
| LOCUS                           | AX505011  | 30 bp DNA linear PAT 27-SRP-2002 |
| DEFINITION                      | Sequence 43 from Patent WO0246378.                                  |                                  |
| ACCESSION                       | AX505011  |                                  |
| VERSION                         | AX505011.1  | GI:23386333                      |
| KEYWORDS                        | synthetic construct   |                                  |
| SOURCE                          | synthetic construct   |                                  |
| ORGANISM                        | other sequences; artificial sequences.                              |                                  |
| REFERENCE                       | 1   |                                  |
| AUTHORS                         | Saus,J.   |                                  |
| TITLE                           | Alternative pol k nucleotide and amino acid sequence and methods    |                                  |
| JOURNAL                         | for using   |                                  |
| FEATURES                        | Patent: WO 0246378-A 43 13-JUN-2002;                                |                                  |
| source                          | Saus, Juan (ES)   |                                  |
| Location/Qualifiers             |   |                                  |
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| Query Match                     | 87.0%; Score 17.4; DB 6; Length 30;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.7e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 2 AGGGAGGGGAGGGGTGG 20  |                                  |
| RESULT 11                       |   |                                  |
| LOCUS                           | AR091423  | 39 bp DNA linear PAT 07-SEP-2000 |
| DEFINITION                      | Sequence 13 from patent US 5994109.                                 |                                  |
| ACCESSION                       | AR091423  |                                  |
| VERSION                         | AR091423.1  | GI:10018178                      |
| KEYWORDS                        | Unknown.  |                                  |
| SOURCE                          | Unknown.  |                                  |
| ORGANISM                        | Unclassified.   |                                  |
| REFERENCE                       | 1 (bases 1 to 39)   |                                  |
| AUTHORS                         | Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J. |                                  |
| TITLE                           | Nucleic acid transporter system and methods of use                  |                                  |
| JOURNAL                         | Patent: US 5994109-A 13 30-NOV-1999;                                |                                  |
| FEATURES                        | Location/Qualifiers   |                                  |
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| ORIGIN                          |   |                                  |
| Query Match                     | 87.0%; Score 17.4; DB 6; Length 39;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.3e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 10 AAGGGAGGGGAGGGGAGGG 28   |                                  |
| RESULT 12                       |   |                                  |
| LOCUS                           | AR125628  | 39 bp DNA linear PAT 16-MAY-2001 |
| DEFINITION                      | Sequence 13 from patent US 6177554.                                 |                                  |
| ACCESSION                       | AR125628  |                                  |
| VERSION                         | AR125628.1  | GI:14111690                      |
| KEYWORDS                        | Unknown.  |                                  |
| SOURCE                          | Unknown.  |                                  |
| ORGANISM                        | Unclassified.   |                                  |
| REFERENCE                       | 1 (bases 1 to 39)   |                                  |
| AUTHORS                         | Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J. |                                  |
| TITLE                           | Nucleic acid transporter systems                                    |                                  |
| JOURNAL                         | Patent: US 6177554-A 13 23-JAN-2001;                                |                                  |
| FEATURES                        | Location/Qualifiers   |                                  |
| source                          | 1..39   |                                  |
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| Query Match                     | 87.0%; Score 17.4; DB 6; Length 39;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.3e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 10 AAGGGAGGGGAGGGGAGGG 28   |                                  |
| RESULT 13                       |   |                                  |
| LOCUS                           | AX505011  | 30 bp DNA linear PAT 27-SRP-2002 |
| DEFINITION                      | Sequence 43 from Patent WO0246378.                                  |                                  |
| ACCESSION                       | AX505011  |                                  |
| VERSION                         | AX505011.1  | GI:23386333                      |
| KEYWORDS                        | synthetic construct   |                                  |
| SOURCE                          | synthetic construct   |                                  |
| ORGANISM                        | other sequences; artificial sequences.                              |                                  |
| REFERENCE                       | 1   |                                  |
| AUTHORS                         | Saus,J.   |                                  |
| TITLE                           | Alternative pol k nucleotide and amino acid sequence and methods    |                                  |
| JOURNAL                         | for using   |                                  |
| FEATURES                        | Patent: WO 0246378-A 43 13-JUN-2002;                                |                                  |
| source                          | Saus, Juan (ES)   |                                  |
| Location/Qualifiers             |   |                                  |
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| /note="Primer ON-TATADel"       |   |                                  |
| ORIGIN                          |   |                                  |
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| Best Local Similarity           | 94.7%; Pred. No. 8.7e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 2 AGGGAGGGGAGGGGTGG   |                                  |

|                                 |   |                                  |
|---------------------------------|---|----------------------------------|
| VERSION                         | AR125630.1  | GI:14111692                      |
| KEYWORDS                        | Unknown.  |                                  |
| SOURCE                          | Unknown.  |                                  |
| ORGANISM                        | Unclassified.   |                                  |
| REFERENCE                       | 1 (bases 1 to 27)   |                                  |
| AUTHORS                         | Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J. |                                  |
| TITLE                           | Nucleic acid transporter systems                                    |                                  |
| JOURNAL                         | Patent: US 6177554-A 15 23-JAN-2001;                                |                                  |
| FEATURES                        | Location/Qualifiers   |                                  |
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| Query Match                     | 87.0%; Score 17.4; DB 6; Length 27;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.8e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 4 AAGGGAGGGGAGGGAGGG 22   |                                  |
| RESULT 9                        |   |                                  |
| LOCUS                           | AX477591  | 30 bp DNA linear PAT 12-AUG-2002 |
| DEFINITION                      | Sequence 43 from Patent WO0246433.                                  |                                  |
| ACCESSION                       | AX477591  |                                  |
| VERSION                         | AX477591.1  | GI:22216771                      |
| KEYWORDS                        | synthetic construct   |                                  |
| SOURCE                          | synthetic construct   |                                  |
| ORGANISM                        | other sequences; artificial sequences.                              |                                  |
| REFERENCE                       | 1   |                                  |
| AUTHORS                         | Saus,J.   |                                  |
| TITLE                           | Tnf-inducible promoters and methods for using                       |                                  |
| JOURNAL                         | Patent: WO 0246433-A 43 13-JUN-2002;                                |                                  |
| FEATURES                        | Saus, Juan (ES)   |                                  |
| source                          | Location/Qualifiers   |                                  |
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| /note="Primer ON-TATADel"       |   |                                  |
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| Query Match                     | 87.0%; Score 17.4; DB 6; Length 30;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.7e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 2 AGGGAGGGGAGGGGTGGG 20   |                                  |
| RESULT 10                       |   |                                  |
| AX505011                        |   |                                  |
| LOCUS                           | AX505011  | 30 bp DNA linear PAT 27-SRP-2002 |
| DEFINITION                      | Sequence 43 from Patent WO0246378.                                  |                                  |
| ACCESSION                       | AX505011  |                                  |
| VERSION                         | AX505011.1  | GI:23386333                      |
| KEYWORDS                        | synthetic construct   |                                  |
| SOURCE                          | synthetic construct   |                                  |
| ORGANISM                        | other sequences; artificial sequences.                              |                                  |
| REFERENCE                       | 1   |                                  |
| AUTHORS                         | Saus,J.   |                                  |
| TITLE                           | Alternative pol k nucleotide and amino acid sequence and methods    |                                  |
| JOURNAL                         | for using   |                                  |
| Patent:                         | WO 0246378-A 43 13-JUN-2002;  |                                  |
| Saus, Juan (ES)                 |   |                                  |
| LOCATION/QUALIFIERS             |   |                                  |
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| /db_xref="taxon:32630"          |   |                                  |
| /note="Primer ON-TATADel"       |   |                                  |
| ORIGIN                          |   |                                  |
| Query Match                     | 87.0%; Score 17.4; DB 6; Length 30;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.7e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 2 AGGGAGGGGAGGGGTGGG 20   |                                  |
| RESULT 11                       |   |                                  |
| AX091423                        |   |                                  |
| LOCUS                           | AR091423  | 39 bp DNA linear PAT 07-SEP-2000 |
| DEFINITION                      | Sequence 13 from patent US 5994109.                                 |                                  |
| ACCESSION                       | AR091423  |                                  |
| VERSION                         | AR091423.1  | GI:10018178                      |
| KEYWORDS                        | Unknown.  |                                  |
| SOURCE                          | Unknown.  |                                  |
| ORGANISM                        | Unclassified.   |                                  |
| REFERENCE                       | 1 (bases 1 to 39)   |                                  |
| AUTHORS                         | Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J. |                                  |
| TITLE                           | Nucleic acid transporter system and methods of use                  |                                  |
| JOURNAL                         | Patent: US 5994109-A 13 30-NOV-1999;                                |                                  |
| FEATURES                        | Location/Qualifiers   |                                  |
| source                          | 1..39   |                                  |
| /organism="unknown"             |   |                                  |
| /mol_type="unassigned DNA"      |   |                                  |
| ORIGIN                          |   |                                  |
| Query Match                     | 87.0%; Score 17.4; DB 6; Length 39;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.3e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 10 AAGGGAGGGGAGGGAGGG 28  |                                  |
| RESULT 12                       |   |                                  |
| AR125628                        |   |                                  |
| LOCUS                           | AR125628  | 39 bp DNA linear PAT 16-MAY-2001 |
| DEFINITION                      | Sequence 13 from patent US 6177554.                                 |                                  |
| ACCESSION                       | AR125628  |                                  |
| VERSION                         | AR125628.1  | GI:14111690                      |
| KEYWORDS                        | Unknown.  |                                  |
| SOURCE                          | Unknown.  |                                  |
| ORGANISM                        | Unclassified.   |                                  |
| REFERENCE                       | 1 (bases 1 to 39)   |                                  |
| AUTHORS                         | Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J. |                                  |
| TITLE                           | Nucleic acid transporter systems                                    |                                  |
| JOURNAL                         | Patent: US 6177554-A 13 23-JAN-2001;                                |                                  |
| FEATURES                        | Location/Qualifiers   |                                  |
| source                          | 1..39   |                                  |
| /organism="unknown"             |   |                                  |
| /mol_type="unassigned DNA"      |   |                                  |
| ORIGIN                          |   |                                  |
| Query Match                     | 87.0%; Score 17.4; DB 6; Length 39;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.3e+03;   |                                  |
| Matches                         | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |                                  |
| Qy                              | 1 AGGGAGGGGAGGGAGGG 19  |                                  |
| Db                              | 10 AAGGGAGGGGAGGGAGGG 28  |                                  |
| RESULT 13                       |   |                                  |
| AX050501                        |   |                                  |
| LOCUS                           | AX050501  | 30 bp DNA linear PAT 27-SRP-2002 |
| DEFINITION                      | Sequence 43 from Patent WO0246378.                                  |                                  |
| ACCESSION                       | AX050501  |                                  |
| VERSION                         | AX050501.1  | GI:23386333                      |
| KEYWORDS                        | synthetic construct   |                                  |
| SOURCE                          | synthetic construct   |                                  |
| ORGANISM                        | other sequences; artificial sequences.                              |                                  |
| REFERENCE                       | 1   |                                  |
| AUTHORS                         | Saus,J.   |                                  |
| TITLE                           | Alternative pol k nucleotide and amino acid sequence and methods    |                                  |
| JOURNAL                         | for using   |                                  |
| Patent:                         | WO 0246378-A 43 13-JUN-2002;  |                                  |
| Saus, Juan (ES)                 |   |                                  |
| LOCATION/QUALIFIERS             |   |                                  |
| 1..30                           |   |                                  |
| /organism="synthetic construct" |   |                                  |
| /mol_type="unassigned DNA"      |   |                                  |
| /db_xref="taxon:32630"          |   |                                  |
| /note="Primer ON-TATADel"       |   |                                  |
| ORIGIN                          |   |                                  |
| Query Match                     | 87.0%; Score 17.4; DB 6; Length 30;                                 |                                  |
| Best Local Similarity           | 94.7%; Pred. No. 8.7e+03;   |                                  |
| Matches</                       |   |                                  |

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RESULT 13
AR356035/c
LOCUS          AR356035          50 bp      DNA          linear      PAT 17-AUG-2003
DEFINITION     Sequence 2153 from patent US 6593114.
ACCESSION      AR356035
VERSION        AR356035.1  GI:33762119
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 50)
AUTHORS       Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and
              Rosen,C.A.
TITLE         Scaphylococcus aureus polynucleotides and sequences
JOURNAL       Patent: US 6593114-A 2153 15-JUL-2003;
              Human Genome Sciences, Inc.; Rockville, MD
FEATURES       source
               1..50
               /organism="unknown"
               /mol_type="genomic DNA"
ORIGIN
Query Match      82.0%; Score 16.4; DB 6; Length 50;
Best Local Similarity 89.5%; Pred. No. 1.9e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  GGGAGGGGGAGGGAGGGG 20
      |||||
Db   28 GGGGGGGGGGGAGGGGG 10

RESULT 14
AR337591/c
LOCUS          AR337591          50 bp      DNA          linear      PAT 08-OCT-2004
DEFINITION     Sequence 2153 from patent US 6737248.
ACCESSION      AR337591
VERSION        AR337591.1  GI:53928808
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 50)
AUTHORS       Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
              Rosen,C.A.
TITLE         Scaphylococcus aureus polynucleotides and sequences
JOURNAL       Patent: US 6737248-A 2153 18-MAY-2004;
              Human Genome Sciences, Inc.; Rockville, MD
FEATURES       source
               1..50
               /organism="unknown"
               /mol_type="genomic DNA"
ORIGIN
Query Match      82.0%; Score 16.4; DB 6; Length 50;
Best Local Similarity 89.5%; Pred. No. 1.9e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  GGGAGGGGGAGGGAGGGG 20
      |||||
Db   28 GGGGGGGGGGGAGGGGG 10

RESULT 15
BD202728/c
LOCUS          BD202728          17 bp      RNA          linear      PAT 17-JUL-2003
DEFINITION     Method and reagent for treating diseases or conditions concerning
              molecule participating in vasculogenic response.
ACCESSION      BD202728
VERSION        BD202728.1  GI:33012498
KEYWORDS       JP 2002509721-A/5754.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
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```
REFERENCE      1 (bases 1 to 17)
AUTHORS       Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE         Method and reagent for treating diseases or conditions concerning
              molecule participating in vasculogenic response
JOURNAL       Patent: JP 2002509721-A 5754 02-APR-2002;
              RIBOZYME PHARMACEUTICALS INC
COMMENT       OS Homo sapiens (human)
              PN JP 2002509721-A/5754
              PD 02-APR-2002
              PF 24-MAR-1999 JP 2000541291
              PR 27-MAR-1998 US 60/079678
              PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
              PI JAMES A MCSWIGGEN
              PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
              PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
              CC Method and reagent for treating diseases or conditions CC
              concerning molecule
              CC participating in vasculogenic response
              FH Key Location/Qualifiers
              FT source 1..17
              FT /organism='Homo sapiens (human)'.
FEATURES       source
               1..17
               /organism="Homo sapiens"
               /mol_type="genomic RNA"
               /db_xref="taxon:9606"
ORIGIN
Query Match      80.0%; Score 16; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3  GGGAGGGGGAGGGAGG 18
      |||||
Db   16 GGGAGGGGGAGGGAGG 1

RESULT 16
E59332
LOCUS          E59332          20 bp      DNA          linear      PAT 31-JAN-2002
DEFINITION     Method for purifying oligonucleotide.
ACCESSION      E59332
VERSION        E59332.1  GI:18622509
KEYWORDS       JP 2000342265-A/13.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Hirose,K. and Yoshida,T.
TITLE         Method for purifying oligonucleotide
JOURNAL       Patent: JP 2000342265-A 13 12-DEC-2000;
              TOAGOSEI CHEM IND CO LTD
COMMENT       OS Artificial Sequence
              PN JP 2000342265-A/13
              PD 12-DEC-2000
              PF 02-JUN-1999 JP 1999154974
              PR KUNIHICO HIROSE,TADAO YOSHIDA
              PI C12N15/09,B01D15/08,C12N15/00
              CC Key Location/Qualifiers
              FH Key 1..20
              FT source /organism='Artificial Sequence'.
              FT Location/Qualifiers
              FT 1..20
              /organism="synthetic construct"
              /mol_type="genomic DNA"
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/db\_xref="taxon:32630"

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 20;  
Best Local Similarity 89.5%; Pred. No. 3.7e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 2 GGGGCGGGGGGGGAGGGG 20

RESULT 17  
BD078154  
LOCUS BD078154.1 GI:22623757 26 bp DNA linear PAT 27-AUG-2002  
DEFINITION Modulator of DNA cytosine-5 methyltransferase and method of using  
the same.

ACCESSION BD078154  
VERSION BD078154.1 GI:22623757  
KEYWORDS JP 2001514862-A/38.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 26)  
AUTHORS Reich,N.O. and Flynn,J.  
TITLE Modulator of DNA cytosine-5 methyltransferase and method of using  
the same

JOURNAL Patent: JP 2001514862-A 38 18-SEP-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

COMMENT OS 'Unidentified  
PN JP 2001514862-A/38  
PD 18-SEP-2001  
PF 12-JUN-1998 JP 2000508978  
PR 29-AUG-1997 US 60/057411  
PI NORBERT O REICH,JAMES FLYNN  
PC C12N9/10,C12Q1/48//C12N15/09,C12N15/00  
CC Strandedness: Double;  
CC Topology: linear;  
CC Modulator of DNA cytosine-5 methyltransferase and method of  
using the same  
FH Key Location/Qualifiers  
FT source 1..26  
FT Location/Qualifiers  
1..26  
/organism='Unidentified'.  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

FEATURES  
source

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 26;  
Best Local Similarity 89.5%; Pred. No. 3.5e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 2 GGGGCGGGGAGGGGAGGGG 20

RESULT 18  
AR362756  
LOCUS AR362756  
DEFINITION Sequence 21 from patent US 5182196.  
ACCESSION AR362756  
VERSION AR362756.1 GI:34423141  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 42)  
AUTHORS Allet,B. and Kawashima,E.H.  
TITLE Expression systems for overproduction of desired proteins  
Patent: US 5182196-A 21 26-JAN-1993;  
JOURNAL

Biogen, Inc.; Cambridge, MA;  
EPX;

FEATURES  
source Location/Qualifiers  
1..42  
/organism='unknown'  
/mol\_type='genomic DNA'

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 42;  
Best Local Similarity 89.5%; Pred. No. 3.3e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 17 GGGGCGGGGGGGGAGGGG 35

RESULT 19  
A28677  
LOCUS A28677 43 bp DNA linear PAT 04-JUN-1995  
DEFINITION Oligonucleotide 1.  
ACCESSION A28677  
VERSION A28677.1 GI:1248716  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 43)  
AUTHORS  
TITLE SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE  
JOURNAL Patent: WO 9014090-A 5 29-NOV-1990;  
FEATURES Location/Qualifiers  
1..43  
/organism='synthetic construct'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:32630'

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 43;  
Best Local Similarity 89.5%; Pred. No. 3.3e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 11 GGGGCGGGGAGGGGAGGGG 29

RESULT 20  
A28678/c  
LOCUS A28678 43 bp DNA linear PAT 04-JUN-1995  
DEFINITION Oligonucleotide 2 (comp.).  
ACCESSION A28678  
VERSION A28678.1 GI:1248717  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 43)  
AUTHORS  
TITLE SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE  
JOURNAL Patent: WO 9014090-A 6 29-NOV-1990;  
FEATURES Location/Qualifiers  
1..43  
/organism='synthetic construct'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:32630'

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 43;  
Best Local Similarity 89.5%; Pred. No. 3.3e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20

```
Db          37 GGGGGGGGAGGGGGGGG 19
||||| ||||| ||||| ||||| |||||
RESULT 21
A28674/c
LOCUS      A28674                44 bp    RNA          linear    PAT 04-JUN-1995
DEFINITION dsRNA with terminal locks (comp.).
ACCESSION  A28674
VERSION    A28674.1 GI:1248713
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1 (bases 1 to 44)
AUTHORS    .
TITLE      SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
JOURNAL    Patent: WO 9014090-A 2 29-NOV-1990;
FEATURES   Location/Qualifiers
            source
            1..44
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      79.0%; Score 15.8; DB 6; Length 44;
Best Local Similarity 89.5%; Pred. No. 3.2e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2 GGGGAGGGGAGGGGAGGGG 20
        ||||| ||||| ||||| |||||
Db      43 GGGGGGGGAGGGGGGGG 25
        ||||| ||||| ||||| |||||
RESULT 22
A28685/c
LOCUS      A28685                47 bp    RNA          linear    PAT 04-JUN-1995
DEFINITION Oligonucleotide 9.
ACCESSION  A28685
VERSION    A28685.1 GI:1248724
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1 (bases 1 to 47)
AUTHORS    .
TITLE      SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
JOURNAL    Patent: WO 9014090-A 13 29-NOV-1990;
FEATURES   Location/Qualifiers
            source
            1..47
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      79.0%; Score 15.8; DB 6; Length 47;
Best Local Similarity 89.5%; Pred. No. 3.2e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2 GGGGAGGGGAGGGGAGGGG 20
        ||||| ||||| ||||| |||||
Db      40 GGGGGGGGAGGGGGGGG 22
        ||||| ||||| ||||| |||||
RESULT 23
CQ003486/c
LOCUS      CQ003486                50 bp    DNA          linear    PAT 16-JAN-2004
DEFINITION Sequence 2126 from Patent WO0147944.
ACCESSION  CQ003486
VERSION    CQ003486.1 GI:41010118
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS    Shimkets,R.A. and Leach,M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL    Patent: WO 0147944-A 2126 05-JUL-2001;
            Curagen Corporation (US)
FEATURES   Location/Qualifiers
            source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            misc_feature
            25..26
            /note="Nucleotide deleted between bases 25 and 26
            Accession number cg44131752"
ORIGIN
Query Match      79.0%; Score 15.8; DB 6; Length 50;
Best Local Similarity 89.5%; Pred. No. 3.2e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2 GGGGAGGGGAGGGGAGGGG 20
        ||||| ||||| ||||| |||||
Db      44 GGGGAGGGGAAGGGGGG 26
        ||||| ||||| ||||| |||||
RESULT 24
CQ003487/c
LOCUS      CQ003487                50 bp    DNA          linear    PAT 16-JAN-2004
DEFINITION Sequence 2127 from Patent WO0147944.
ACCESSION  CQ003487
VERSION    CQ003487.1 GI:41010119
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE 1
AUTHORS    Shimkets,R.A. and Leach,M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL    Patent: WO 0147944-A 2127 05-JUL-2001;
            Curagen Corporation (US)
FEATURES   Location/Qualifiers
            source
            1..50
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            misc_feature
            25..26
            /note="Nucleotide deleted between bases 25 and 26
            Accession number cg44131752"
ORIGIN
Query Match      79.0%; Score 15.8; DB 6; Length 50;
Best Local Similarity 89.5%; Pred. No. 3.2e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2 GGGGAGGGGAGGGGAGGGG 20
        ||||| ||||| ||||| |||||
Db      36 GGGGAGGGGAAGGGGGG 18
        ||||| ||||| ||||| |||||
RESULT 25
CQ006699
LOCUS      CQ006699                50 bp    DNA          linear    PAT 16-JAN-2004
DEFINITION Sequence 5339 from Patent WO0147944.
ACCESSION  CQ006699
VERSION    CQ006699.1 GI:41013331
KEYWORDS   .
SOURCE     Homo sapiens (human)
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Shimkets, R.A. and Leach, M.  
AUTHORS Nucleic acids containing single nucleotide polymorphisms and  
TITLE methods of use thereof  
JOURNAL Patent: WO 0147944-A 5339 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
misc\_feature 25..26  
/note="Nucleotide deleted between bases 25 and 26"  
Accession number CG43267341"  
ORIGIN  
Query Match 79.0%; Score 15.8; DB 6; Length 50;  
Best Local Similarity 89.5%; Pred. No. 3.2e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AGGGAGGGAGGGAGGG 19  
|| ||||| ||||| |||||  
Db 10 AGAGGAGGAGAGGGAGGG 28  
|| ||||| ||||| |||||  
RESULT 26  
LOCUS CQ006700 50 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 5340 from Patent WO0147944.  
ACCESSION CQ006700  
VERSION CQ006700.1 GI:41013332  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Shimkets, R.A. and Leach, M.  
AUTHORS Nucleic acids containing single nucleotide polymorphisms and  
TITLE methods of use thereof  
JOURNAL Patent: WO 0147944-A 5340 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
source 1..50  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
misc\_feature 25..26  
/note="Nucleotide deleted between bases 25 and 26"  
Accession number CG43267341"  
ORIGIN  
Query Match 79.0%; Score 15.8; DB 6; Length 50;  
Best Local Similarity 89.5%; Pred. No. 3.2e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AGGGAGGGAGGGAGGG 19  
|| ||||| ||||| |||||  
Db 7 AGAGGAGGAGAGGGAGGG 25  
|| ||||| ||||| |||||  
RESULT 27  
LOCUS BD202727/c 17 bp RNA linear PAT 17-JUL-2003  
DEFINITION Method and reagent for treating diseases or conditions concerning  
TITLE molecule participating in vasculogenic response.  
ACCESSION BD202727  
VERSION BD202727.1 GI:33012497

KEYWORDS JP 2002509721-A/5753.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 17)  
REFERENCE Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswigen, J.A.  
AUTHORS Method and reagent for treating diseases or conditions concerning  
TITLE molecule participating in vasculogenic response  
JOURNAL Patent: JP 2002509721-A 5753 02-APR-2002;  
RIBOZYME PHARMACEUTICALS INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002509721-A/5753  
PD 02-APR-2002  
PF 24-MAR-1999 JP 2000541291  
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,  
PI JAMES A MCSWIGGEN  
PC  
C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC  
A61P29/00,  
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC  
C12N5/00  
CC Method and reagent for treating diseases or conditions CC  
concerning molecule  
CC participating in vasculogenic response  
FH Key Location/Qualifiers  
FT source 1..17  
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FEATURES Location/Qualifiers  
source 1..17  
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/mol\_type="genomic RNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 77.0%; Score 15.4; DB 6; Length 17;  
Best Local Similarity 94.1%; Pred. No. 5.3e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 GGGGAGGGAGGGAGGG 18  
|| ||||| ||||| |||||  
Db 17 GGGGAGGGAGGGAGGGACG 1  
|| ||||| ||||| |||||  
RESULT 28  
LOCUS AR110134 37 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 2 from patent US 6114154.  
ACCESSION AR110134  
VERSION AR110134.1 GI:12826410  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 37)  
AUTHORS Li, H.  
TITLE Method of constructing full-length target cDNA molecules  
JOURNAL Patent: US 6114154-A 2 05-SEP-2000;  
FEATURES Location/Qualifiers  
source 1..37  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 76.0%; Score 15.2; DB 6; Length 37;  
Best Local Similarity 85.0%; Pred. No. 5.6e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 AGGGAGGGAGGGAGGGGGG 20  
|| ||||| ||||| |||||  
Db 16 AGGGAAGGGGGGGGGGGGG 35  
|| ||||| ||||| |||||

```
RESULT 29
I41099/c
LOCUS           I41099           38 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION      Sequence 2 from patent US 5624803.
ACCESSION       I41099
VERSION         I41099.1 GI:2081689
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 38)
AUTHORS         Noonberg S.B. and Hunt C.Anthony.
TITLE           In vivo oligonucleotide generator, and methods of testing the
                binding affinity of triplex forming oligonucleotides derived
                therefrom
JOURNAL
FEATURES        Patent: US 5624803-A 2 29-APR-1997;
                Location/Qualifiers
                1..38
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match    76.0%; Score 15.2; DB 6; Length 38;
Best Local Similarity 85.0%; Pred. No. 5.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 27 AGGGGAAGGAAGGAAGGG 8

RESULT 30
A23688/c
LOCUS           A23688           41 bp      DNA      linear      PAT 25-NOV-1994
DEFINITION      L. monocytogenes HlyA gene probe-primer.
ACCESSION       A23688
VERSION         A23688.1 GI:641736
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        other sequences; artificial sequences.
REFERENCE       1 (bases 1 to 41)
AUTHORS         METHODS OF DETECTING OR QUANTITATING NUCLEIC ACIDS AND OF PRODUCING
                LABELLED IMMOBILISED NUCLEIC ACIDS
JOURNAL         Patent: WO 9304199-A 4 04-MAR-1993;
FEATURES        Location/Qualifiers
                1..41
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
ORIGIN
Query Match    76.0%; Score 15.2; DB 6; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 21 AGGGGGGGGGGGGGGGGG 2

RESULT 31
A23689/c
LOCUS           A23689           41 bp      DNA      linear      PAT 25-NOV-1994
DEFINITION      L. monocytogenes HlyA gene probe-primer.
ACCESSION       A23689
VERSION         A23689.1 GI:641737
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        synthetic construct
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other sequences; artificial sequences.
REFERENCE       1 (bases 1 to 41)
AUTHORS         METHODS OF DETECTING OR QUANTITATING NUCLEIC ACIDS AND OF PRODUCING
                LABELLED IMMOBILISED NUCLEIC ACIDS
JOURNAL         Patent: WO 9304199-A 5 04-MAR-1993;
FEATURES        Location/Qualifiers
                1..41
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
ORIGIN
Query Match    76.0%; Score 15.2; DB 6; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 21 AGGGGGGGGGGGGGGGGG 2

RESULT 32
AX058552
LOCUS           AX058552           15 bp      DNA      linear      PAT 17-JAN-2001
DEFINITION      Sequence 4 from Patent WO0077250.
ACCESSION       AX058552
VERSION         AX058552.1 GI:12310894
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        synthetic construct
                other sequences; artificial sequences.
REFERENCE       1
AUTHORS         Escude, C., Garestier, T., Helene, C. and Roulon, T.
TITLE           Method for circularizing oligonucleotides around a double stranded
                nucleic acid, resulting structures and uses thereof
JOURNAL         Patent: WO 0077250-A 4 21-DEC-2000;
                INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
                (FR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES        Location/Qualifiers
                1..15
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"
ORIGIN
Query Match    75.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GAGGGGAGGGGAGGGG 19
    ||||| ||||| ||||| |||||
Db 1 GAGGGGAGGGGAGGGG 15

RESULT 33
AX514983
LOCUS           AX514983           41 bp      DNA      linear      PAT 05-OCT-2002
DEFINITION      Sequence 1181 from Patent WO02052044.
ACCESSION       AX514983
VERSION         AX514983.1 GI:23561811
KEYWORDS        .
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE       1
AUTHORS         Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE           Detection of genetic polymorphisms
JOURNAL         Patent: WO 02052044-A 1181 04-JUL-2002;
                Riken (JP)
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FEATURES
  source
    Location/Qualifiers
      1..41
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
ORIGIN
  Query Match 75.0%; Score 15; DB 6; Length 41;
  Best Local Similarity 88.2%; Pred. No. 6.6e+04;
  Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GGAGGGGAGGGAGGGG 20
  ||| |||||:|||||
Db 10 GGAAGGGAGGGAGGGG 26

RESULT 34
AX519178 AX519178 41 bp DNA linear PAT 05-OCT-2002
LOCUS
DEFINITION Sequence 5376 from Patent WO02052044.
ACCESSION AX519178
VERSION AX519178.1 GI:23569300
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1 Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  Detection of genetic polymorphisms
  TITLE Patent: WO 02052044-A 5376 04-JUL-2002;
  Riken (JP)
FEATURES
  source
    Location/Qualifiers
      1..41
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
ORIGIN
  Query Match 75.0%; Score 15; DB 6; Length 41;
  Best Local Similarity 88.2%; Pred. No. 6.6e+04;
  Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GGAGGGGAGGGAGGGG 20
  ||| |||||:|||||
Db 10 GGAAGGGAGGGAGGGG 26

RESULT 35
BD078171 BD078171 26 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Modulator of DNA cytosine-5 methyltransferase and method of using
the same.
ACCESSION BD078171
VERSION BD078171.1 GI:22623774
KEYWORDS JP 2001514862-A/55.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
  1 (bases 1 to 26)
  Reich,N.O. and Flynn,J.
  Modulator of DNA cytosine-5 methyltransferase and method of using
  the same
  TITLE Patent: JP 2001514862-A 55 18-SEP-2001;
  THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
JOURNAL
COMMENT OS Unidentified
PN JP 2001514862-A/55
PF 12-JUN-1998 JP 2000508978
PP 29-AUG-1997 US 60/057411
PI NORBERT O REICH,JAMES FLYNN
PC C12N9/10,C12Q1/48//C12N15/09,C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
CC Modulator of DNA cytosine-5 methyltransferase and method of
using the same
  Key 1..26
  Location/Qualifiers
  FT source
    Location/Qualifiers
      1..26
      /organism="Unidentified".
FEATURES
  source
    Location/Qualifiers
      1..26
      /organism="Unidentified"
      /mol_type="genomic DNA"
      /db_xref="taxon:32644"
ORIGIN
  Query Match 74.0%; Score 14.8; DB 6; Length 26;
  Best Local Similarity 88.9%; Pred. No. 8.4e+04;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 GGGAGGGGAGGGAGGGG 20
  ||| |||||:|||||
Db 3 GGGGGGGGAGCGAGGGG 20

RESULT 36
BD078223 BD078223 26 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Modulator of DNA cytosine-5 methyltransferase and method of using
the same.
ACCESSION BD078223
VERSION BD078223.1 GI:22623826
KEYWORDS JP 2001514862-A/107.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
  1 (bases 1 to 26)
  Reich,N.O. and Flynn,J.
  Modulator of DNA cytosine-5 methyltransferase and method of using
  the same
  TITLE Patent: JP 2001514862-A 107 18-SEP-2001;
  THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
JOURNAL
COMMENT OS Unidentified
PN JP 2001514862-A/107
PF 12-JUN-1998 JP 2000508978
PP 29-AUG-1997 US 60/057411
PI NORBERT O REICH,JAMES FLYNN
PC C12N9/10,C12Q1/48//C12N15/09,C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
CC Modulator of DNA cytosine-5 methyltransferase and method of
using the same
  Key 1..26
  Location/Qualifiers
  FT source
    Location/Qualifiers
      1..26
      /organism="Unidentified"
      /mol_type="genomic DNA"
      /db_xref="taxon:32644"
FEATURES
  source
    Location/Qualifiers
      1..26
      /organism="Unidentified"
      /mol_type="genomic DNA"
      /db_xref="taxon:32644"
ORIGIN
  Query Match 74.0%; Score 14.8; DB 6; Length 26;
  Best Local Similarity 88.9%; Pred. No. 8.4e+04;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 GGGAGGGGAGGGAGGGG 20
  ||| |||||:|||||
Db 3 GGGGGGGGAGCGAGGGG 20

RESULT 37
AR121366 AR121366 30 bp DNA linear PAT 16-MAY-2001
LOCUS

```

DEFINITION Sequence 18 from patent US 6159720.  
ACCESSION AR121366  
VERSION AR121366.1 GI:14104942  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Murashima,K., Moriya,T., Hamaya,T., Koga,J., Sumida,N., Aoyagi,K., Murakami,T. and Kono,T.  
TITLE Enzyme endoglucanase and cellulase preparations containing the same  
JOURNAL Patent: US 6159720-A 18 12-DEC-2000;  
FEATURES Location/Qualifiers  
source 1..30  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 30;  
Best Local Similarity 88.9%; Pred. No. 8.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCGAGGGGAGGGAGG 18  
||| ||||| ||||| |||||  
Db 25 AGCGAGGAGAGGGGAGG 8

RESULT 38  
AR213275/c  
LOCUS AR213275 30 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 25 from patent US 6403362.  
ACCESSION AR213275  
VERSION AR213275.1 GI:23310445  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Moriya,T., Murashima,K., Aoyagi,K., Sumida,N., Watanabe,M., Hamaya,T., Koga,J., Kono,T. and Murakami,T.  
TITLE Systems for the mass production of proteins or peptides by microorganisms of the genus humicola  
JOURNAL Patent: US 6403362-A 25 11-JUN-2002;  
Meiji Seika Kaisha, Ltd.; Tokyo;  
JPX;

FEATURES Location/Qualifiers  
source 1..30  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 30;  
Best Local Similarity 88.9%; Pred. No. 8.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCGAGGGGAGGGAGG 18  
||| ||||| ||||| |||||  
Db 25 AGCGAGGAGAGGGGAGG 8

RESULT 39  
AR202976  
LOCUS AR202976 31 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 31 from patent US 6365350.  
ACCESSION AR202976  
VERSION AR202976.1 GI:21499243  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Hayashizaki,Y.  
TITLE Method of DNA sequencing

JOURNAL Patent: US 6365350-A 31 02-APR-2002;  
FEATURES Location/Qualifiers  
source 1..31  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 88.9%; Pred. No. 8.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGGGGAGGGAGGGG 20  
||| ||||| ||||| |||||  
Db 1 GGGAGGGGGGGGGGGGG 18

RESULT 40  
AR643452  
LOCUS AR643452 31 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 17 from patent US 6867027.  
ACCESSION AR643452  
VERSION AR643452.1 GI:62781753  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Hayashizaki,Y. and Watahiki,M.  
TITLE RNA polymerase  
JOURNAL Patent: US 6867027-A 17 15-MAR-2005;  
The Institute of Physical and Chemical Research, Nippon Gene Co., Ltd. and Nippon Genetech Co., Ltd.; Wako;  
JPX;

FEATURES Location/Qualifiers  
source 1..31  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 88.9%; Pred. No. 8.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGGGGAGGGAGGGG 20  
||| ||||| ||||| |||||  
Db 1 GGGAGGGGGGGGGGGGG 18

RESULT 41  
AX158892/c  
LOCUS AX158892 50 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 2220 from Patent WO0140521.  
ACCESSION AX158892  
VERSION AX158892.1 GI:14540223  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 2220 07-JUN-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
source 1..50  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

misc\_feature 25..26  
/note="Nucleotide deleted between bases 25 and 26"

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misc_feature
26
Accession number cg393311132"
/note="2 of 2 allelic variants (2219 is other entry)"

ORIGIN
Query Match 74.0%; Score 14.8; DB 6; Length 50;
Best Local Similarity 88.9%; Pred. No. 7.6e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGGGAGGGAGGGG 20
|||||
Db 39 GGGAGGAGGGAGGGG 22
|||||

RESULT 42
AR121583/c
LOCUS AR121583 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 16 from patent US 6159934.
ACCESSION AR121583
VERSION AR121583.1 GI:14105159
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Peskovitz,O.H.
TITLE Use of GHRH-RP to stimulate stem cell factor production
JOURNAL Patent: US 6159934-A 16 12-DEC-2000;
FEATURES
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GAGGGAGGGAGGGG 20
|||||
Db 20 GAGGGAGGTGAGGGG 5
|||||

RESULT 43
AR630012
LOCUS AR630012 25 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 66 from patent US 6838556.
ACCESSION AR630012
VERSION AR630012.1 GI:59762204
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 66 04-JAN-2005;
FEATURES
source 1..25
/mol_type="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGAGGGAGGGAGGGG 17
|||||
Db 1 GGTGAGGGAGGGAGG 16
|||||

RESULT 44
AX351114
LOCUS AX351114 25 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 66 from Patent WO0194600.
ACCESSION AX351114
VERSION AX351114.1 GI:18616468
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: WO 0194600-A 66 13-DEC-2001;
FEATURES
source 1..25
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGAGGGAGGGAGGGG 17
|||||
Db 1 GGTGAGGGAGGGAGG 16
|||||

RESULT 45
AR137709/c
LOCUS AR137709 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 2 from patent US 6197554.
ACCESSION AR137709
VERSION AR137709.1 GI:14479218
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Lin,S.-L., Chuong,C.-M. and Ying,S.-Y.
TITLE Method for generating full-length cDNA library from single cells
JOURNAL Patent: US 6197554-A 2 06-MAR-2001;
FEATURES
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 71.0%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGAGGGAGGGG 20
|||||
Db 20 GGGGGGGGGGGGGGGG 2
|||||

RESULT 46
CQ892090
LOCUS CQ892090 20 bp DNA linear PAT 01-NOV-2004
DEFINITION Sequence 133 from Patent WO2004087203.
ACCESSION CQ892090
VERSION CQ892090.1 GI:55164648
KEYWORDS
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SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
1  
AUTHORS Davis,H.L. and Mccluskie,M.J.  
TITLE Immunostimulatory nucleic acid oil-in-water formulations and related methods of use  
JOURNAL Patent: WO 2004087203-A 133 14-OCT-2004;  
Coley Pharmaceutical Group, Ltd. (CA)  
FEATURES Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"  
ORIGIN  
Query Match 71.0%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.5e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 GGGGAGGGGAGGGAGGGG 20  
|||||  
Db 1 GGGGGGGGGGGGGGGGGG 19  
RESULT 47  
CS130448/c  
LOCUS CS130448 20 bp DNA linear PAT 02-AUG-2005  
DEFINITION Sequence 3 from Patent WO2005063300.  
ACCESSION CS130448  
VERSION CS130448.1 GI:71792416  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Kippenberger,S.  
TITLE Cosmetics or pharmaceutical preparations containing nucleic acid sequences forming a superstructure  
JOURNAL Patent: WO 2005063300-A 3 14-JUL-2005;  
Phenion GmbH & Co KG (DE)  
FEATURES Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="phosphorothioate or phosphodiester"  
ORIGIN  
Query Match 71.0%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.5e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 GGGGAGGGGAGGGAGGGG 20  
|||||  
Db 20 GGGGGGGGGGGGGGGGGG 2  
RESULT 48  
CS130449  
LOCUS CS130449 20 bp DNA linear PAT 02-AUG-2005  
DEFINITION Sequence 4 from Patent WO2005063300.  
ACCESSION CS130449  
VERSION CS130449.1 GI:71792417  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Kippenberger,S.  
TITLE Cosmetics or pharmaceutical preparations containing nucleic acid sequences forming a superstructure

JOURNAL Patent: WO 2005063300-A 4 14-JUL-2005;  
Phenion GmbH & Co KG (DE)  
FEATURES Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="phosphorothioate or phosphodiester"  
ORIGIN  
Query Match 71.0%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.5e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 GGGGAGGGGAGGGAGGGG 20  
|||||  
Db 1 GGGGGGGGGGGGGGGGGG 19  
RESULT 49  
E12675/c  
LOCUS E12675 20 bp DNA linear PAT 27-APR-1998  
DEFINITION Anti-HTLV-1 antisense oligonucleotide.  
ACCESSION E12675  
VERSION E12675.1 GI:3251507  
KEYWORDS JP 1997052898-A/9.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Mizuguchi,M., Kurosaki,N., Makino,K., Koyanagi,Y. and Yamamoto,N.  
TITLE ANTI-HTLV-1 ANTI-SENSE OLIGONUCLEOTIDE  
JOURNAL Patent: JP 1997052898-A 9 25-FEB-1997;  
SOYAKU GIJUTSU KENKYUSHO:KK  
COMMENT OS None  
OC Artificial sequences.  
PN JP 1997052898-A/9  
PD 25-FEB-1997  
PF 09-AUG-1995 JP 1995224606  
PI MIZUGUCHI MASATSUGU, KUROSAKI NAOKO, MAKINO KEISUKE, PI  
KOYANAGI YOSHIO, PI  
YAMAMOTO NAOKI  
PC C07H21/04//A61K31/70;  
CC strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: Yes;  
FH Key  
FT source 1..20  
Location/Qualifiers  
/organism='Artificial sequences'.  
1..20  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
FEATURES source  
ORIGIN  
Query Match 71.0%; Score 14.2; DB 6; Length 20;  
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DEFINITION Sequence 55 from patent US 6339068.  
ACCESSION AR182883  
VERSION AR182883.1 GI:20226090

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
            Unclassified.
AUTHORS     Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE       Vectors and methods for immunization or therapeutic protocols
JOURNAL     Patent: US 6339068-A 55 15-JAN-2002;
FEATURES    Location/Qualifiers
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                        /mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Search completed: February 15, 2006, 18:56:04  
Job time : 486.835 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:25:23 ; Search time 150.744 Seconds  
(without alignments)  
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Title: US-09-669-187A-906

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 58 | 15.2 | 76.0 | 35 | 12 | ADJ87120 | Adj87120 Nucleotid |
| 59 | 15.2 | 76.0 | 35 | 12 | ADL92249 | Adl92249 MBL gene  |
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| 61 | 15.2 | 76.0 | 38 | 2  | AAQ8038  | Aaq8038 U6-type R  |
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| 69 | 15.2 | 76.0 | 41 | 6  | ABL60242 | Abi60242 Citrate s |
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| C 95  | 14.2 | 71.0 | 20 | 3  | AAZ57147  | Aaz57147 | Exemplary  | 168   | 14.2 | 71.0 | 24 | 2  | AAQ49955 | Aa49955  | Sequence   |
| C 96  | 14.2 | 71.0 | 20 | 3  | AAZ57136  | Aaz57136 | Quadruple  | 169   | 14.2 | 71.0 | 24 | 2  | AAQ36277 | Aa36277  | APP7par,   |
| C 97  | 14.2 | 71.0 | 20 | 4  | AAC87242  | Ac87242  | Poly C ol  | 170   | 14.2 | 71.0 | 24 | 2  | AAQ36278 | Aa36278  | APP7anti,  |
| C 98  | 14.2 | 71.0 | 20 | 4  | AAC87229  | Ac87229  | Digoxigen  | 171   | 14.2 | 71.0 | 24 | 2  | AAT99285 | Aa99285  | POLYG, a   |
| C 99  | 14.2 | 71.0 | 20 | 4  | AAC87239  | Ac87239  | Phosphoro  | 172   | 14.2 | 71.0 | 24 | 2  | AAV31742 | Aa31742  | Nucleotid  |
| C 100 | 14.2 | 71.0 | 20 | 4  | AAF77533  | Af77533  | CDNA libr  | 173   | 14.2 | 71.0 | 24 | 2  | AAX04085 | Aa04085  | Oligonucle |
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| C 102 | 14.2 | 71.0 | 20 | 4  | AAF99402  | Af99402  | Immunosti  | C 175 | 14.2 | 71.0 | 24 | 4  | AAF99758 | Aa99758  | Immunosti  |
| C 103 | 14.2 | 71.0 | 20 | 4  | AAF99782  | Af99782  | Immunosti  | C 176 | 14.2 | 71.0 | 24 | 6  | ABS78479 | Ab78479  | Angiogene  |
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| C 105 | 14.2 | 71.0 | 20 | 4  | AAF99130  | Af99130  | Immunosti  | C 178 | 14.2 | 71.0 | 24 | 6  | ABL38793 | Ab38793  | Immunosti  |
| C 106 | 14.2 | 71.0 | 20 | 4  | AAF99401  | Af99401  | Immunosti  | C 179 | 14.2 | 71.0 | 24 | 9  | ACH03286 | Ac03286  | Immunosti  |
| C 107 | 14.2 | 71.0 | 20 | 5  | AAD18515  | Ad18515  | Biotinyl   | C 180 | 14.2 | 71.0 | 24 | 9  | ACH03286 | Ac03286  | Immunosti  |
| C 108 | 14.2 | 71.0 | 20 | 6  | ABS78046  | Ab78046  | Angiogene  | C 181 | 14.2 | 71.0 | 24 | 9  | ADB36801 | Ad36801  | Immunosti  |
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| C 111 | 14.2 | 71.0 | 20 | 6  | ABS78047  | Ab78047  | Angiogene  | C 184 | 14.2 | 71.0 | 24 | 13 | ADR48247 | Adr48247 | Microarra  |
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| C 113 | 14.2 | 71.0 | 20 | 6  | ABL38792  | Ab38792  | Immunosti  | C 186 | 14.2 | 71.0 | 24 | 13 | ADU89744 | Adu89744 | Allergic   |
| C 114 | 14.2 | 71.0 | 20 | 6  | ABL39026  | Ab39026  | Immunosti  | C 187 | 14.2 | 71.0 | 24 | 13 | ADU90279 | Adu90279 | Allergic   |
| C 115 | 14.2 | 71.0 | 20 | 6  | ABL38791  | Ab38791  | Immunosti  | C 188 | 14.2 | 71.0 | 24 | 13 | ADU90279 | Adu90279 | Allergic   |
| C 116 | 14.2 | 71.0 | 20 | 6  | ABL39025  | Ab39025  | Immunosti  | C 189 | 14.2 | 71.0 | 25 | 6  | ABK10411 | Abk10411 | Synthetic  |
| C 117 | 14.2 | 71.0 | 20 | 8  | ABX89934  | Abx89934 | Cancer me  | C 190 | 14.2 | 71.0 | 25 | 11 | ADL99557 | Adl99557 | Single ch  |
| C 118 | 14.2 | 71.0 | 20 | 9  | ACA92790  | Ac92790  | Immunosti  | C 191 | 14.2 | 71.0 | 26 | 2  | AAX40755 | Aa40755  | Oligonucle |
| C 119 | 14.2 | 71.0 | 20 | 9  | ACD99822  | Ac99822  | Immunosti  | C 192 | 14.2 | 71.0 | 26 | 8  | AAD48367 | Ad48367  | Oligonucle |
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| C 121 | 14.2 | 71.0 | 20 | 9  | ACD99821  | Ac99821  | Immunosti  | C 194 | 14.2 | 71.0 | 26 | 13 | ADV51233 | Adv51233 | Hepatitis  |
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| C 125 | 14.2 | 71.0 | 20 | 9  | ADB36632  | Ad36632  | Immunosti  | C 198 | 14.2 | 71.0 | 28 | 6  | ABS78286 | Ab78286  | Angiogene  |
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| C 129 | 14.2 | 71.0 | 20 | 10 | ADE86160  | De86160  | RET gene   | C 202 | 14.2 | 71.0 | 28 | 12 | ADF82756 | Adf82756 | Antiviral  |
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| C 131 | 14.2 | 71.0 | 20 | 10 | ABX76122  | Abx76122 | Immunosti  | C 204 | 14.2 | 71.0 | 30 | 2  | AAT09304 | Aat09304 | Murine an  |
| C 132 | 14.2 | 71.0 | 20 | 10 | ACA58787  | Ac58787  | Gastric u  | C 205 | 14.2 | 71.0 | 30 | 4  | AAF99890 | Aaf99890 | Immunosti  |
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| C 137 | 14.2 | 71.0 | 20 | 12 | ADL57919  | Adl57919 | Human ESM  | C 210 | 14.2 | 71.0 | 30 | 13 | ADG70063 | Adg70063 | Terminal   |
| C 138 | 14.2 | 71.0 | 20 | 12 | ADL57899  | Adl57899 | Human ESM  | C 211 | 14.2 | 71.0 | 30 | 13 | ADG70063 | Adg70063 | Terminal   |
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| C 141 | 14.2 | 71.0 | 20 | 13 | ADS75744  | Ads75744 | DNA molec  | C 214 | 14.2 | 71.0 | 30 | 14 | ADZ36927 | Adz36927 | Rice zmCe  |
| C 142 | 14.2 | 71.0 | 20 | 13 | ADS08444  | Ads08444 | Poly-C pr  | C 215 | 14.2 | 71.0 | 31 | 6  | ABK10413 | Abk10413 | Oligonucle |
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| C 144 | 14.2 | 71.0 | 20 | 13 | ADU90127  | Adu90127 | Allergic   | C 217 | 14.2 | 71.0 | 32 | 6  | ABK10414 | Abk10414 | Synthetic  |
| C 145 | 14.2 | 71.0 | 20 | 13 | ADU90303  | Adu90303 | Allergic   | C 218 | 14.2 | 71.0 | 32 | 9  | ACC58756 | Acc58756 | Anti-rest  |
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| C 152 | 14.2 | 71.0 | 20 | 14 | AEA39366  | Aea39366 | H-RAS gen  | C 225 | 14.2 | 71.0 | 35 | 6  | AAF99571 | Aaf99571 | Immunosti  |
| C 153 | 14.2 | 71.0 | 20 | 14 | AEB28253  | Aeb28253 | Oligonucle | C 226 | 14.2 | 71.0 | 35 | 6  | ABS78287 | Ab78287  | Angiogene  |
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| C 158 | 14.2 | 71.0 | 21 | 2  | AAQ35038  | Aaq35038 | Triplex-f  | C 231 | 14.2 | 71.0 | 35 | 12 | ADL92244 | Adl92244 | MXA gene   |
| C 159 | 14.2 | 71.0 | 21 | 3  | AAZ99630  | Aaz99630 | Prototypic | C 232 | 14.2 | 71.0 | 35 | 13 | ADU90087 | Adu90087 | Allergic   |
| C 160 | 14.2 | 71.0 | 21 | 5  | AAH88948  | Aah88948 | Human pol  | C 233 | 14.2 | 71.0 | 36 | 13 | ADF82760 | Adf82760 | Antiviral  |
| C 161 | 14.2 | 71.0 | 21 | 5  | AAH62060  | Aah62060 | PDGF A ha  | C 234 | 14.2 | 71.0 | 37 | 2  | AAQ98446 | Aa98446  | Antisense  |
| C 162 | 14.2 | 71.0 | 21 | 5  | ACC58752  | Acc58752 | Anti-rest  | C 235 | 14.2 | 71.0 | 37 | 2  | AAZ06500 | Aaz06500 | G-free bi  |
| C 163 | 14.2 | 71.0 | 21 | 13 | ADW24473  | Adw24473 | Nucleotid  | C 236 | 14.2 | 71.0 | 37 | 2  | AAZ06497 | Aaz06497 | Competito  |
| C 164 | 14.2 | 71.0 | 22 | 8  | ACF03717  | Acf03717 | PCR prime  | C 237 | 14.2 | 71.0 | 37 | 2  | AAZ24985 | Aaz24985 | Oligonucle |
| C 165 | 14.2 | 71.0 | 23 | 2  | AAQ33897  | Aaq33897 | Microsate  | C 238 | 14.2 | 71.0 | 37 | 12 | ADF82770 | Adf82770 | Antiviral  |



239 14.2 71.0 38 2 AAV03769 Hepatitis  
 c 240 14.2 71.0 38 12 ADF82761  
 c 241 14.2 71.0 38 13 ADS75741 DNA molec  
 c 242 14.2 71.0 38 13 ADS08441 Poly-C pr  
 c 243 14.2 71.0 38 13 ADV93321 PCR prime  
 c 244 14.2 71.0 40 2 AAQ25029 Oligonuc  
 c 245 14.2 71.0 40 2 AAQ22624 Sense oli  
 c 246 14.2 71.0 40 2 AAQ25022 Anti-sens  
 c 247 14.2 71.0 40 2 AAQ25026 Anti-sens  
 c 248 14.2 71.0 40 2 AAQ25030 Oligonuc  
 c 249 14.2 71.0 40 2 AAQ25017 Sense oli  
 c 250 14.2 71.0 40 2 AAQ22626 Sense oli  
 c 251 14.2 71.0 40 2 AAQ25018 Sense oli  
 c 252 14.2 71.0 40 2 AAQ50877 HSV2 prim  
 c 253 14.2 71.0 40 4 AAC83643 Human c-f  
 c 254 14.2 71.0 40 4 AAC83641 Human c-f  
 c 255 14.2 71.0 40 12 ADF82762 Antiviral  
 c 256 14.2 71.0 40 13 ADV51231 Linker ol  
 c 257 14.2 71.0 40 14 AEB28262 Oligonuc  
 c 258 14.2 71.0 41 2 AAQ72283 Rat serot  
 c 259 14.2 71.0 41 6 ABQ79324 Human pro  
 c 260 14.2 71.0 41 12 ADK17714 Cytochrom  
 c 261 14.2 71.0 41 13 ADV25730 Primer BA  
 c 262 14.2 71.0 42 3 AA71923 E. coli 2  
 c 263 14.2 71.0 42 6 ABZ50869 Human ATP  
 c 264 14.2 71.0 42 6 ABZ48406 Human ATP  
 c 265 14.2 71.0 42 6 ABZ44642 Human ATP  
 c 266 14.2 71.0 45 2 AAX76410 Sequencin  
 c 267 14.2 71.0 45 5 AAC91549 Human PRO  
 c 268 14.2 71.0 45 13 ADV25731 Primer BA  
 c 269 14.2 71.0 46 7 ADI94435 Human IL-  
 c 270 14.2 71.0 46 7 ADI94432 Human IL-  
 c 271 14.2 71.0 47 3 AAZ65938 Human map  
 c 272 14.2 71.0 47 3 AAZ68865 Human map  
 c 273 14.2 71.0 47 7 ADI93449 Human bet  
 c 274 14.2 71.0 48 2 AAQ12358 European-  
 c 275 14.2 71.0 49 2 AAT80463 Hepatoma  
 c 276 14.2 71.0 49 7 ADI94426 Human IL-  
 c 277 14.2 71.0 49 7 ADI94427 Human IL-  
 c 278 14.2 71.0 49 7 ADI93448 Human bet  
 c 279 14.2 71.0 49 12 ADH76831 MCHR1 loc  
 c 280 14.2 71.0 49 12 ADH76662 MCHR1 loc  
 c 281 14.2 71.0 49 13 ADV25732 Primer BA  
 c 282 14.2 71.0 50 2 AAQ69772 Herpes si  
 c 283 14.2 71.0 50 2 AAT64234 HSV-1 b'g  
 c 284 14.2 71.0 50 2 AAX76438 Sequencin  
 c 285 14.2 71.0 50 2 AAX17522 Test sequ  
 c 286 14.2 71.0 50 3 AAA38175 Primer us  
 c 287 14.2 71.0 50 4 AAH4830 Probe use  
 c 288 14.2 71.0 50 6 ABK83013 DNA bindi  
 c 289 14.2 71.0 50 6 ABZ02124 Human leu  
 c 290 14.2 71.0 50 6 ABZ04174 Human leu  
 c 291 14.2 71.0 50 10 ADC56858 Micro gol  
 c 292 14.2 71.0 50 10 ADC56859 Micro gol  
 c 293 14.2 71.0 50 12 ADG33323 Human DNA  
 c 294 14.2 71.0 50 10 ADE80552 Duplex ol  
 c 295 14.2 71.0 50 14 ADV97064 Chimeric  
 c 296 14.2 71.0 50 14 ADV71296 Human ACh  
 c 297 14 70.0 14 12 ADH70438 Human Vbe  
 c 298 14 70.0 50 6 ABZ04828 Human leu  
 c 299 14 70.0 50 6 ABZ04829 Human leu  
 c 300 13.8 69.0 17 12 ADI83485 HCV DNaza

## ALIGNMENTS

RESULT 1

AAF99701

ID AAF99701 standard; DNA; 20 BP.

XX

AC AAF99701;

XX

DT 12-JUN-2001 (first entry)  
 XX Immunostimulatory nucleic acid #817.  
 DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; ashma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 OS Synthetic.  
 XX WO200122972-A2.  
 PN 05-APR-2001.  
 PD 25-SEP-2000; 2000WO-US026383.  
 XX 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 PA Krieg AM, Schetter C, Vollmer J;  
 PI WPI; 2001-273485/28.  
 DR Vaccinating against tumors, infectious diseases, allergies and asthma  
 XX using immunostimulatory Py-rich and TG nucleic acids.  
 PT Claim 101; Page 56; 338pp; English.  
 PS The present invention relates to a method for stimulating an immune  
 XX response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 20; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGGGGAGGGGAGGGGAGGGG 20  
 |||||  
 Db 1 AGGGGAGGGGAGGGGAGGGG 20  
 |||||  
 RESULT 2  
 ABS78422  
 ID ABS78422 standard; DNA; 20 BP.  
 XX  
 AC ABS78422;  
 XX  
 XX 13-DEC-2002 (first entry)  
 DE Angiogenesis inhibitory oligonucleotide #906.  
 XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX Synthetic.  
XX WO200253141-A2.  
PN  
XX  
XX 11-JUL-2002.  
PD  
XX  
XX 14-DEC-2001; 2001WO-US048458.  
PF  
XX  
XX 14-DEC-2000; 2000US-0255534P.  
PR  
XX  
FA (COLE-) COLEY PHARM GROUP INC.  
XX  
XX Bratzler RL;  
PI  
XX  
XX WPI; 2002-566690/60.  
DR  
XX  
XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.  
XX  
XX Claim 2; Page 35; 276pp; English.  
PS  
XX  
XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth.  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
XX  
SQ Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 AGGGAGGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | |  
Db 1 AGGGAGGGGAGGGAGGGG 20  
  
RESULT 3  
ACH03240  
ID ACH03240 standard; DNA; 20 BP.  
XX  
XX  
AC ACH03240;  
XX  
XX 25-SEP-2003 (first entry)  
DT  
XX  
XX Immunostimulatory nucleic acid #875.  
DE  
XX  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX US2003050268-A1.  
PN  
XX  
XX 13-MAR-2003.  
PD  
XX  
XX

PF 29-MAR-2002; 2002US-00112653.  
XX  
PR 29-MAR-2001; 2001US-0279642P.  
XX  
PA (KRIE/) KRIEG A M.  
PA (BERG/) BERG D J.  
XX  
XX Krieg AM, Berg DJ;  
PI  
XX  
XX WPI; 2003-521815/49.  
DR  
XX  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX  
XX Disclosure; Page 32; 229pp; English.  
PS  
XX  
XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
XX  
SQ Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 AGGGAGGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | |  
Db 1 AGGGAGGGGAGGGAGGGG 20  
  
RESULT 4  
ADB37203  
ID ADB37203 standard; DNA; 20 BP.  
XX  
XX ADB37203;  
AC  
XX  
XX 04-DEC-2003 (first entry)  
DT  
XX  
XX Immunostimulatory nucleic acid #817.  
DE  
XX  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
KW  
XX  
XX Synthetic.  
OS  
XX  
XX US2003087848-A1.  
PN  
XX  
XX 08-MAY-2003.  
PD  
XX  
XX 02-FEB-2001; 2001US-00776479.  
PF  
XX  
XX 03-FEB-2000; 2000US-0179991P.  
PR  
XX  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURN Y.  
XX  
XX Bratzler RL, Petersen DM, Fourn Y;  
PI  
XX  
XX WPI; 2003-657977/62.  
DR  
XX  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
PT  
XX  
XX Disclosure; Page 17; 221pp; English.  
PS  
XX  
XX

CC The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.

XX Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGGAGGGGAGGGAGGGG 20  
|||||  
Db 1 AGGGAGGGGAGGGAGGGG 20

## RESULT 5

ADU90222

ID ADU90222 standard; DNA; 20 BP.

XX AC

ADU90222;

DT 10-FEB-2005 (first entry)

XX Allergic response suppressor oligonucleotide #906.

ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;  
KW antibacterial; virucide; immunoglobulin E antagonist; allergy;  
KW immunostimulator; asthma; rhinitis; urticaria; dermatitis;  
KW bacterial infection; viral infection.

XX Synthetic.

XX US2004235774-A1.

XX 25-NOV-2004.

XX 23-APR-2004; 2004US-00831778.

XX 03-FEB-2000; 2000US-0179991P.

PR 02-FEB-2001; 2001US-00776479.

XX (BRATZLER R L.

PA (PETE//) PETERSEN D M.

PA (FOUR//) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;

XX WPI; 2004-833006/82.

XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
PT dermatitis, in a subject, comprises administering a first and second dose  
PT of an immunostimulatory nucleic acid.

XX Disclosure; SEQ ID NO 906; 235pp; English.

XX The invention relates to a method of suppressing a symptom of an allergic  
CC response in a subject by administering a first and second dose of an  
CC immunostimulatory nucleic acid that comprises a nucleotide sequence  
CC comprising 5'-cg-3', and where the second dose is administered from 1 day  
CC to 8 weeks after the first dose. The methods and compositions of the  
CC present invention are useful for the treatment or prevention of asthma  
CC and allergy, including rhinitis, urticaria and atopic dermatitis, using  
CC an immunostimulatory nucleic acid alone or in combination with other  
CC medicaments. This can also be used in preventing bacterial and viral  
CC infections. This sequence represents an oligonucleotide used in the  
CC method of the invention.

XX Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;

Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGGAGGGGAGGGAGGGG 20  
|||||  
Db 1 AGGGAGGGGAGGGAGGGG 20

## RESULT 6

ABL56735

ID ABL56735 standard; DNA; 50 BP.

XX AC

ABL56735;

XX 20-AUG-2002 (first entry)

XX Sequence of a fragment of the murine androgen receptor promoter.

XX Nucleic acid detection; nucleic acid labelling; gene therapy;  
KW nucleic acid purification; androgen receptor promoter; triple helix; ss.

XX Synthetic.

OS Mus sp.

XX WO200077250-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-FR001655.

XX 14-JUN-1999; 99FR-00007503.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX Escude C, Garestier T, Helene C, Roulon T;

XX WPI; 2001-080698/09.

XX Circularizing oligonucleotide around double-stranded nucleic acid, useful  
PT e.g. for detecting mutations, using target-binding oligonucleotide with  
PT complementary end sequences.

XX Disclosure; Page 20; 91pp; French.

XX The specification describes a process for circularizing an  
CC oligonucleotide around a double-stranded nucleic acid that contains a  
CC target sequence. The method is used to detect or label nucleic acids,  
CC particularly plasmids, to detect target sequences in the nucleic acid,  
CC and to distinguish between two sequences that differ in only 1 or 2  
CC mutations. It can be used to select, e.g. from degenerate single-stranded  
CC nucleic acids, sequences that can bind to the nucleic acid, particularly  
CC sequences that promote entry of the nucleic acid into cells or can target  
CC the nucleic acid to specific cellular compartments. The method can also  
CC be used to purify nucleic acids, particularly plasmids, and in gene  
CC therapy for specific inhibition of a gene contained in the nucleic acid.  
CC ABL56735-36 represent a fragment of the murine androgen receptor  
CC promoter. They were used in the course of the invention, during  
CC construction of triple helices

XX Sequence 50 BP; 19 A; 0 C; 30 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 50;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGGAGGGGAGGGAGGGG 20  
|||||  
Db 16 AGGGAGGGGAGGGAGGGG 35

## RESULT 7

ABL56736/c

```

ID  ABL56736 standard; DNA; 50 BP.
XX
AC  ABL56736;
XX
DT  20-AUG-2002 (first entry)
XX
DE  Sequence of a fragment of the murine androgen receptor promoter.
XX
KW  Nucleic acid detection; nucleic acid labelling; gene therapy;
KW  nucleic acid purification; androgen receptor promoter; triple helix; ss.
XX
OS  Synthetic.
OS  Mus sp.
XX
FN  WO200077250-A2.
XX
PD  21-DEC-2000.
XX
XX  14-JUN-2000; 2000WO-FR001655.
XX
PF  14-JUN-1999; 99FR-00007503.
XX
PR  (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA  (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI  Escude C, Garestier T, Helene C, Roulon T;
XX
DR  WPI; 2001-080698/09.
XX
PT  Circularizing oligonucleotide around double-stranded nucleic acid, useful
PT  e.g. for detecting mutations, using target-binding oligonucleotide with
PT  complementary end sequences.
XX
XX  Disclosure; Page 20; 91pp; French.
XX
CC  The specification describes a process for circularizing an
CC  oligonucleotide around a double-stranded nucleic acid that contains a
CC  target sequence. The method is used to detect or label nucleic acids,
CC  particularly plasmids, to detect target sequences in the nucleic acid,
CC  and to distinguish between two sequences that differ in only 1 or 2
CC  mutations. It can be used to select, e.g. from degenerate single-stranded
CC  nucleic acids, sequences that can bind to the nucleic acid, particularly
CC  sequences that promote entry of the nucleic acid into cells or can target
CC  the nucleic acid to specific cellular compartments. The method can also
CC  be used to purify nucleic acids, particularly plasmids, and in gene
CC  therapy for specific inhibition of a gene contained in the nucleic acid.
CC  ABL56735-36 represent a fragment of the murine androgen receptor
CC  promoter. They were used in the course of the invention, during
CC  construction of triple helices
XX
SQ  Sequence 50 BP; 1 A; 30 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGGG 20
    |||||
Db 35 AGGGGAGGGGAGGGAGGGG 16

RESULT 8
AAA36647
ID AAA36647 standard; cDNA; 27 BP.
XX
AC AAA36647;
XX
XX 31-JUL-2000 (first entry)
DT
DE Nucleic acid transporter system purine series sequence #5.
XX
KW Transporter system; nucleic acid delivery; gene therapy; cancer;
KW carcinogenesis; cardiovascular disease; infection; ss.

Query Match 87.0%; Score 17.4; DB 3; Length 27;
Best Local Similarity 94.7%; Pred. No. 4.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGGG 19
    |||||
Db 4 AAGGGAGGGGAGGGAGGGG 22

RESULT 9
AAA36646/c
ID AAA36646 standard; DNA; 27 BP.
XX
AC AAA36646;
XX
XX 31-JUL-2000 (first entry)
DT
DE Nucleic acid transporter system ligand containing template #5.
XX
KW Transporter system; nucleic acid delivery; gene therapy; cancer;
KW carcinogenesis; cardiovascular disease; infection; ss.
XX
OS Synthetic.
OS US6033884-A.
XX
FN US6033884-A.
XX
PD 07-MAR-2000.
XX
XX 14-DEC-1993; 93US-00167641.
PF
```



XX WPI; 2000-038262/03.  
 DR Nucleic acid transport system, useful for creating transgenic animals for  
 XX assessing human disease such as cancer in an animal model.  
 FT  
 XX Disclosure; Fig 15A; 107pp; English.  
 PS  
 XX The invention relates to a nucleic acid transport system (NTS) for  
 CC delivering nucleic acid into a cell. The NTS contains but is not limited  
 CC to 5 components: (a) the nucleic acid or a macromolecule to be delivered;  
 CC (b) a moiety that recognizes and binds to a cell surface receptor or  
 CC antigen or is capable of entering a cell through cytosol; (c) a nucleic  
 CC acid or macromolecular molecule binding moiety; (d) a moiety that is  
 CC capable of moving or initiating movement through a nuclear membrane; and/  
 CC or (e) a lysis moiety that enables the transport of the entire complex  
 CC from the cell surface directly into the cytoplasm of the cell. The NTS  
 CC delivers nucleic acid into the cellular interior as well as the nucleus  
 CC of specific cells. The NTS can be used to treat disorders by targeting  
 CC specific nucleic acid accordingly. The NTS can also be used to create  
 CC transgenic animals for assessing human disease, such as cancer, in an  
 CC animal model. The NTS can be used in vitro with tissue culture cells  
 CC which allows the role of various nucleic acids to be studied by targeting  
 CC specific expression into specifically targeted tissue culture cells. The  
 CC lysis agent within the NTS avoids the problem of endosomal/lysosomal  
 CC degradation  
 XX  
 SQ Sequence 27 BP; 13 A; 0 C; 14 G; 0 T; 0 U; 0 Other;  
 Query Match 87.0%; Score 17.4; DB 3; Length 27;  
 Best Local Similarity 94.7%; Pred. No. 4.2e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 AGGGAGGGAGGGAGGG 19  
 Db | | | | | | | | | | | | | | | | | | | |  
 4 AAGGGAGGGAGGGAGGG 22  
 RESULT 12  
 AAC82867  
 ID AAC82867 standard; DNA; 27 BP.  
 XX  
 AC AAC82867;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Nucleic acid transporter system primer SEQ ID NO 15.  
 KW Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;  
 KW growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene;  
 KW tumor antigen; tumor suppressor; viral antigen; parasitic antigen;  
 KW bacterial antigen; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 XX US6150168-A.  
 PN  
 XX  
 PD 21-NOV-2000.  
 XX  
 XX 05-JUN-1995; 95US-00460971.  
 XX  
 XX 20-MAR-1992; 92US-00855389.  
 PR  
 PR 19-MAR-1993; 93WO-US002725.  
 PR  
 PR 14-DEC-1993; 93US-00167641.  
 XX  
 XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
 PA  
 XX Gottchalk S, Sparrow J, Cristiano RJ, Smith LC, Woo SLC;  
 PI  
 XX WPI; 2001-049093/06.  
 DR  
 XX Nucleic acid transporter system for delivering nucleic acid into a cell,  
 XX useful for delivering proteins and polypeptides to cells, including  
 PT

PT growth factors, enzymes, hormones, and tumor suppressors.  
 XX  
 PS Disclosure; Col 97-98; 105pp; English.  
 XX  
 CC This invention describes a novel system (I) for delivering a nucleic acid  
 CC to a cell, comprising a binding complex comprising a ligand binding  
 CC molecule noncovalently bound to a nucleic acid and covalently linked to a  
 CC surface ligand, and a second binding complex comprising a second binding  
 CC molecule noncovalently bound to a nucleic acid and covalently linked to a  
 CC nuclear ligand. The complexes are simultaneously bound to the nucleic  
 CC acid. The nucleic acid transporter system can also be used in a method  
 CC for the in vivo targeting of the insertion of DNA into a cell. It can  
 CC also be used in processes for producing transformed cell lines. The  
 CC system can be used to deliver a variety of proteins and polypeptides,  
 CC such as hormones, growth factors, enzymes, clotting factors, tumor  
 CC apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor  
 CC suppressors, viral antigens, parasitic antigens, and bacterial antigens.  
 CC The transporter system uses lysis agents to overcome the problems of  
 CC endosomal/lysosomal degradation seen with prior art systems  
 XX  
 SQ Sequence 27 BP; 13 A; 0 C; 14 G; 0 T; 0 U; 0 Other;  
 Query Match 87.0%; Score 17.4; DB 4; Length 27;  
 Best Local Similarity 94.7%; Pred. No. 4.2e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 AGGGAGGGAGGGAGGG 19  
 Db | | | | | | | | | | | | | | | | | | | |  
 4 AAGGGAGGGAGGGAGGG 22  
 RESULT 13  
 AAC82866/c  
 ID AAC82866 standard; DNA; 27 BP.  
 XX  
 AC AAC82866;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Nucleic acid transporter system primer SEQ ID NO 14.  
 KW Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;  
 KW growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene;  
 KW tumor antigen; tumor suppressor; viral antigen; parasitic antigen;  
 KW bacterial antigen; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 6  
 FT /\*tag= a  
 FT /mod\_base= Other  
 FT /note= "5-methylcytosine"  
 FT modified\_base 7  
 FT /\*tag= b  
 FT /mod\_base= Other  
 FT /note= "5-methylcytosine"  
 FT modified\_base 8  
 FT /\*tag= c  
 FT /mod\_base= Other  
 FT /note= "5-methylcytosine"  
 FT modified\_base 10  
 FT /\*tag= d  
 FT /mod\_base= Other  
 FT /note= "5-methylcytosine"  
 FT modified\_base 11  
 FT /\*tag= e  
 FT /mod\_base= Other  
 FT /note= "5-methylcytosine"  
 FT modified\_base 12  
 FT /\*tag= f  
 FT /mod\_base= Other  
 FT /note= "5-methylcytosine"



CC binding molecules (surface ligands), lysis agents, spacer molecules or  
CC their intermediates. The ligands, binding molecules, lysis agents and  
CC spacer molecules are used in nucleic acid transporter systems to deliver  
CC nucleic acid into specific cells e.g. in gene therapy to deliver nucleic  
CC acid into hepatocytes, muscle cells or bone forming cells  
XX  
SQ Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 4; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 24 AAGGAGGGAGGGAGGG 6

RESULT 15  
AAS08477  
ID AAS08477 standard; DNA; 27 BP.

XX AAS08477;

DT 23-OCT-2001 (first entry)

DE Purine-rich oligonucleotide #5 used in nucleic acid transporter system.

XX Nucleic acid transport; cytosine; ligand; lysis agent; spacer molecule;  
KW gene therapy; hepatocyte; muscle; bone forming cell; oligonucleotide; ss.  
XX Synthetic.

PN US6177554-B1.

PD 23-JAN-2001.

XX 05-JUN-1995; 95US-00462040.

XX 20-MAR-1992; 92US-00855389.

PR 19-MAR-1993; 93WO-US002725.

PR 14-DEC-1993; 93US-00167641.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

PI Woo SLC, Smith LC, Cristiano RJ, Gottchalk S, Sparrow J;

DR WPI; 2001-365933/38.  
XX Nucleic acid transport system, useful for creating transgenic animals for  
XX assessing human disease such as cancer in an animal model.

PS Disclosure; Fig 15; 11pp; English.

XX The sequence represents the purine-rich oligonucleotide #5 used in used  
CC in a nucleic acid transporter system. The nucleic acid transporter system  
CC uses nucleic acid binding complexes containing surface ligands which are  
CC capable of binding to a cell surface receptor and entering the cell  
CC through cytosine. The compounds of the invention are either ligands,  
CC binding molecules (surface ligands), lysis agents, spacer molecules or  
CC their intermediates. The ligands, binding molecules, lysis agents and  
CC spacer molecules are used in nucleic acid transporter systems to deliver  
CC nucleic acid into specific cells e.g. in gene therapy to deliver nucleic  
CC acid into hepatocytes, muscle cells or bone forming cells  
XX

SQ Sequence 27 BP; 13 A; 0 C; 14 G; 0 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 4; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 4 AAGGAGGGAGGGAGGG 22

RESULT 16  
AAD41066  
ID AAD41066 standard; DNA; 30 BP.  
XX  
AC AAD41066;  
XX  
DT 30-OCT-2002 (first entry)  
XX  
DE Primer ON-TAPAdel used for DNA sequencing.  
XX

KW Tumour necrosis-factor; TNF; promoter; autoimmune disorder; cancer;  
KW therapy; primer; ss.

XX Unidentified.

XX WO200246433-A2.

XX 13-JUN-2002.

XX 07-DEC-2001; 2001WO-EP014412.

XX 08-DEC-2000; 2000US-0254649P.

XX (SAUS/) SAUS J.

XX Saus J;

XX WPI; 2002-519670/55.

XX Novel tumor necrosis-factor inducible promoter useful for identifying  
XX candidate compounds for treating/preventing autoimmune disorders/cancer,  
XX or for identifying promoters that are regulated by tumor necrosis factor.  
XX Example; Page 17; 95pp; English.

XX The invention relates to a tumour necrosis-factor TNF inducible promoter.  
XX The invention is useful for identifying candidate TNF inducible promoters  
XX by aligning a test sequence consisting of a nucleic acid sequence with a  
XX comparison sequence selected from the invention, using a gap opening  
XX penalty of 50 and a gap extension penalty of 3 to define a test  
XX alignment, shuffling the nucleic sequence of the test sequence at least  
XX one hundred times, while maintaining its length and composition, to  
XX produce a series of randomised sequences, aligning the randomised  
XX sequences with the comparison sequence using a gap opening penalty of 50  
XX and a gap extension penalty of 3, to produce a series of randomised  
XX alignments, determining an average alignment quality of the randomised  
XX alignments, where the average alignment quality of the randomised  
XX alignments represent an alignment expected by chance, comparing the test  
XX alignment with the average alignment quality of the randomised alignments  
XX and identifying a test alignment with a probability value of less than  
XX 0.05 that the alignment is obtained by chance as a candidate TNF  
XX inducible promoter. The invention is useful for identifying candidate  
XX compounds for treating or preventing autoimmune disorders or cancer. The  
XX present sequence is a primer used in the exemplification of the invention  
XX  
SQ Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 6; Length 30;  
Best Local Similarity 94.7%; Pred. No. 4.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 2 AGGGAGGGAGGGAGGG 20

RESULT 17  
ABT03901  
ID ABT03901 standard; DNA; 30 BP.

XX  
AC ABT03901;



```
XX 18-SEP-2002 (first entry)
XX Human pol kappa 76 DNA polymerase sequencing primer #7.
XX
XX
XX Human; pol kappa 76; Goodpasture antigen binding protein; GPBP;
KW chromosome 5q12-13; apoptosis; autoimmune disorder; cancer; cytostatic;
KW immunosuppressive; PCR; primer; sequencing; ss.
XX
XX Homo sapiens.
XX WO200246378-A2.
XX
XX 13-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-EP014409.
XX
XX 08-DEC-2000; 2000US-0254649P.
XX (SAUS/) SAUS J.
XX Saus J;
XX WPI; 2002-537563/57.
XX
XX Novel isolated pol kappa76 polypeptide, a 76 kDa alternatively spliced
XX variant of DNA polymerase kappa, useful as target for treating a patient
XX with autoimmune disorder or cancer.
XX
XX Example; Page 15; 90pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX DNA polymerase pol kappa 76. The gene is found on human chromosome 5q12-
XX 13, in a head-to-head arrangement with the Goodpasture antigen binding
XX protein (GPBP). The detection of the coding sequence can be used for
XX diagnosing an autoimmune condition and identifying cells undergoing
XX apoptosis, and the sequences can be used in the treatment of autoimmune
XX diseases and cancer. The present sequence is a sequencing primer
XX described in the invention
XX
XX Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 87.0%; Score 17.4; DB 6; Length 30;
XX Best Local Similarity 94.7%; Pred. No. 4.2e+03;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 AGGGGAGGGGAGGGGAGGG 19
XX 2 AGGGGAGGGGAGGGGAGGG 20
XX
XX
XX RESULT 18
XX ACD13504
XX ID ACD13504 standard; DNA; 30 BP.
XX
XX AC ACD13504;
XX
XX 14-AUG-2003 (first entry)
XX
XX Human bi-directional promoter PCR/sequencing primer ON-TATAdel.
XX
XX Human; ss; Goodpasture antigen binding protein; GPBP; COL4A3BP;
KW collagen 4 alpha 3 binding protein; DNA polymerase kappa; Pol kappa;
KW Goodpasture disease; cutaneous lupus; polk76; bi-directional promoter;
KW autoimmune disease; cancer; antisense therapy; PCR; primer.
XX
XX Homo sapiens.
XX
XX US2003027165-A1.
XX
XX 06-FEB-2003.
XX
XX 07-DEC-2001; 2001US-00010920.
```

```
XX 08-DEC-2000; 2000US-0254649P.
XX (SAUS/) SAUS J.
XX Saus J;
XX WPI; 2003-479531/45.
XX
XX New isolated DNA polymerase, pol kappa 76, useful in identifying
XX autoimmune disorders and in treating cancer and autoimmune disorders by
XX modifying its expression.
XX
XX Example; Page 6; 54pp; English.
XX
XX The invention relates to an isolated pol kappa (k) 76 polypeptide (an
XX alternatively spliced form of DNA polymerase kappa), appearing as
XX AB007327 (encoded by the cDNA appearing as ACD13492). The gene for
XX Polkappa is located on chromosome 5q12-13 in a head-head arrangement with
XX the gene encoding Goodpasture antigen binding protein (GPBP or collagen 4
XX alpha 3 binding protein (COL4A3BP), associated with autoimmune diseases
XX such as Goodpasture's disease and cutaneous lupus) i.e. has a bi-
XX directional promoter. Also included are a recombinant expression vector
XX comprising the polk76 cDNA, a host cell transfected with the vector,
XX detecting (M1) polk76 (comprising providing a protein sample to be
XX screened, contacting the protein sample to be screened with an anti-
XX polk76 antibody and detecting the formation of an antibody- polypeptide
XX complexes, where the presence of the antibody-polypeptide complexes
XX indicates the presence of polk76), detecting (M2) the polk76 nucleic acid
XX in a sample (comprising contacting the sample with one or more polk76 PCR
XX primer, carrying out PCR to generate PCR products, and identifying the
XX polk76-specific PCR), detecting an autoimmune condition in a patient
XX (comprising providing a tissue or body fluid sample from the patient,
XX providing a control tissue or body fluid sample in which no autoimmune
XX condition is present, and detecting an increase in pol k76 RNA expression
XX in the tissue of body fluid samples compared to the control sample, where
XX the increase indicates the presence of an autoimmune condition) and
XX treating (M3) a patient with an autoimmune disorder or cancer by
XX modifying the expression or activity of pol k76 in the patient. Modifying
XX the expression or activity of polk76 or polk76 nucleic acid, such as by
XX increasing or decreasing their expression or activity using antibodies or
XX antisense therapy, is useful for treating an autoimmune disorder or
XX cancer. The present sequence is a PCR and/or sequencing primer used in
XX the analysis of bi-directional promoters of other genes (and/or of
XX polkappa/GPBP), whose structure and sequence were compared to the
XX polkappa/GPBP bi-directional promoter
XX
XX Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 87.0%; Score 17.4; DB 9; Length 30;
XX Best Local Similarity 94.7%; Pred. No. 4.2e+03;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 AGGGGAGGGGAGGGGAGGG 19
XX 2 AGGGGAGGGGAGGGGAGGG 20
XX
XX
XX RESULT 19
XX ADA97805
XX ID ADA97805 standard; DNA; 30 BP.
XX
XX AC ADA97805;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human tumour necrosis factor (TNF) inducible promoter PCR primer #7.
XX
XX Human; tumour necrosis factor inducible promoter; TNF;
KW autoimmune disorder; cancer; PCR; immunosuppressive; cytostatic; ss;
KW primer.
XX
XX Homo sapiens.
XX
XX OS
```





|           |             |   |     |              |    |            |    |        |    |      |    |
|-----------|-------------|---|-----|--------------|----|------------|----|--------|----|------|----|
|           |             | Matches   | 18; | Conservative | 0; | Mismatches | 1; | Indels | 0; | Gaps | 0; |
| Qy        | 1           | AGGGAGGGAGGGAGGG 19   |     |              |    |            |    |        |    |      |    |
|           |             |   |     |              |    |            |    |        |    |      |    |
| Db        | 10          | AAGGGAGGGAGGGAGGG 28  |     |              |    |            |    |        |    |      |    |
|           |             |   |     |              |    |            |    |        |    |      |    |
| RESULT 24 |             |   |     |              |    |            |    |        |    |      |    |
| ID        | ABK98155    | standard; DNA; 39 BP.   |     |              |    |            |    |        |    |      |    |
| XX        | AC          | ABK98155;   |     |              |    |            |    |        |    |      |    |
| DT        | 07-OCT-2002 | (first entry)   |     |              |    |            |    |        |    |      |    |
| XX        | DE          | Triple helix forming associated DNA sequence #19.                         |     |              |    |            |    |        |    |      |    |
| XX        | KW          | Triple-helix formation; purine-rich target sequence; double-helix DNA;    |     |              |    |            |    |        |    |      |    |
| KW        | KW          | gene expression; regulatory sequence; pathogenic double-stranded DNA;     |     |              |    |            |    |        |    |      |    |
| KW        | KW          | pathogenic bacteria; virus; replication; virulence; cancer;               |     |              |    |            |    |        |    |      |    |
| KW        | KW          | oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.      |     |              |    |            |    |        |    |      |    |
| OS        | OS          | Synthetic.  |     |              |    |            |    |        |    |      |    |
| XX        | PN          | US6403302-B1.   |     |              |    |            |    |        |    |      |    |
| XX        | PD          | 11-JUN-2002.  |     |              |    |            |    |        |    |      |    |
| XX        | PF          | 16-DEC-1993; 93US-00168920.   |     |              |    |            |    |        |    |      |    |
| XX        | PR          | 17-SEP-1992; 92US-00946976.   |     |              |    |            |    |        |    |      |    |
| XX        | PA          | (CALY ) CALIFORNIA INST OF TECHNOLOGY.                                    |     |              |    |            |    |        |    |      |    |
| XX        | PI          | Dervan PB, Beal PA;   |     |              |    |            |    |        |    |      |    |
| XX        | DR          | WPI; 2002-536030/57.  |     |              |    |            |    |        |    |      |    |
| XX        | PT          | A triple-helix comprising a double helical nucleic acid (DHNA) and an     |     |              |    |            |    |        |    |      |    |
| PT        | PT          | oligonucleotide which binds in parallel and antiparallel orientation,     |     |              |    |            |    |        |    |      |    |
| PT        | PT          | respectively, for targetting sequences on alternate strands of DHNA to    |     |              |    |            |    |        |    |      |    |
| XX        | XX          | control gene expression.  |     |              |    |            |    |        |    |      |    |
| XX        | PS          | Example 4; Fig 8B; 108pp; English.  |     |              |    |            |    |        |    |      |    |
| XX        | CC          | The present invention relates to methods and oligonucleotides for forming |     |              |    |            |    |        |    |      |    |
| CC        | CC          | a triple-helix comprising a double helical nucleic acid comprising first  |     |              |    |            |    |        |    |      |    |
| CC        | CC          | and second substantially complementary strands, and an oligonucleotide    |     |              |    |            |    |        |    |      |    |
| CC        | CC          | bound to a purine-rich target sequence within the double helical nucleic  |     |              |    |            |    |        |    |      |    |
| CC        | CC          | acid, where the oligonucleotide binds in a parallel and antiparallel      |     |              |    |            |    |        |    |      |    |
| CC        | CC          | orientation, respectively, to target sequences on alternate strands of    |     |              |    |            |    |        |    |      |    |
| CC        | CC          | the double helical nucleic acid. The method has therapeutic applications, |     |              |    |            |    |        |    |      |    |
| CC        | CC          | where gene expression is controlled by selective triple-helix formation   |     |              |    |            |    |        |    |      |    |
| CC        | CC          | within expression regulatory sequences of a target gene. The              |     |              |    |            |    |        |    |      |    |
| CC        | CC          | oligonucleotides can be used to form triple-helices, and are useful to    |     |              |    |            |    |        |    |      |    |
| CC        | CC          | detect the presence or absence of specific sequences within genomic DNA   |     |              |    |            |    |        |    |      |    |
| CC        | CC          | for diagnostic and therapeutic purposes. The oligonucleotides can be      |     |              |    |            |    |        |    |      |    |
| CC        | CC          | selected to specifically bind to pathogenic double-stranded DNA including |     |              |    |            |    |        |    |      |    |
| CC        | CC          | specific sequences required by pathogenic bacteria or viruses for         |     |              |    |            |    |        |    |      |    |
| CC        | CC          | replication or virulence, reducing their pathogenicity. Alternatively,    |     |              |    |            |    |        |    |      |    |
| CC        | CC          | the oligonucleotide can be chosen to target a unique sequence of the      |     |              |    |            |    |        |    |      |    |
| CC        | CC          | pathogen which is not found in the genome of pathogen's host. The         |     |              |    |            |    |        |    |      |    |
| CC        | CC          | oligonucleotides can be used in cancer treatment by way of triple-helix   |     |              |    |            |    |        |    |      |    |
| CC        | CC          | suppression of specific oncogenes including those of endogenous or viral  |     |              |    |            |    |        |    |      |    |
| CC        | CC          | origin. Such therapeutic oligonucleotides are capable of forming triple-  |     |              |    |            |    |        |    |      |    |
| CC        | CC          | helices with such sequences in cancerous cells containing the activated   |     |              |    |            |    |        |    |      |    |
| CC        | CC          | oncogene, so preferentially killing or repressing the cancer causing      |     |              |    |            |    |        |    |      |    |
| CC        | CC          | cell. The present sequence represents a DNA sequence used in the methods  |     |              |    |            |    |        |    |      |    |
| CC        | CC          | of the present invention  |     |              |    |            |    |        |    |      |    |
| XX        | XX          | Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;                       |     |              |    |            |    |        |    |      |    |
| SQ        | SQ          | 87.0%; Score 17.4; DB 6; Length 39;                                       |     |              |    |            |    |        |    |      |    |

|           |             |   |        |                    |    |            |    |        |    |      |    |
|-----------|-------------|---|--------|--------------------|----|------------|----|--------|----|------|----|
|           |             | Best Local Similarity   | 94.7%; | Pred. NO..4.1e+03; |    |            |    |        |    |      |    |
|           |             | Matches   | 18;    | Conservative       | 0; | Mismatches | 1; | Indels | 0; | Gaps | 0; |
| Qy        | 1           | AGGGAGGGAGGGAGGG 19   |        |                    |    |            |    |        |    |      |    |
|           |             |   |        |                    |    |            |    |        |    |      |    |
| Db        | 10          | AAGGGAGGGAGGGAGGG 28  |        |                    |    |            |    |        |    |      |    |
|           |             |   |        |                    |    |            |    |        |    |      |    |
| RESULT 25 |             |   |        |                    |    |            |    |        |    |      |    |
| ID        | ABK98154/c  | standard; DNA; 39 BP.   |        |                    |    |            |    |        |    |      |    |
| XX        | AC          | ABK98154;   |        |                    |    |            |    |        |    |      |    |
| DT        | 07-OCT-2002 | (first entry)   |        |                    |    |            |    |        |    |      |    |
| XX        | DE          | Triple helix forming associated DNA sequence #18.                         |        |                    |    |            |    |        |    |      |    |
| XX        | KW          | Triple-helix formation; purine-rich target sequence; double-helix DNA;    |        |                    |    |            |    |        |    |      |    |
| KW        | KW          | gene expression; regulatory sequence; pathogenic double-stranded DNA;     |        |                    |    |            |    |        |    |      |    |
| KW        | KW          | pathogenic bacteria; virus; replication; virulence; cancer;               |        |                    |    |            |    |        |    |      |    |
| KW        | KW          | oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.      |        |                    |    |            |    |        |    |      |    |
| OS        | OS          | Synthetic.  |        |                    |    |            |    |        |    |      |    |
| XX        | PN          | US6403302-B1.   |        |                    |    |            |    |        |    |      |    |
| XX        | PD          | 11-JUN-2002.  |        |                    |    |            |    |        |    |      |    |
| XX        | PF          | 16-DEC-1993; 93US-00168920.   |        |                    |    |            |    |        |    |      |    |
| XX        | PR          | 17-SEP-1992; 92US-00946976.   |        |                    |    |            |    |        |    |      |    |
| XX        | PA          | (CALY ) CALIFORNIA INST OF TECHNOLOGY.                                    |        |                    |    |            |    |        |    |      |    |
| XX        | PI          | Dervan PB, Beal PA;   |        |                    |    |            |    |        |    |      |    |
| XX        | DR          | WPI; 2002-536030/57.  |        |                    |    |            |    |        |    |      |    |
| XX        | PT          | A triple-helix comprising a double helical nucleic acid (DHNA) and an     |        |                    |    |            |    |        |    |      |    |
| PT        | PT          | oligonucleotide which binds in parallel and antiparallel orientation,     |        |                    |    |            |    |        |    |      |    |
| PT        | PT          | respectively, for targetting sequences on alternate strands of DHNA to    |        |                    |    |            |    |        |    |      |    |
| XX        | XX          | control gene expression.  |        |                    |    |            |    |        |    |      |    |
| XX        | PS          | Example 4; Fig 8B; 108pp; English.  |        |                    |    |            |    |        |    |      |    |
| XX        | CC          | The present invention relates to methods and oligonucleotides for forming |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | a triple-helix comprising a double helical nucleic acid comprising first  |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | and second substantially complementary strands, and an oligonucleotide    |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | bound to a purine-rich target sequence within the double helical nucleic  |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | acid, where the oligonucleotide binds in a parallel and antiparallel      |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | orientation, respectively, to target sequences on alternate strands of    |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | the double helical nucleic acid. The method has therapeutic applications, |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | where gene expression is controlled by selective triple-helix formation   |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | within expression regulatory sequences of a target gene. The              |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | oligonucleotides can be used to form triple-helices, and are useful to    |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | detect the presence or absence of specific sequences within genomic DNA   |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | for diagnostic and therapeutic purposes. The oligonucleotides can be      |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | selected to specifically bind to pathogenic double-stranded DNA including |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | specific sequences required by pathogenic bacteria or viruses for         |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | replication or virulence, reducing their pathogenicity. Alternatively,    |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | the oligonucleotide can be chosen to target a unique sequence of the      |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | pathogen which is not found in the genome of pathogen's host. The         |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | oligonucleotides can be used in cancer treatment by way of triple-helix   |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | suppression of specific oncogenes including those of endogenous or viral  |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | origin. Such therapeutic oligonucleotides are capable of forming triple-  |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | helices with such sequences in cancerous cells containing the activated   |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | oncogene, so preferentially killing or repressing the cancer causing      |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | cell. The present sequence represents a DNA sequence used in the methods  |        |                    |    |            |    |        |    |      |    |
| CC        | CC          | of the present invention  |        |                    |    |            |    |        |    |      |    |
| XX        | XX          | Sequence 39 BP; 6 A; 14 C; 6 G; 13 T; 0 U; 0 Other;                       |        |                    |    |            |    |        |    |      |    |
| SQ        | SQ          | 87.0%; Score 17.4; DB 6; Length 39;                                       |        |                    |    |            |    |        |    |      |    |

|           |   |                       |        |                    |    |            |    |        |    |      |    |
|-----------|---|-----------------------|--------|--------------------|----|------------|----|--------|----|------|----|
|           |   | Best Local Similarity | 94.7%; | Pred. No. 4.1e+03; |    |            |    |        |    |      |    |
|           |   | Matches               | 18;    | Conservative       | 0; | Mismatches | 1; | Indels | 0; | Gaps | 0; |
| QY        | 1   | AGGGAGGGAGGGAGGG 19   |        |                    |    |            |    |        |    |      |    |
|           |   |                       |        |                    |    |            |    |        |    |      |    |
| DB        | 10  | AAGGGAGGGAGGGAGGG 28  |        |                    |    |            |    |        |    |      |    |
|           |   |                       |        |                    |    |            |    |        |    |      |    |
| RESULT 25 |   |                       |        |                    |    |            |    |        |    |      |    |
| ID        | ABK98154/c  |                       |        |                    |    |            |    |        |    |      |    |
| XX        | ABK98154 standard; DNA; 39 BP.  |                       |        |                    |    |            |    |        |    |      |    |
| AC        | ABK98154;   |                       |        |                    |    |            |    |        |    |      |    |
| XX        | 07-OCT-2002 (first entry)   |                       |        |                    |    |            |    |        |    |      |    |
| XX        | Triple helix forming associated DNA sequence #18.                         |                       |        |                    |    |            |    |        |    |      |    |
| DE        |   |                       |        |                    |    |            |    |        |    |      |    |
| XX        | Triple-helix formation; purine-rich target sequence; double-helix DNA;    |                       |        |                    |    |            |    |        |    |      |    |
| KW        | gene expression; regulatory sequence; pathogenic double-stranded DNA;     |                       |        |                    |    |            |    |        |    |      |    |
| KW        | pathogenic bacteria; virus; replication; virulence; cancer;               |                       |        |                    |    |            |    |        |    |      |    |
| KW        | oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.      |                       |        |                    |    |            |    |        |    |      |    |
| OS        | Synthetic.  |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| PN        | US6403302-B1.   |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| PD        | 11-JUN-2002.  |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| PF        | 16-DEC-1993; 93US-00168920.   |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| PR        | 17-SEP-1992; 92US-00946976.   |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| PA        | (CALY ) CALIFORNIA INST OF TECHNOLOGY.                                    |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| PI        | Dervan PB, Beal PA;   |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| DR        | WPI; 2002-536030/57.  |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| PT        | A triple-helix comprising a double helical nucleic acid (DHNA) and an     |                       |        |                    |    |            |    |        |    |      |    |
| PT        | oligonucleotide which binds in parallel and antiparallel orientation,     |                       |        |                    |    |            |    |        |    |      |    |
| PT        | respectively, for targetting sequences on alternate strands of DHNA to    |                       |        |                    |    |            |    |        |    |      |    |
| PT        | control gene expression.  |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| XX        | Example 4; Fig 8B; 108pp; English.  |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| CC        | The present invention relates to methods and oligonucleotides for forming |                       |        |                    |    |            |    |        |    |      |    |
| CC        | a triple-helix comprising a double helical nucleic acid comprising first  |                       |        |                    |    |            |    |        |    |      |    |
| CC        | and second substantially complementary strands, and an oligonucleotide    |                       |        |                    |    |            |    |        |    |      |    |
| CC        | bound to a purine-rich target sequence within the double helical nucleic  |                       |        |                    |    |            |    |        |    |      |    |
| CC        | acid, where the oligonucleotide binds in a parallel and antiparallel      |                       |        |                    |    |            |    |        |    |      |    |
| CC        | orientation, respectively, to target sequences on alternate strands of    |                       |        |                    |    |            |    |        |    |      |    |
| CC        | the double helical nucleic acid. The method has therapeutic applications, |                       |        |                    |    |            |    |        |    |      |    |
| CC        | where gene expression is controlled by selective triple-helix formation   |                       |        |                    |    |            |    |        |    |      |    |
| CC        | within expression regulatory sequences of a target gene. The              |                       |        |                    |    |            |    |        |    |      |    |
| CC        | oligonucleotides can be used to form triple-helices, and are useful to    |                       |        |                    |    |            |    |        |    |      |    |
| CC        | detect the presence or absence of specific sequences within genomic DNA   |                       |        |                    |    |            |    |        |    |      |    |
| CC        | for diagnostic and therapeutic purposes. The oligonucleotides can be      |                       |        |                    |    |            |    |        |    |      |    |
| CC        | selected to specifically bind to pathogenic double-stranded DNA including |                       |        |                    |    |            |    |        |    |      |    |
| CC        | specific sequences required by pathogenic bacteria or viruses for         |                       |        |                    |    |            |    |        |    |      |    |
| CC        | replication or virulence, reducing their pathogenicity. Alternatively,    |                       |        |                    |    |            |    |        |    |      |    |
| CC        | the oligonucleotide can be chosen to target a unique sequence of the      |                       |        |                    |    |            |    |        |    |      |    |
| CC        | pathogen which is not found in the genome of pathogen's host. The         |                       |        |                    |    |            |    |        |    |      |    |
| CC        | oligonucleotides can be used in cancer treatment by way of triple-helix   |                       |        |                    |    |            |    |        |    |      |    |
| CC        | suppression of specific oncogenes including those of endogenous or viral  |                       |        |                    |    |            |    |        |    |      |    |
| CC        | origin. Such therapeutic oligonucleotides are capable of forming triple-  |                       |        |                    |    |            |    |        |    |      |    |
| CC        | helices with such sequences in cancerous cells containing the activated   |                       |        |                    |    |            |    |        |    |      |    |
| CC        | oncogene, so preferentially killing or repressing the cancer causing      |                       |        |                    |    |            |    |        |    |      |    |
| CC        | cell. The present sequence represents a DNA sequence used in the methods  |                       |        |                    |    |            |    |        |    |      |    |
| CC        | of the present invention  |                       |        |                    |    |            |    |        |    |      |    |
| XX        |   |                       |        |                    |    |            |    |        |    |      |    |
| SQ        | Sequence 39 BP; 6 A; 14 C; 6 G; 13 T; 0 U; 0 Other;                       |                       |        |                    |    |            |    |        |    |      |    |

|                       |        |                    |               |                   |
|-----------------------|--------|--------------------|---------------|-------------------|
| Query Match           | 87.0%; | Score 17.4;        | DB 6;         | Length 39;        |
| Best Local Similarity | 94.7%; | Pred. NO. 4.1e+03; |               |                   |
| Matches               | 18;    | Conservative 0;    | Mismatches 1; | Indels 0; Gaps 0; |

  

|    |    |                    |    |
|----|----|--------------------|----|
| QY | 1  | AGGGGAGGGAGGGAGGGG | 19 |
| DB | 30 | AAGGGAGGGAGGGAGGGG | 12 |

  

|           |  |
|-----------|--|
| RESULT 26 |  |
| ABK98106  |  |
| ID        | ABK98106 standard; DNA; 43 BP.   |
| XX        |  |
| AC        | ABK98106;  |
| DT        | 07-OCT-2002 (first entry)  |
| XX        |  |
| DE        | Triple helix forming associated oligonucleotide #3.                    |
| XX        |  |
| KW        | Triple-helix formation; purine-rich target sequence; double-helix DNA; |
| KW        | gene expression; regulatory sequence; pathogenic double-stranded DNA;  |
| KW        | pathogenic bacteria; virus; replication; virulence; cancer;            |
| KW        | oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.   |
| XX        |  |
| OS        | Synthetic.   |
| XX        |  |
| PN        | US6403302-B1.  |
| XX        |  |
| PD        | 11-JUN-2002.   |
| XX        |  |
| PF        | 16-DEC-1993; 93US-00168920.  |
| XX        |  |
| PR        | 17-SEP-1992; 92US-00946976.  |
| XX        |  |
| PA        | (CALY ) CALIFORNIA INST OF TECHNOLOGY.                                 |
| XX        |  |
| PI        | Dervan PB, Beal PA;  |
| XX        |  |
| DR        | WPI; 2002-536030/57.   |
| XX        |  |
| PT        | A triple-helix comprising a double helical nucleic acid (DHNA) and an  |
| PT        | oligonucleotide which binds in parallel and antiparallel orientation,  |
| PT        | respectively, for targeting sequences on alternate strands of DHNA to  |
| PT        | control gene expression.   |
| XX        |  |
| PS        | Example 4; Col 29; 108pp; English.                                     |
| XX        |  |

  

|    |   |
|----|---|
| CC | The present invention relates to methods and oligonucleotides for forming |
| CC | a triple-helix comprising a double helical nucleic acid comprising first  |
| CC | and second substantially complementary strands, and an oligonucleotide    |
| CC | bound to a purine-rich target sequence within the double helical nucleic  |
| CC | acid, where the oligonucleotide binds in a parallel and antiparallel      |
| CC | orientation, respectively, to target sequences on alternate strands of    |
| CC | the double helical nucleic acid. The method has therapeutic applications, |
| CC | where gene expression is controlled by selective triple-helix formation   |
| CC | within expression regulatory sequences of a target gene. The              |
| CC | oligonucleotides can be used to form triple-helices, and are useful to    |
| CC | detect the presence or absence of specific sequences within genomic DNA   |
| CC | for diagnostic and therapeutic purposes. The oligonucleotides can be      |
| CC | selected to specifically bind to pathogenic double-stranded DNA including |
| CC | specific sequences required by pathogenic bacteria or viruses for         |
| CC | replication or virulence, reducing their pathogenicity. Alternatively,    |
| CC | the oligonucleotide can be chosen to target a unique sequence of the      |
| CC | pathogen which is not found in the genome of pathogen's host. The         |
| CC | oligonucleotides can be used in cancer treatment by way of triple-helix   |
| CC | suppression of specific oncogenes including those of endogenous or viral  |
| CC | origin. Such therapeutic oligonucleotides are capable of forming triple-  |
| CC | helices with such sequences in cancerous cells containing the activated   |
| CC | oncogene, so preferentially killing or repressing the cancer causing      |
| CC | cell. The present invention represents an oligonucleotide used in the     |
| CC | methods of the present invention  |
| XX |   |

  

|          |  |
|----------|--|
| Sequence | 43 BP; 15 A; 6 C; 14 G; 8 T; 0 U; 0 Other; |
| XX       |  |

  

|                       |        |                  |               |                   |
|-----------------------|--------|------------------|---------------|-------------------|
| Query Match           | 87.0%; | Score 17.4;      | DB 6;         | Length 43;        |
| Best Local Similarity | 94.7%; | Pred. NO. 4e+03; |               |                   |
| Matches               | 18;    | Conservative 0;  | Mismatches 1; | Indels 0; Gaps 0; |

  

|    |    |                    |    |
|----|----|--------------------|----|
| QY | 1  | AGGGGAGGGAGGGAGGGG | 19 |
| DB | 14 | AAGGGAGGGAGGGAGGGG | 32 |

  

|           |  |
|-----------|--|
| RESULT 27 |  |
| ABK98104  |  |
| ID        | ABK98104 standard; DNA; 19 BP.   |
| XX        |  |
| AC        | ABK98104;  |
| DT        | 07-OCT-2002 (first entry)  |
| XX        |  |
| DE        | Triple helix forming associated DNA sequence #1.                       |
| XX        |  |
| KW        | Triple-helix formation; purine-rich target sequence; double-helix DNA; |
| KW        | gene expression; regulatory sequence; pathogenic double-stranded DNA;  |
| KW        | pathogenic bacteria; virus; replication; virulence; cancer;            |
| KW        | oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.   |
| XX        |  |
| OS        | Synthetic.   |
| XX        |  |
| PN        | US6403302-B1.  |
| XX        |  |
| PD        | 11-JUN-2002.   |
| XX        |  |
| PF        | 16-DEC-1993; 93US-00168920.  |
| XX        |  |
| PR        | 17-SEP-1992; 92US-00946976.  |
| XX        |  |
| PA        | (CALY ) CALIFORNIA INST OF TECHNOLOGY.                                 |
| XX        |  |
| PI        | Dervan PB, Beal PA;  |
| XX        |  |
| DR        | WPI; 2002-536030/57.   |
| XX        |  |
| PT        | A triple-helix comprising a double helical nucleic acid (DHNA) and an  |
| PT        | oligonucleotide which binds in parallel and antiparallel orientation,  |
| PT        | respectively, for targeting sequences on alternate strands of DHNA to  |
| PT        | control gene expression.   |
| XX        |  |
| PS        | Example 4; Col 29; 108pp; English.                                     |
| XX        |  |

  

|    |   |
|----|---|
| CC | The present invention relates to methods and oligonucleotides for forming |
| CC | a triple-helix comprising a double helical nucleic acid comprising first  |
| CC | and second substantially complementary strands, and an oligonucleotide    |
| CC | bound to a purine-rich target sequence within the double helical nucleic  |
| CC | acid, where the oligonucleotide binds in a parallel and antiparallel      |
| CC | orientation, respectively, to target sequences on alternate strands of    |
| CC | the double helical nucleic acid. The method has therapeutic applications, |
| CC | where gene expression is controlled by selective triple-helix formation   |
| CC | within expression regulatory sequences of a target gene. The              |
| CC | oligonucleotides can be used to form triple-helices, and are useful to    |
| CC | detect the presence or absence of specific sequences within genomic DNA   |
| CC | for diagnostic and therapeutic purposes. The oligonucleotides can be      |
| CC | selected to specifically bind to pathogenic double-stranded DNA including |
| CC | specific sequences required by pathogenic bacteria or viruses for         |
| CC | replication or virulence, reducing their pathogenicity. Alternatively,    |
| CC | the oligonucleotide can be chosen to target a unique sequence of the      |
| CC | pathogen which is not found in the genome of pathogen's host. The         |
| CC | oligonucleotides can be used in cancer treatment by way of triple-helix   |
| CC | suppression of specific oncogenes including those of endogenous or viral  |
| CC | origin. Such therapeutic oligonucleotides are capable of forming triple-  |
| CC | helices with such sequences in cancerous cells containing the activated   |
| CC | oncogene, so preferentially killing or repressing the cancer causing      |
| CC | cell. The present invention represents a DNA sequence used in the methods |
| CC | of the present invention  |
| XX |   |

SQ Sequence 19 BP; 5 A; 0 C; 14 G; 0 T; 0 U; 0 Other;  
 Query Match 85.0%; Score 17; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GGGAGGGGAGGGAGGG 19  
 DB 2 GGGAGGGGAGGGAGGG 18  
 RESULT 28  
 ADH70505/c  
 ID ADH70505 standard; DNA; 23 BP.  
 XX AC ADH70505;  
 XX DT 25-MAR-2004 (first entry)  
 XX DE Human Vbeta gene repeat sequence #295.  
 XX KW human; T-cell associated disease; Vbeta; autoimmune disease;  
 KW degenerative nervous system disease; graft versus host disease;  
 KW hypersensitivity disease; infectious disease; neoplastic disease;  
 KW Addison's disease; atrophic gastritis;  
 KW degenerative nervous system disease; multiple sclerosis;  
 KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;  
 KW allergy; type II hypersensitivity; Goodpasture's syndrome;  
 KW type IV hypersensitivity; leprosy; infectious disease; viral infection;  
 KW HIV; fungal infection; Candida; parasitic infection; schistosoma;  
 KW filaria; bacterial infection; Mycobacterium; neoplastic disease;  
 KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;  
 KW breast cancer; ds.  
 XX OS Homo sapiens.  
 XX FT US2002150891-A1.  
 XX FT 17-OCT-2002.  
 XX PF 05-MAR-1999; 99US-00263959.  
 XX PR 19-SEP-1994; 94US-00309335.  
 XX PR 19-SEP-1995; 95US-00531241.  
 XX XX (HOOD//) HOOD L E.  
 XX FA (ROWE//) ROWEN L.  
 XX PI Hood LE, Rowen L;  
 XX WPI; 2004-059052/06.  
 XX FT Kit for diagnosing and treating T-cell associated diseases e.g.  
 FT autoimmune, degenerative nervous system and infectious disease, comprises  
 FT nucleic acid primers specifically priming and allowing amplification of a  
 FT Vbeta gene.  
 XX PS Disclosure; SEQ ID NO 699; 164pp; English.  
 XX CC The invention relates to a kit for diagnosing and treating T-cell  
 CC associated diseases which comprises a panel of nucleic acid primers  
 CC specifically priming and allowing amplification of each Vbeta gene,  
 CC VbetatRNA or cDNA. The kit is useful for diagnosing organ transplant  
 CC rejection and diagnosing and treating T-cell associated diseases  
 CC including autoimmune diseases, degenerative nervous system diseases,  
 CC graft versus host disease, hypersensitivity diseases, infectious diseases  
 CC and neoplastic diseases. Autoimmune diseases include Addison's disease,  
 CC atrophic gastritis. Degenerative nervous system diseases include multiple  
 CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type  
 CC I hypersensitivities such as contact with allergens that lead to  
 CC allergies, type II hypersensitivities such as those present in  
 CC Goodpasture's syndrome and Type IV hypersensitivities such as those  
 CC manifested in leprosy. Infectious diseases include viral infections

CC caused by viruses such as HIV, fungal infections such as those caused by  
 CC the yeast genus Candida, parasitic infections such as those caused by  
 CC schistosomes, filaria and bacterial infections such as those caused by  
 CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases  
 CC such as leukaemias, lymphomas and cancers such as cancer of the brain,  
 CC breast. The present sequence represents a Vbeta gene repeat sequence.  
 XX Sequence 23 BP; 1 A; 17 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 84.0%; Score 16.8; DB 12; Length 23;  
 Best Local Similarity 90.0%; Pred. No. 6.7e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AGGGAGGGGAGGGAGGGG 20  
 DB 23 AGGGGCGGGAGGGAGGGG 4  
 RESULT 29  
 AAQ46253  
 ID AAQ46253 standard; DNA; 43 BP.  
 XX AC AAQ46253;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 24-MAR-1994 (first entry)  
 XX DE 39mer duplex forming DNA.  
 XX KW Duplex; T4 polynucleotide kinase; nebularine; triple helix; triplex;  
 KW detection; diagnosis; pathogen; bacteria; virus; virulence; cancer;  
 KW oncogene; ss.  
 XX OS Synthetic.  
 XX FT Key Location/Qualifiers  
 FT misc\_difference 19 /\*tag= a  
 FT /note= "A, G, C or T"  
 XX W09318187-A1.  
 XX PD 16-SEP-1993.  
 XX PF 11-MAR-1993; 93WO-US002352.  
 XX PR 13-MAR-1992; 92US-00850503.  
 XX PA (CALY ) CALIFORNIA INST OF TECHN.  
 XX PI Dervan PB;  
 XX WPI; 1993-303498/38.  
 XX FT Triple helix formation for diagnosis and therapy - by specific  
 FT recognition by oligo:nucleotide probe of target sequence in double-  
 FT stranded nucleic acid.  
 XX PS Example 1; Page 18; 42pp; English.  
 XX CC This sequence was used to form a 39mer duplex an example to illustrate  
 CC the invention. Oligonucleotides conforming to this sequence were 5' and  
 CC radioactively labeled using T4 polynucleotide kinase and gamma-32P ATP.  
 CC The annealed oligomers form a purine-rich target sequence to which an  
 CC oligonucleotide (TFO) containing a nebularine nucleotide binds, forming a  
 CC triple helix. These triplex- forming oligomers may be used to detect the  
 CC presence or absence of specific sequences within genomic DNA by the  
 CC formation in situ or in vivo of triple helices for diagnostic and  
 CC therapeutic purposes. TFO can be selected which specifically bind to  
 CC pathogenic double-stranded DNA including specific sequences required by  
 CC pathogenic bacteria or viruses for replication or virulence.  
 CC Alternatively, TFO can be chosen to target a unique sequence of the  
 CC pathogen which is not found in the genome of the host. It may include a

CC therapeutic agent to kill the pathogen or the cell containing it. Triple  
 CC helix technology can also be used for cancer treatment by way of triple  
 CC helix suppression of specific oncogenes including those of endogenous or  
 CC viral origin. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 2; Length 43;

Best Local Similarity 89.5%; Pred. No. 8.6e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGGAGGG 19

DB 14 AAGGGGAGGGGAGGGGAGGG 32

RESULT 30

AAQ46257/c

ID AAQ46257 standard; DNA; 43 BP.

AC AAQ46257;

DT 25-MAR-2003 (revised)

DT 24-MAR-1994 (first entry)

DE Duplex forming DNA #2.

Duplex; T4 polynucleotide kinase; nebularine; triple helix; triplex;  
 KW detection; diagnosis; pathogen; bacteria; virus; virulence; cancer;  
 KW oncogene; ss.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT misc\_difference 29 /\*tag= a

FT /\*note= "A, G, C or T"

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CC correct PN field.)

XX

SQ Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 2; Length 43;

Best Local Similarity 89.5%; Pred. No. 8.6e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGGAGGG 19

DB 34 AAGGGGAGGGGAGGGGAGGG 16

RESULT 31

AAQ46256

ID AAQ46256 standard; DNA; 43 BP.

AC AAQ46256;

DT 21-OCT-2004 (revised)

DT 25-MAR-2003 (revised)

DT 24-MAR-1994 (first entry)

DE Duplex forming DNA #1.

Duplex; T4 polynucleotide kinase; nebularine; triple helix; triplex;  
 KW detection; diagnosis; pathogen; bacteria; virus; virulence; cancer;  
 KW oncogene; ss.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT modified\_base 1

FT /\*tag= a

FT /\*mod\_base= OTHER

FT /\*note= "32P-A"

FT misc\_difference 19

FT /\*tag= b

FT /\*note= "A, G, C or T"

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The sequences given in AAQ46256-57 form a duplex which was used to  
 evaluate the binding of triplex forming oligomers (TFO). The annealed  
 oligomers form a purine-rich target sequence to which the TFO which  
 contain a nebularine nucleotide binds, bind, forming a triple helix.  
 These triplex-forming oligomers may be used to detect the presence or  
 absence of specific sequences within genomic DNA by the formation in situ  
 or in vivo of triple helices for diagnostic and therapeutic purposes. TFO  
 can be selected which specifically bind to pathogenic double-stranded DNA  
 including specific sequences required by pathogenic bacteria or viruses  
 for replication or virulence. Alternatively, TFO can be chosen to target  
 a unique sequence of the pathogen which is not found in the genome of the  
 host. It may include a therapeutic agent to kill the pathogen or the cell  
 containing it. Triple helix technology can also be used for cancer

CC treatment by way of triple helix suppression of specific oncogenes  
CC including those of endogenous or viral origin. (Updated on 25-MAR-2003 to  
CC correct PN field.)

CC Revised record issued on 21-OCT-2004 : Correction to feature table key

XX  
SQ Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 2; Length 43;  
Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 14 AAGGGGGGAGGGGAGGG 32

RESULT 32  
ABK98158/c  
ID ABK98158 standard; DNA; 43 BP.

XX  
AC ABK98158;

XX  
DT 07-OCT-2002 (first entry)

XX  
DE Triple helix forming associated DNA sequence #21.

XX  
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
KW pathogenic bacteria; virus; replication; virulence; cancer;  
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX  
OS Synthetic.

XX  
FN US6403302-B1.

XX  
PD 11-JUN-2002.

XX  
PF 16-DEC-1993; 93US-00168920.

XX  
PR 17-SEP-1992; 92US-00946976.

XX  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.

XX  
PI Dervan PB, Beal PA;

XX  
DR WPI; 2002-536030/57.

XX  
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an  
PT oligonucleotide which binds in parallel and antiparallel orientation,  
PT respectively, for targetting sequences on alternate strands of DHNA to  
PT control gene expression.

XX  
PS Example 5; Fig 11; 108pp; English.

XX  
CC The present invention relates to methods and oligonucleotides for forming  
CC a triple-helix comprising a double helical nucleic acid comprising first  
CC and second substantially complementary strands, and an oligonucleotide  
CC bound to a purine-rich target sequence within the double helical nucleic  
CC acid, where the oligonucleotide binds in a parallel and antiparallel  
CC orientation, respectively, to target sequences on alternate strands of  
CC the double helical nucleic acid. The method has therapeutic applications,  
CC where gene expression is controlled by selective triple-helix formation,  
CC within expression regulatory sequences of a target gene. The  
CC oligonucleotides can be used to form triple-helices, and are useful to  
CC detect the presence or absence of specific sequences within genomic DNA  
CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
CC selected to specifically bind to pathogenic double-stranded DNA including  
CC specific sequences required by pathogenic bacteria or viruses for  
CC replication or virulence, reducing their pathogenicity. Alternatively,  
CC the oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The  
CC oligonucleotides can be used in cancer treatment by way of triple-helix

CC suppression of specific oncogenes including those of endogenous or viral  
CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
CC helices with such sequences in cancerous cells containing the activated  
CC oncogene, so preferentially killing or repressing the cancer causing  
CC cell. The present sequence represents a DNA sequence used in the methods  
CC of the present invention

SQ Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 6; Length 43;  
Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 34 AAGGGGGGAGGGGAGGG 16

RESULT 33  
ABK98112/c  
ID ABK98112 standard; DNA; 43 BP.

XX  
AC ABK98112;

XX  
DT 07-OCT-2002 (first entry)

XX  
DE Triple helix forming associated DNA sequence #3.

XX  
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
KW pathogenic bacteria; virus; replication; virulence; cancer;  
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX  
OS Synthetic.

XX  
FN US6403302-B1.

XX  
PD 11-JUN-2002.

XX  
PF 16-DEC-1993; 93US-00168920.

XX  
PR 17-SEP-1992; 92US-00946976.

XX  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.

XX  
PI Dervan PB, Beal PA;

XX  
DR WPI; 2002-536030/57.

XX  
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an  
PT oligonucleotide which binds in parallel and antiparallel orientation,  
PT respectively, for targetting sequences on alternate strands of DHNA to  
PT control gene expression.

XX  
PS Example 5; Col 35; 108pp; English.

XX  
CC The present invention relates to methods and oligonucleotides for forming  
CC a triple-helix comprising a double helical nucleic acid comprising first  
CC and second substantially complementary strands, and an oligonucleotide  
CC bound to a purine-rich target sequence within the double helical nucleic  
CC acid, where the oligonucleotide binds in a parallel and antiparallel  
CC orientation, respectively, to target sequences on alternate strands of  
CC the double helical nucleic acid. The method has therapeutic applications,  
CC where gene expression is controlled by selective triple-helix formation,  
CC within expression regulatory sequences of a target gene. The  
CC oligonucleotides can be used to form triple-helices, and are useful to  
CC detect the presence or absence of specific sequences within genomic DNA  
CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
CC selected to specifically bind to pathogenic double-stranded DNA including  
CC specific sequences required by pathogenic bacteria or viruses for  
CC replication or virulence, reducing their pathogenicity. Alternatively,  
CC the oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The



CC oligonucleotides can be used in cancer treatment by way of triple-helix  
 CC suppression of specific oncogenes including those of endogenous or viral  
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
 CC helices with such sequences in cancerous cells containing the activated  
 CC oncogene, so preferentially killing or repressing the cancer causing  
 CC cell. The present sequence represents a DNA sequence used in the methods  
 CC of the present invention

XX SQ Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 6; Length 43;  
 Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGGAGGG 19  
 |||||  
 Db 34 AAGGGGAGGGGAGGGGAGGG 16

RESULT 34  
 ABK98111  
 ID ABK98111 standard; DNA; 43 BP.

XX AC ABK98111;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated DNA sequence #2.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
 KW pathogenic bacteria; virus; replication; virulence; cancer;  
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX FN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-00168920.

XX PR 17-SEP-1992; 92US-00946976.

XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX DR WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an  
 PT oligonucleotide which binds in parallel and antiparallel orientation,  
 PT respectively, for targeting sequences on alternate strands of DHNA to  
 PT control gene expression.

XX Example 5; Col 35; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming  
 CC a triple-helix comprising a double helical nucleic acid comprising first  
 CC and second substantially complementary strands, and an oligonucleotide  
 CC bound to a purine-rich target sequence within the double helical nucleic  
 CC acid, where the oligonucleotide binds in a parallel and antiparallel  
 CC orientation, respectively, to target sequences on alternate strands of  
 CC the double helical nucleic acid. The method has therapeutic applications,  
 CC where gene expression is controlled by selective triple-helix formation  
 CC within expression regulatory sequences of a target gene. The  
 CC oligonucleotides can be used to form triple-helices, and are useful to  
 CC detect the presence or absence of specific sequences within genomic DNA  
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
 CC selected to specifically bind to pathogenic double-stranded DNA including  
 CC specific sequences required by pathogenic bacteria or viruses for  
 CC replication or virulence, reducing their pathogenicity. Alternatively,  
 CC the oligonucleotide can be chosen to target a unique sequence of the

CC pathogen which is not found in the genome of pathogen's host. The  
 CC oligonucleotides can be used in cancer treatment by way of triple-helix  
 CC suppression of specific oncogenes including those of endogenous or viral  
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
 CC helices with such sequences in cancerous cells containing the activated  
 CC oncogene, so preferentially killing or repressing the cancer causing  
 CC cell. The present sequence represents a DNA sequence used in the methods  
 CC of the present invention

XX SQ Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 6; Length 43;  
 Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGGAGGG 19  
 |||||  
 Db 14 AAGGGGAGGGGAGGGGAGGG 32

RESULT 35  
 ABK98107  
 ID ABK98107 standard; DNA; 43 BP.

XX AC ABK98107;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated oligonucleotide #4.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
 KW pathogenic bacteria; virus; replication; virulence; cancer;  
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX FN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-00168920.

XX PR 17-SEP-1992; 92US-00946976.

XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX DR WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an  
 PT oligonucleotide which binds in parallel and antiparallel orientation,  
 PT respectively, for targeting sequences on alternate strands of DHNA to  
 PT control gene expression.

XX Example 5; Col 33; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming  
 CC a triple-helix comprising a double helical nucleic acid comprising first  
 CC and second substantially complementary strands, and an oligonucleotide  
 CC bound to a purine-rich target sequence within the double helical nucleic  
 CC acid, where the oligonucleotide binds in a parallel and antiparallel  
 CC orientation, respectively, to target sequences on alternate strands of  
 CC the double helical nucleic acid. The method has therapeutic applications,  
 CC where gene expression is controlled by selective triple-helix formation  
 CC within expression regulatory sequences of a target gene. The  
 CC oligonucleotides can be used to form triple-helices, and are useful to  
 CC detect the presence or absence of specific sequences within genomic DNA  
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
 CC selected to specifically bind to pathogenic double-stranded DNA including  
 CC specific sequences required by pathogenic bacteria or viruses for  
 CC replication or virulence, reducing their pathogenicity. Alternatively,

CC the oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The  
CC oligonucleotides can be used in cancer treatment by way of triple-helix  
CC suppression of specific oncogenes including those of endogenous or viral  
CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
CC helices with such sequences in cancerous cells containing the activated  
CC oncogene, so preferentially killing or repressing the cancer causing  
CC cell. The present sequence represents an oligonucleotide used in the  
CC methods of the present invention

XX SQ Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 6; Length 43;  
Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGAGGGAGGG 19  
Db 14 AAGGGGGAGGGAGGGAGGG 32

#### RESULT 36

ABK98157  
ID ABK98157 standard; DNA; 45 BP.

XX AC ABK98157;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated DNA sequence #20.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
XX KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
XX KW pathogenic bacteria; virus; replication; virulence; cancer;  
XX KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX PN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-00168920.

XX PR 17-SEP-1992; 92US-00946976.

XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX DR WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an  
FT oligonucleotide which binds in parallel and antiparallel orientation,  
PT respectively, for targeting sequences on alternate strands of DHNA to  
PT control gene expression.

XX Example 5; Fig 11; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming  
CC a triple-helix comprising a double helical nucleic acid comprising first  
CC and second substantially complementary strands, and an oligonucleotide  
CC bound to a purine-rich target sequence within the double helical nucleic  
CC acid, where the oligonucleotide binds in a parallel and antiparallel  
CC orientation, respectively, to target sequences on alternate strands of  
CC the double helical nucleic acid. The method has therapeutic applications,  
CC where gene expression is controlled by selective triple-helix formation  
CC within expression regulatory sequences of a target gene. The  
CC oligonucleotides can be used to form triple-helices, and are useful to  
CC detect the presence or absence of specific sequences within genomic DNA  
CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
CC selected to specifically bind to pathogenic double-stranded DNA including  
CC specific sequences required by pathogenic bacteria or viruses for

CC replication or virulence, reducing their pathogenicity. Alternatively,  
CC the oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The  
CC oligonucleotides can be used in cancer treatment by way of triple-helix  
CC suppression of specific oncogenes including those of endogenous or viral  
CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
CC helices with such sequences in cancerous cells containing the activated  
CC oncogene, so preferentially killing or repressing the cancer causing  
CC cell. The present sequence represents a DNA sequence used in the methods  
CC of the present invention

XX SQ Sequence 45 BP; 14 A; 7 C; 14 G; 9 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 6; Length 45;  
Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGAGGGAGGG 19  
Db 16 AAGGGGGAGGGAGGGAGGG 34

#### RESULT 37

AAV76464/C

ID AAV76464 standard; DNA; 50 BP.

XX AC AAV76464;

XX DT 16-MAR-1999 (first entry)

XX DE Staphylococcus aureus contig SEQ ID #2153.

XX KW Computer readable medium; vaccine; S. aureus infection; immunodetection;  
XX KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
XX KW skin infection; surgical wound infection; scalded skin syndrome;  
XX KW toxic shock syndrome; ds.

XX OS Staphylococcus aureus.

XX PN EP786519-A2.

XX PD 30-JUL-1997.

XX PF 07-JAN-1997; 97EP-00100117.

XX PR 05-JAN-1996; 96US-0009861P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

XX DR WPI; 1997-374922/35.

XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
PT stored on computer readable medium and used in the production of anti-  
PT S. aureus vaccines.

XX Claim 1; Page 2159; 3271pp; English.

XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
CC of the invention. The DNA sequences are recorded on a computer readable  
CC medium, preferably selected from a floppy or hard disk, random access  
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
CC the S. aureus DNA sequences allows putative functions to be assigned so  
CC that protein-encoding or regulatory regions of commercial, therapeutic or  
CC industrial importance can be obtained. Specifically, sequences which are  
CC likely to encode antigens have been identified and these polypeptides can  
CC be used in a vaccine composition against S. aureus infection. The  
CC polypeptides can also be used in a kit for the immunodetection of  
CC S. aureus in a sample. S. aureus is implicated in numerous human diseases,  
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CC syndrome, etc. Organisms transformed with the DNA sequences can be used

CC for recombinant production of the polypeptides. The new DNA sequences  
 CC (and their fragments) are useful as primers or probes for isolating  
 CC homologues of any of the S.aureus DNA sequences contained on the computer  
 CC readable medium

XX Sequence 50 BP; 0 A; 46 C; 1 G; 2 T; 0 U; 1 Other;  
 SQ Query Match 82.0%; Score 16.4; DB 2; Length 50;  
 Best Local Similarity 89.5%; Pred. No. 8.5e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGAGGGGGGGGGGGGGG 20  
 ||||| ||||| ||||| |||||  
 Db 28 GGGGGGGGGGGGGGGGGG 10

RESULT 38  
 AAA22528/C  
 ID AAA22528 standard; RNA; 17 BP.

XX AC AAA22528;

XX DT 19-JUN-2000 (first entry)

XX DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5754.

XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;  
 KW ophthalmologic; antiinflammatory; antiarthritis; antipsoriatic; ARMD;  
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome;  
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

OS WO9950403-A2.

XX PN 07-OCT-1999.

XX PD 24-MAR-1999; 98WO-US006507.

XX PF 27-MAR-1998; 98US-0079678P.

XX PR (RIBO-) RIBOZYME PHARM INC.

XX PA Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

XX PI WPI; 1999-591315/50.

XX DR Novel ribozymes for modulating the synthesis, expression and/or stability  
 of an mRNA encoding an angiogenic factors.

XX PS Claim 54; Page 226; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA  
 CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
 CC AAA19184 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
 CC AAA21596 to AAA21688 represent their corresponding target sequences;  
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
 CC AAA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or

CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tuberculous sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3

XX SQ Sequence 17 BP; 0 A; 13 C; 1 G; 0 T; 3 U; 0 Other;

Query Match 80.0%; Score 16; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGAGGGGGGGGGGGG 18  
 ||||| ||||| ||||| |||||  
 Db 16 GGGAGGGGGGGGGGGG 1

RESULT 39

ADH70729

ID ADH70729 standard; DNA; 19 BP.

XX AC ADH70729;

XX DT 25-MAR-2004 (first entry)

XX DE Human Vbeta gene repeat sequence #519.

XX human; T-cell associated disease; Vbeta; autoimmune disease;  
 KW degenerative nervous system disease; graft versus host disease;  
 KW hypersensitivity disease; infectious disease; neoplastic disease;  
 KW Addison's disease; atrophic gastritis;  
 KW degenerative nervous system disease; multiple sclerosis;  
 KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;  
 KW allergy; type II hypersensitivity; Goodpasture's syndrome;  
 KW type IV hypersensitivity; leprosy; infectious disease; viral infection;  
 KW HIV; fungal infection; Candida; parasitic infection; schistosoma;  
 KW filaria; bacterial infection; Mycobacterium; neoplastic disease;  
 KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;  
 KW breast cancer; ds.

XX Homo sapiens.

OS US2002150891-A1.

XX PN 17-OCT-2002.

XX PD 05-MAR-1999; 99US-00263959.

XX PF 19-SEP-1994; 94US-00309335.

XX PR 19-SEP-1995; 95US-00531241.

XX PA (HOOD/) HOOD L E.

XX PI (ROWE/) ROWEN L.

XX PI Hood LE, Rowen L;

XX DR WPI; 2004-059052/06.

XX Kit for diagnosing and treating T-cell associated diseases e.g.  
 PT autoimmune, degenerative nervous system and infectious disease, comprises  
 PT nucleic acid primers specifically priming and allowing amplification of a  
 PT Vbeta gene.

PS Disclosure; SEQ ID NO 923; 164pp; English.

XX The invention relates to a kit for diagnosing and treating T-cell  
 CC associated diseases which comprises a panel of nucleic acid primers  
 CC specifically priming and allowing amplification of each Vbeta gene,  
 CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant

CC rejection and diagnosing and treating T-cell associated diseases  
CC including autoimmune diseases, degenerative nervous system diseases,  
CC graft versus host disease, hypersensitivity diseases, infectious diseases,  
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,  
CC atrophic gastritis. Degenerative nervous system diseases include multiple  
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type  
CC I hypersensitivities such as contact with allergens that lead to  
CC allergies, Type II hypersensitivities such as those present in  
CC Goodpasture's syndrome and Type IV hypersensitivities such as those  
CC manifested in leprosy. Infectious diseases include viral infections  
CC caused by viruses such as HIV, fungal infections such as those caused by  
CC the yeast genus Candida, parasitic infections such as those caused by  
CC schistosomes, filaria and bacterial infections such as those caused by  
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases  
CC such as leukemias, lymphomas and cancers such as cancer of the brain,  
CC breast. The present sequence represents a Vbeta gene repeat sequence.

XX Sequence 19 BP; 1 A; 2 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 12; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.5e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 1 GGGGCGGGGAGGGGCGGGG 19  
|||||

RESULT 40  
AAF99947  
ID AAF99947 standard; DNA; 20 BP.

XX AAF99947;

XX 12-JUL-2001 (first entry)

XX Synthetic oligonucleotide #13.

XX Oligonucleotide purification; liquid chromatography;  
KW hydrophobic protective group; deprotection; ds.

XX Synthetic.

XX JP2000342265-A.

XX 12-DEC-2000.

XX 02-JUN-1999; 99JP-00154974.

XX 02-JUN-1999; 99JP-00154974.

XX (TOAG ) TOA GOSHI CHEM IND LTD.

XX WPI; 2001-268251/28.

XX A process for purification of oligonucleotides using liquid  
PT chromatography.

XX Example 1; Page 4; 13pp; Japanese.

XX The present sequence is an oligonucleotide provided in a specification  
XX relating to the simplified purification of oligonucleotides by liquid  
XX chromatography. The process comprises: (a) pouring oligonucleotides  
XX protected with a hydrophobic group and oligonucleotide with no protective  
XX group into a liquid chromatography column packed with an acid and alkali  
XX resistant packing agent, such as polystyrene resin; (b) pouring a mixed  
XX developing solvent composed of a buffer made from a volatile salt and a  
XX water soluble organic solvent at a suitable concentration gradient into  
XX the column; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into  
XX the column to deprotect the oligonucleotides protected with the  
XX hydrophobic group; (d) pouring a mixed developing solvent composed of a  
XX buffer made from a volatile salt, particularly 0.05-0.5 N aqueous  
XX ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water

CC soluble organic solvent at a suitable concentration gradient to elute the  
CC deprotected oligonucleotides; and (e) removal of the solvent and the salt  
CC from the eluted oligonucleotides

XX Sequence 20 BP; 1 A; 1 C; 17 G; 1 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 4; Length 20;  
Best Local Similarity 89.5%; Pred. No. 1.5e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 2 GGGGCGGGGAGGGGAGGGG 20  
|||||

RESULT 41

AAAX40753  
ID AAAX40753 standard; DNA; 26 BP.

XX AAAX40753;

XX 16-JUN-1999 (first entry)

XX Oligonucleotide used for screening DCMase binding discrimination.

XX DNA cytosine methyltransferase; DCMase; binding discrimination;

XX C-5 methylcytosine; allosteric site; synthetic inhibitor; cancer cell;

XX proliferation; development disorder; Huntington's disease;

XX Down's syndrome; Hox gene; ss.

XX Synthetic.

XX WO9912027-A1.

XX 11-MAR-1999.

XX 12-JUN-1998; 98WO-US012351.

XX 29-AUG-1997; 97US-0057411P.

XX (REGC ) UNIV CALIFORNIA.

XX Reich NO, Flynn J;

XX WPI; 1999-205256/17.

XX DNA cytosine methyltransferase modulator containing 5-C methylcytosine -  
XX used to inhibit methylation of DNA, and proliferation of cancer cells.

XX Example 1; Fig 7; 114pp; English.

XX Oligonucleotides AAAX40733-815 represent cloned and sequenced isolates  
XX from pooled generations used for screening DNA cytosine methyltransferase  
XX (DCMase) binding discrimination. The oligonucleotides are double  
XX stranded, and the guanine containing strand is shown. The specification  
XX describes a synthetic oligonucleotide comprising a C-5 methylcytosine  
XX which recognizes and binds an allosteric site on DCMase, thereby  
XX modulating DCMase activity associated with the allosteric site. The  
XX synthetic inhibitor can be used to inhibit methylation of DNA. It can  
XX also be used to inhibit proliferation of cancer cells. The inhibitor can  
XX also be used to treat a disorder of development, which is linked to a  
XX genetic locus regulated by methylation, such as Huntington's disease,  
XX Down's syndrome, and disorders associated with a Hox gene

XX Sequence 26 BP; 3 A; 1 C; 20 G; 2 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 2; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 2 GGGGTGGGAGCGGAGGGG 20  
|||||

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RESULT 42
AAF28800/c
ID AAF28800 standard; DNA; 27 BP.
XX
AC AAF28800;
XX
DT 09-APR-2001 (first entry)
XX
DE Human GABA(b) receptor 1 promoter Plb primer 2057 PR1b CGVI Fwd.
XX
KW Neuroprotective; nootropic; antidepressant; tranquilizer; anticonvulsant;
KW cardiant; antiasthmatic; antiinflammatory; human; GABA; promoter; CNS;
KW gamma-amino butyric acid B receptor 1; splice isoform; spinal spasticity;
KW transcription modulator; central nervous system disorder; dementia;
KW muscle relaxation; Alzheimer's disease; depression; anxiety; epilepsy;
KW cardiovascular disorder; asthma; irritable bowel syndrome; emesis;
KW reflux disease; neurological disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200068268-A1.
XX
PD 16-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-SE000878.
XX
PR 06-MAY-1999; 99SE-00001659.
XX
PA (ASTR ) ASTRAZENECA AB.
XX
PI Ekstrand J, Edlund A, Johansson T, Leonardsson G;
XX WPI; 2001-024861/03.
XX
PT New nucleic acid molecules constituting the human gamma amino butyric
PT acid-B receptor 1 promoters, useful for screening modulators of the
PT receptors transcription or therapeutic agents regulating the expression
PT of its splice isoforms.
XX
PS Example 6; Page 21; 46pp; English.
XX
CC The invention relates to novel nucleic acid molecules constituting the
CC human gamma-amino butyric acid (GABA)B receptor 1 promoters PlA and/or
CC Plb (AAF28781 and AAF28782), or their functionally equivalent modified
CC forms or active fragments. PCR primers AAF28788-AAF28805 were used for
CC PCR mutagenesis of the GABA(b) promoter sequences for mutational analysis
CC of promoter element function. Nucleic acid molecules containing the human
CC GABAB receptor 1 promoters PlA and/or Plb are useful for screening
CC therapeutic agents that selectively regulate the expression of GABAB
CC receptor 1a- and 1b-type splice isoforms. These compounds, which are
CC modulators of GABAB receptor 1 transcription, are potentially useful in
CC the treatment of disorders that are related to neurally-controlled
CC physiological responses regulated by GABAB receptors such as central
CC nervous system (CNS) disorders, e.g. muscle relaxation in spinal
CC spasticity, Alzheimer's disease and other dementias, psychiatric and
CC neurological disorders, e.g. depression, anxiety or epilepsy,
CC cardiovascular disorders, asthma, gut motility disorders, e.g. irritable
CC bowel syndrome, emesis or reflux disease
XX
SQ Sequence 27 BP; 3 A; 16 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 4; Length 27;
Best Local Similarity 89.5%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 AGGGGAGGGGAGGGAGGG 19
Db 19 AGGTTAGGGGAGGGAGGG 1
RESULT 43
AAF28801
ID AAF28801 standard; DNA; 27 BP.
XX
AC AAF28801;
XX
DT 09-APR-2001 (first entry)
XX
DE Human GABA(b) receptor 1 promoter Plb primer 2058 PR1b CGVI Rev.
XX
KW Neuroprotective; nootropic; antidepressant; tranquilizer; anticonvulsant;
KW cardiant; antiasthmatic; antiinflammatory; human; GABA; promoter; CNS;
KW gamma-amino butyric acid B receptor 1; splice isoform; spinal spasticity;
KW transcription modulator; central nervous system disorder; dementia;
KW muscle relaxation; Alzheimer's disease; depression; anxiety; epilepsy;
KW cardiovascular disorder; asthma; irritable bowel syndrome; emesis;
KW reflux disease; neurological disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200068268-A1.
XX
PD 16-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-SE000878.
XX
PR 06-MAY-1999; 99SE-00001659.
XX
PA (ASTR ) ASTRAZENECA AB.
XX
PI Ekstrand J, Edlund A, Johansson T, Leonardsson G;
XX WPI; 2001-024861/03.
XX
PT New nucleic acid molecules constituting the human gamma amino butyric
PT acid-B receptor 1 promoters, useful for screening modulators of the
PT receptors transcription or therapeutic agents regulating the expression
PT of its splice isoforms.
XX
PS Example 6; Page 21; 46pp; English.
XX
CC The invention relates to novel nucleic acid molecules constituting the
CC human gamma-amino butyric acid (GABA)B receptor 1 promoters PlA and/or
CC Plb (AAF28781 and AAF28782), or their functionally equivalent modified
CC forms or active fragments. PCR primers AAF28788-AAF28805 were used for
CC PCR mutagenesis of the GABA(b) promoter sequences for mutational analysis
CC of promoter element function. Nucleic acid molecules containing the human
CC GABAB receptor 1 promoters PlA and/or Plb are useful for screening
CC therapeutic agents that selectively regulate the expression of GABAB
CC receptor 1a- and 1b-type splice isoforms. These compounds, which are
CC modulators of GABAB receptor 1 transcription, are potentially useful in
CC the treatment of disorders that are related to neurally-controlled
CC physiological responses regulated by GABAB receptors such as central
CC nervous system (CNS) disorders, e.g. muscle relaxation in spinal
CC spasticity, Alzheimer's disease and other dementias, psychiatric and
CC neurological disorders, e.g. depression, anxiety or epilepsy,
CC cardiovascular disorders, asthma, gut motility disorders, e.g. irritable
CC bowel syndrome, emesis or reflux disease
XX
SQ Sequence 27 BP; 6 A; 2 C; 16 G; 3 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 4; Length 27;
Best Local Similarity 89.5%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 AGGGGAGGGGAGGGAGGG 19
Db 9 AGGTTAGGGGAGGGAGGG 27
RESULT 44
AAL28918/c
ID AAL28918 standard; DNA; 50 BP.
XX
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AC AAL28918;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #2126.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Claim 1; Page 1990; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 50 BP; 9 A; 26 C; 3 G; 12 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 4; Length 50;
Best Local Similarity 89.5%; Pred. No. 1.3e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GGGGAGGGGGAGGGAGGGG 20
DB 44 GGGGAGGGGGAGGGGGGGG 26
RESULT 45
AAL32132
ID AAL32132 standard; DNA; 50 BP.
XX
AC AAL32132;
XX
DT 24-JAN-2002 (first entry)
XX

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XX DE Human SNP oligonucleotide #5340.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Claim 1; Page 2224; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 50 BP; 11 A; 12 C; 22 G; 5 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 4; Length 50;
Best Local Similarity 89.5%; Pred. No. 1.3e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGGGAGGGGGAGGGAGGGG 19
DB 7 AGAGGAGGGAGGGAGGGG 25
RESULT 46
AAL32131
ID AAL32131 standard; DNA; 50 BP.
XX
AC AAL32131;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #5339.
XX

```





KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
KW tuberos sclerosi; pot-wine stain; Sturge Weber syndrome;  
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO9950403-A2.  
XX  
PD 07-OCT-1999.  
XX  
XX  
PF 24-MAR-1999; 99WO-US006507.  
XX  
PR 27-MAR-1998; 98US-0079678P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;  
PI WPI; 1999-591315/50.  
XX  
DR Novel ribozymes for modulating the synthesis, expression and/or stability  
PT of an mRNA encoding an angiogenic factors.  
XX  
XX Claim 54; Page 226; 305pp; English.  
XX  
XX The present invention describes enzymatic nucleic acid molecules with RNA  
CC cleaving activity, which specifically cleave RNA encoded by an aryl  
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
CC AAA21596 to AAA21688 represent their corresponding target sequences;  
CC AAA21689 to AAA22475 and AAA223263 to AAA23342 represent ribozyme sequence  
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
CC AAA23422 represent their corresponding target sequences. The ribozymes of  
CC the invention are used for modulating the synthesis, expression and/or  
CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
CC especially used to treat cancer, diabetic retinopathy, age related  
CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
CC angiofibroma of tuberos sclerosi, pot-wine stains, Sturge Weber  
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
CC integrin subunit alpha-6, or integrin subunit beta-3  
XX  
SQ Sequence 17 BP; 0 A; 13 C; 1 G; 0 T; 3 U; 0 Other;  
  
Query Match 77.0%; Score 15.4; DB 2; Length 17;  
Best Local Similarity 94.1%; Pred. NO. 2e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GGGGAGGGGGGGGAGG 18  
|||||  
Db 17 GGGGAGGGGGGGGAGG 1  
  
RESULT 49  
AB244397  
ID AB244397 standard; DNA; 41 BP.  
XX  
AC AB244397;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
XX Human catechol-O-methyltransferase COMT gene polymorphic site, #1181.  
DE  
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;  
KW

KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT variation replace(21,A)  
FT /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism (SNP)"  
XX  
XX WO200252044-A2.  
PN  
XX  
PD 04-JUL-2002.  
XX  
XX 27-DEC-2001; 2001WO-JP011592.  
PF  
XX  
XX 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
XX (RIKE ) RIKEN KK.  
PA  
XX  
XX Nakamura Y, Sekine A, Iida A, Saito S;  
PI WPI; 2002-583571/62.  
XX  
DR Identifying individuals having a polymorphism, useful for determining the  
XX effectiveness or side effect of a drug or treatment protocol, comprises  
XX detecting at least one polymorphism in the drug metabolizing enzyme  
XX nucleic acid.  
XX  
XX Claim 23; Page 83; 2785pp; English.  
XX  
XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from AB243217-AB250887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphism data, particularly that relating to single nucleotide  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy  
XX  
SQ Sequence 41 BP; 7 A; 11 C; 21 G; 2 T; 0 U; 0 Other;  
  
Query Match 77.0%; Score 15.4; DB 6; Length 41;  
Best Local Similarity 94.1%; Pred. No. 1.8e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



CC Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy

XX  
SQ Sequence 41 BP; 7 A; 11 C; 21 G; 2 T; 0 U; 0 Other;

Query Match 77.0%; Score 15.4; DB 6; Length 41;  
Best Local Similarity 94.1%; Pred. No. 1.8e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGAGGGGAGGGAGGGG 20  
||| ||||| ||||| |||||  
Db 10 GGAAGGGAGGGAGGGG 26

Search completed: February 15, 2006, 18:07:23  
Job time : 157.744 secs

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||| ||||| ||||| |||||  
Db 10 GGAAGGGAGGGAGGGG 26

RESULT 50  
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ID ABZ48593 standard; DNA; 41 BP.  
XX  
AC ABZ48593;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human catechol-O-methyltransferase COMT gene polymorphic site, #5376.  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation replace(21,A)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
PN WO200252044-A2.  
XX  
PD 04-JUL-2002.  
XX  
PF 27-DEC-2001; 2001WO-JP011592.  
XX  
PR 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
PA (RIKE ) RIKEN KK.  
XX  
PI Nakamura Y, Sekine A, Iida A, Saito S;  
XX  
WPI; 2002-583571/62.

Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.

Claim 23; Page 169; 2785pp; English.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety.

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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:07:43 ; Search time 1330.25 Seconds  
(without alignments)  
703.434 Million cell updates/sec

Title: US-09-669-187A-906  
Perfect score: 20  
Sequence: 1 agggaggaggaggaggagg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues  
Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database :

- EST:\*
- 1: gb\_est1:\*
  - 2: gb\_est2:\*
  - 3: gb\_est3:\*
  - 4: gb\_hic:\*
  - 5: gb\_est4:\*
  - 6: gb\_est5:\*
  - 7: gb\_est6:\*
  - 8: gb\_est7:\*
  - 9: gb\_gss1:\*
  - 10: gb\_gss2:\*
  - 11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 16       | 16.8  | 84.0        | 38     | 9  | AZ424085    |
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| C 18       | 16.8  | 84.0        | 43     | 9  | AZ877472    |
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| AZ331988 | 1M0060B11 |
| AZ447246 | 1M0244E23 |
| AZ607348 | 1M0429D18 |
| AZ645874 | 1M0511C07 |
| AZ488138 | 1M0318E13 |
| AZ581259 | 1M0369N11 |
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| AZ404465 | 1M0172P09 |
| AZ607348 | 1M0503D04 |
| AZ789161 | 2M0036A15 |
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| AZ468549 | 1M0281D10 |
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| AL453376 | T. brucei |
| BX626114 | BX626114  |
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| AZ810458 | 2M0076C02 |
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| AZ604434 | 1M0425I18 |
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| AZ27022  | 1M0050I12 |
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| AZ640161 | 1M0501G23 |
| AZ806290 | 2M0068C13 |
| AZ872959 | 2M0186F03 |
| AZ423751 | 1M0203B22 |
| AZ662726 | 1M0542C01 |
| AZ468615 | 1M0281D22 |
| AZ650045 | 1M0520S05 |
| AZ783172 | 2M0024F08 |
| AZ853274 | 2M0156D23 |
| CZ918653 | 4021010C1 |
| AZ325963 | 1M0048M24 |
| AZ798034 | 2M0054C10 |
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| AZ375613 | 1M0129N05 |
| AZ825930 | 2M0101E23 |
| CZ915624 | 4013012D0 |
| A1721161 | as73h12.x |
| AZ321115 | 1M0041H02 |
| AZ389253 | 1M0149K07 |
| AZ588848 | 1M0397M24 |
| AZ636745 | 1M0495F14 |
| AZ831930 | 2M0110I21 |
| AZ858898 | 2M0164H14 |
| AZ627849 | 1M0474I13 |
| AZ629871 | 1M0483B08 |
| AZ643259 | 1M0506G06 |
| AZ777125 | 2M0011O18 |
| AA903696 | ok54h06.s |
| AZ666510 | 1M0548M11 |
| CZ919256 | 4021012D1 |
| AL940792 | Arabidops |
| BX002745 | Arabidops |
| AZ829800 | 2M0107I09 |
| AZ949765 | 2M0213D06 |
| AZ643646 | 1M0507A17 |
| AL764506 | Arabidops |
| CG729057 | 1119107A1 |
| AL985306 | Danio rer |
| DR025738 | Osmo00605 |
| AZ423755 | 1M0203C23 |

|       |      |      |    |    |           |                     |       |      |      |    |    |           |                     |
|-------|------|------|----|----|-----------|---------------------|-------|------|------|----|----|-----------|---------------------|
| C 96  | 15.8 | 79.0 | 41 | 9  | AZ871797  | AZ871797 2M0184C24  | 169   | 15.2 | 76.0 | 47 | 10 | CZ910062  | CZ910062 4012001B0  |
| C 97  | 15.8 | 79.0 | 41 | 10 | CW956912  | CW956912 TcB51.4_C  | C 170 | 15.2 | 76.0 | 48 | 9  | AZ652813  | AZ652813 1M0526M08  |
| C 98  | 15.8 | 79.0 | 41 | 10 | EX001342  | EX001342 Arabidops  | 171   | 15.2 | 76.0 | 48 | 10 | CZ258850  | CZ258850 AH0165_Sa  |
| C 99  | 15.8 | 79.0 | 42 | 9  | AZ499950  | AZ499950 1M0338101  | C 172 | 15.2 | 76.0 | 49 | 3  | B1762841  | B1762841 603048373  |
| C 100 | 15.8 | 79.0 | 42 | 9  | AZ764537  | AZ764537 1M0560M21  | C 173 | 15.2 | 76.0 | 50 | 1  | AU256770  | AU256770 AU256770   |
| C 101 | 15.8 | 79.0 | 42 | 9  | AZ801055  | AZ801055 2M0059C22  | 174   | 15.2 | 76.0 | 50 | 11 | CR041958  | CR041958 Forward S  |
| C 102 | 15.8 | 79.0 | 43 | 1  | A1811876  | A1811876 tw45G01.x  | 175   | 15.2 | 76.0 | 50 | 11 | CR166872  | CR166872 Forward S  |
| C 103 | 15.8 | 79.0 | 43 | 9  | AZ345493  | AZ345493 1M0080E05  | C 176 | 14.8 | 74.0 | 19 | 9  | AZ760597  | AZ760597 1M0554N21  |
| C 104 | 15.8 | 79.0 | 43 | 9  | AZ484846  | AZ484846 1M0318F17  | C 177 | 14.8 | 74.0 | 20 | 9  | AZ969440  | AZ969440 2M0242012  |
| C 105 | 15.8 | 79.0 | 43 | 9  | AZ864816  | AZ864816 2M0174A11  | C 178 | 14.8 | 74.0 | 21 | 9  | AZ476392  | AZ476392 1M0295F12  |
| C 106 | 15.8 | 79.0 | 44 | 1  | AM046897  | AM046897 AM046897   | C 179 | 14.8 | 74.0 | 22 | 1  | AL158208  | AL158208 ar96B07.x  |
| C 107 | 15.8 | 79.0 | 44 | 1  | AZ860493  | AZ860493 2M0166F02  | 180   | 14.8 | 74.0 | 22 | 5  | BQ585098  | BQ585098 E011826-0  |
| C 108 | 15.8 | 79.0 | 45 | 9  | AZ366532  | AZ366532 1M0115L18  | C 181 | 14.8 | 74.0 | 22 | 9  | AQ5811419 | AQ5811419 1M0437D15 |
| C 109 | 15.8 | 79.0 | 45 | 9  | AZ442112  | AZ442112 1M0234K08  | C 182 | 14.8 | 74.0 | 22 | 9  | AZ871408  | AZ871408 2M0184E16  |
| C 110 | 15.8 | 79.0 | 45 | 9  | AZ473613  | AZ473613 1M0289O03  | C 183 | 14.8 | 74.0 | 23 | 9  | AZ618720  | AZ618720 1M0450O19  |
| C 111 | 15.8 | 79.0 | 45 | 9  | AZ776609  | AZ776609 2M0010J20  | C 184 | 14.8 | 74.0 | 25 | 1  | AI363940  | AI363940 qw4b12.x   |
| C 112 | 15.8 | 79.0 | 45 | 10 | AL753618  | AL753618 Arabidops  | C 185 | 14.8 | 74.0 | 26 | 11 | TA185B02Q | TA185B02Q           |
| C 113 | 15.8 | 79.0 | 45 | 10 | AL763837  | AL763837 Arabidops  | C 186 | 14.8 | 74.0 | 26 | 9  | AZ816353  | AZ816353 2M0085K06  |
| C 114 | 15.8 | 79.0 | 46 | 9  | AZ325773  | AZ325773 1M0048J12  | C 187 | 14.8 | 74.0 | 30 | 5  | BX624507  | BX624507 BX624507   |
| C 115 | 15.8 | 79.0 | 46 | 10 | CZ906361  | CZ906361 BCB236_Ba  | C 188 | 14.8 | 74.0 | 30 | 9  | AZ875577  | AZ875577 2M0190G06  |
| C 116 | 15.8 | 79.0 | 47 | 9  | AZ769421  | AZ769421 1M0570O01  | C 189 | 14.8 | 74.0 | 33 | 11 | TA95A01P  | TA95A01P            |
| C 117 | 15.8 | 79.0 | 48 | 5  | BQ591368  | BQ591368 E012714-0  | C 190 | 14.8 | 74.0 | 34 | 1  | AI224571  | AI224571 qw36A07.x  |
| C 118 | 15.8 | 79.0 | 48 | 5  | AZ650456  | AZ650456 1M0520G09  | 191   | 14.8 | 74.0 | 34 | 9  | AZ432435  | AZ432435 1M0217B21  |
| C 119 | 15.8 | 79.0 | 48 | 9  | AZ860712  | AZ860712 2M0166P18  | C 192 | 14.8 | 74.0 | 34 | 10 | AL759611  | AL759611 Arabidops  |
| C 120 | 15.8 | 79.0 | 49 | 1  | A1189618  | A1189618 qd32h02.x  | C 193 | 14.8 | 74.0 | 34 | 11 | TA128E02Q | TA128E02Q           |
| C 121 | 15.8 | 79.0 | 49 | 5  | CX033453  | CX033453 pw54h05.y  | 194   | 14.8 | 74.0 | 39 | 11 | DR41D12S  | DR41D12S Danio rer  |
| C 122 | 15.8 | 79.0 | 50 | 9  | AZ506149  | AZ506149 1M0347U05  | 195   | 14.8 | 74.0 | 39 | 11 | TA200E07Q | TA200E07Q           |
| C 123 | 15.8 | 79.0 | 50 | 9  | AZ456166  | AZ456166 1M0258B20  | 196   | 14.8 | 74.0 | 48 | 10 | AL752522  | AL752522 Arabidops  |
| C 124 | 15.8 | 79.0 | 50 | 9  | AZ776242  | AZ776242 2M0009P12  | 197   | 14.8 | 74.0 | 50 | 11 | CR025955  | CR025955 Reverse S  |
| C 125 | 15.8 | 79.0 | 50 | 9  | AZ787456  | AZ787456 2M0033O06  | 198   | 14.8 | 74.0 | 50 | 11 | CR042155  | CR042155 Reverse S  |
| C 126 | 15.8 | 79.0 | 50 | 10 | BX987794  | BX987794 Reverse S  | 199   | 14.4 | 72.0 | 36 | 10 | AL763948  | AL763948 Arabidops  |
| C 127 | 15.8 | 79.0 | 50 | 11 | CR117295  | CR117295 Reverse S  | 200   | 14.4 | 72.0 | 47 | 10 | AG220079  | AG220079 Lotus cor  |
| C 128 | 15.8 | 79.0 | 50 | 11 | CR138789  | CR138789 Forward S  | C 201 | 14.4 | 72.0 | 49 | 11 | TA33D12P  | TA33D12P            |
| C 129 | 15.8 | 79.0 | 50 | 11 | CR165643  | CR165643 Reverse S  | C 202 | 14.2 | 71.0 | 19 | 1  | AJ659543  | AJ659543            |
| C 130 | 15.4 | 77.0 | 49 | 1  | A1687811  | A1687811 tp39a10.x  | C 203 | 14.2 | 71.0 | 19 | 1  | AJ747090  | AJ747090 AJ747090   |
| C 131 | 15.2 | 76.0 | 22 | 9  | AZ6556873 | AZ6556873 1M0532M09 | 204   | 14.2 | 71.0 | 19 | 6  | CF280692  | CF280692 14ETL--07  |
| C 132 | 15.2 | 76.0 | 23 | 9  | AZ305188  | AZ305188 1M0005C17  | 205   | 14.2 | 71.0 | 19 | 6  | CF282249  | CF282249 14ETL--09  |
| C 133 | 15.2 | 76.0 | 23 | 9  | AZ968672  | AZ968672 2M0241B09  | C 206 | 14.2 | 71.0 | 19 | 6  | CF295184  | CF295184 30DGS--05  |
| C 134 | 15.2 | 76.0 | 24 | 9  | AZ642567  | AZ642567 1M0505H12  | C 207 | 14.2 | 71.0 | 19 | 6  | CF312583  | CF312583 ABF--08-G  |
| C 135 | 15.2 | 76.0 | 26 | 10 | CZ906862  | CZ906862 4011003E0  | C 208 | 14.2 | 71.0 | 19 | 6  | CF323353  | CF323353 HDN--03-K  |
| C 136 | 15.2 | 76.0 | 27 | 1  | AM047386  | AM047386 AM047386   | C 209 | 14.2 | 71.0 | 19 | 8  | CX007735  | CX007735 HDN--07-   |
| C 137 | 15.2 | 76.0 | 27 | 9  | AZ776617  | AZ776617 2M0010D23  | C 210 | 14.2 | 71.0 | 19 | 8  | CX007735  | CX007735 1030B01.9  |
| C 138 | 15.2 | 76.0 | 27 | 11 | TA289G07Q | TA289G07Q           | C 211 | 14.2 | 71.0 | 19 | 8  | DN953961  | DN953961 1t66h11.g  |
| C 139 | 15.2 | 76.0 | 29 | 6  | CF295257  | CF295257 30DGS--05  | C 212 | 14.2 | 71.0 | 19 | 8  | DR062674  | DR062674 iq20d11.g  |
| C 140 | 15.2 | 76.0 | 29 | 9  | AZ642459  | AZ642459 1M0505P06  | 213   | 14.2 | 71.0 | 19 | 8  | DR072910  | DR072910 ik79a02.g  |
| C 141 | 15.2 | 76.0 | 31 | 9  | AZ648445  | AZ648445 1M0517A02  | 214   | 14.2 | 71.0 | 19 | 8  | DR074124  | DR074124 ik98d12.g  |
| C 142 | 15.2 | 76.0 | 31 | 9  | AZ761993  | AZ761993 1M0556D11  | 215   | 14.2 | 71.0 | 19 | 9  | AZ314181  | AZ314181 1M0030822  |
| C 143 | 15.2 | 76.0 | 32 | 9  | AZ758290  | AZ758290 1M0550A16  | C 216 | 14.2 | 71.0 | 19 | 9  | AZ328696  | AZ328696 1M0052006  |
| C 144 | 15.2 | 76.0 | 32 | 10 | CZ910279  | CZ910279 4012001H1  | C 217 | 14.2 | 71.0 | 19 | 9  | AZ328727  | AZ328727 1M0052F10  |
| C 145 | 15.2 | 76.0 | 32 | 10 | CZ918374  | CZ918374 4021009B0  | 218   | 14.2 | 71.0 | 19 | 9  | AZ330766  | AZ330766 1M0056N07  |
| C 146 | 15.2 | 76.0 | 34 | 1  | A1521590  | A1521590 t065b11.x  | 219   | 14.2 | 71.0 | 19 | 9  | AZ338927  | AZ338927 1M0070N07  |
| C 147 | 15.2 | 76.0 | 34 | 1  | AM047178  | AM047178 AM047178   | 220   | 14.2 | 71.0 | 19 | 9  | AZ342171  | AZ342171 1M0075P01  |
| C 148 | 15.2 | 76.0 | 34 | 9  | AZ776846  | AZ776846 2M0010A20  | 221   | 14.2 | 71.0 | 19 | 9  | AZ345792  | AZ345792 1M0080G12  |
| C 149 | 15.2 | 76.0 | 34 | 11 | TA367E10Q | TA367E10Q           | 222   | 14.2 | 71.0 | 19 | 9  | AZ390115  | AZ390115 1M0151L15  |
| C 150 | 15.2 | 76.0 | 35 | 9  | AZ807171  | AZ807171 2M0069H18  | 223   | 14.2 | 71.0 | 19 | 9  | AZ412494  | AZ412494 1M0186A06  |
| C 151 | 15.2 | 76.0 | 35 | 10 | CZ916366  | CZ916366 4021001B0  | 224   | 14.2 | 71.0 | 19 | 9  | AZ423757  | AZ423757 1M0203D19  |
| C 152 | 15.2 | 76.0 | 36 | 9  | AZ462645  | AZ462645 1M0269M12  | C 225 | 14.2 | 71.0 | 19 | 9  | AZ439205  | AZ439205 1M0229B15  |
| C 153 | 15.2 | 76.0 | 36 | 10 | CZ906811  | CZ906811 4011003B0  | C 226 | 14.2 | 71.0 | 19 | 9  | AZ447234  | AZ447234 1M0224L16  |
| C 154 | 15.2 | 76.0 | 36 | 10 | CZ917576  | CZ917576 4021006B1  | C 227 | 14.2 | 71.0 | 19 | 9  | AZ447245  | AZ447245 1M0244A22  |
| C 155 | 15.2 | 76.0 | 37 | 1  | A1433088  | A1433088 th41c06.x  | C 228 | 14.2 | 71.0 | 19 | 9  | AZ466785  | AZ466785 1M0277A16  |
| C 156 | 15.2 | 76.0 | 37 | 9  | AZ784558  | AZ784558 2M0027G15  | C 229 | 14.2 | 71.0 | 19 | 9  | AZ468226  | AZ468226 1M0288D10  |
| C 157 | 15.2 | 76.0 | 38 | 2  | B788802   | B788802 601475711   | C 230 | 14.2 | 71.0 | 19 | 9  | AZ481469  | AZ481469 1M0303B15  |
| C 158 | 15.2 | 76.0 | 38 | 6  | CF291715  | CF291715 14ROOT--0  | C 231 | 14.2 | 71.0 | 19 | 9  | AZ499200  | AZ499200 1M0336O22  |
| C 159 | 15.2 | 76.0 | 38 | 9  | AZ314682  | AZ314682 1M0031B07  | 232   | 14.2 | 71.0 | 19 | 9  | AZ587841  | AZ587841 1M0395J14  |
| C 160 | 15.2 | 76.0 | 39 | 2  | B878080   | B878080 601487463   | 233   | 14.2 | 71.0 | 19 | 9  | AZ611179  | AZ611179 1M0436B01  |
| C 161 | 15.2 | 76.0 | 39 | 9  | AZ949370  | AZ949370 2M0212O18  | C 234 | 14.2 | 71.0 | 19 | 9  | AZ611509  | AZ611509 1M0437B21  |
| C 162 | 15.2 | 76.0 | 39 | 10 | AL947253  | AL947253 Arabidops  | C 235 | 14.2 | 71.0 | 19 | 9  | AZ615843  | AZ615843 1M0445E23  |
| C 163 | 15.2 | 76.0 | 39 | 10 | CG724099  | CG724099 1119079F0  | C 236 | 14.2 | 71.0 | 19 | 9  | AZ618258  | AZ618258 1M0449G23  |
| C 164 | 15.2 | 76.0 | 40 | 1  | A1205954  | A1205954 gg26f01.x  | C 237 | 14.2 | 71.0 | 19 | 9  | AZ625211  | AZ625211 1M0464P22  |
| C 165 | 15.2 | 76.0 | 40 | 10 | BX185628  | BX185628 Danio rer  | C 238 | 14.2 | 71.0 | 19 | 9  | AZ625605  | AZ625605 1M0465D17  |
| C 166 | 15.2 | 76.0 | 41 | 1  | AJ806745  | AJ806745 AJ806745   | C 239 | 14.2 | 71.0 | 19 | 9  | AZ634205  | AZ634205 1M0489D19  |
| C 167 | 15.2 | 76.0 | 41 | 8  | CW998414  | CW998414 iv49a12.b  | C 240 | 14.2 | 71.0 | 19 | 9  | AZ648703  | AZ648703 1M0517A20  |
| C 168 | 15.2 | 76.0 | 43 | 10 | BX001839  | BX001839 Arabidops  | C 241 | 14.2 | 71.0 | 19 | 9  | AZ649856  | AZ649856 1M0519O07  |

|       |      |      |    |    |            |
|-------|------|------|----|----|------------|
| C 242 | 14.2 | 71.0 | 19 | 9  | A2654733   |
| C 243 | 14.2 | 71.0 | 19 | 9  | A2654842   |
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| C 245 | 14.2 | 71.0 | 19 | 9  | A2657564   |
| C 246 | 14.2 | 71.0 | 19 | 9  | A2764500   |
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| C 250 | 14.2 | 71.0 | 19 | 9  | A2795057   |
| C 251 | 14.2 | 71.0 | 19 | 9  | A2799834   |
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| C 261 | 14.2 | 71.0 | 19 | 10 | CL657666   |
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| C 263 | 14.2 | 71.0 | 20 | 6  | CF279207   |
| C 264 | 14.2 | 71.0 | 20 | 6  | CF309954   |
| C 265 | 14.2 | 71.0 | 20 | 6  | CF311285   |
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| C 273 | 14.2 | 71.0 | 20 | 9  | A2342269   |
| C 274 | 14.2 | 71.0 | 20 | 9  | A2358156   |
| C 275 | 14.2 | 71.0 | 20 | 9  | A2360709   |
| C 276 | 14.2 | 71.0 | 20 | 9  | A2436223   |
| C 277 | 14.2 | 71.0 | 20 | 9  | A2437804   |
| C 278 | 14.2 | 71.0 | 20 | 9  | A2441557   |
| C 279 | 14.2 | 71.0 | 20 | 9  | A2445158   |
| C 280 | 14.2 | 71.0 | 20 | 9  | A2447205   |
| C 281 | 14.2 | 71.0 | 20 | 9  | A2448206   |
| C 282 | 14.2 | 71.0 | 20 | 9  | A2464607   |
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| C 284 | 14.2 | 71.0 | 20 | 9  | A2466043   |
| C 285 | 14.2 | 71.0 | 20 | 9  | A2470070   |
| C 286 | 14.2 | 71.0 | 20 | 9  | A2473415   |
| C 287 | 14.2 | 71.0 | 20 | 9  | A2486866   |
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ALIGNMENTS

RESULT 1  
AZ867169  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

AZ867169  
2M0177120R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0177120 R, genomic survey sequence.

AZ867169.1 GI:13069207  
Mus musculus (house mouse)

ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0177 row: I column: 20  
Seq primer: CACACAGGAACACGTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC2M0177120"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gil4732114[gb|AF129072.1]), a copy-number  
inducible derivative of plasmid R1, a copy-number  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGGGAGGGAGGGAGGGG 20  
DB 1 AGGGAGGGAGGGAGGGG 20

RESULT 2  
AZ359724  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

AZ359724  
1M0102M11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0102M11 R, genomic survey sequence.

AZ359724  
GI:10473424  
GSS.

**SOURCE**  
**ORGANISM** Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
**REFERENCE**  
**AUTHORS** 1 (bases 1 to 35)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0102 row: M column: 11  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 35.  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0102M11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

**ORIGIN**  
 Query Match 100.0%; Score 20; DB 9; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 AGGGGAGGGGAGGGGAGGGG 20  
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 Db 4 AGGGGAGGGGAGGGGAGGGG 23  
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 RESULT 3  
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 LOCUS  
 DEFINITION 2M0225G02R Mouse 10kb plasmid UUC2M library Mus musculus genomic  
 clone UUC2M0225G02 R, genomic survey sequence.  
 ACCESSION AZ958287  
 VERSION AZ958287.1 GI:13829514

**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 22)  
**AUTHORS** Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0225 row: G column: 02  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 22.  
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 /sex="Female"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

**ORIGIN**  
 Query Match 92.0%; Score 18.4; DB 9; Length 22;  
 Best Local Similarity 95.0%; Pred. No. 2.1e+04;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 AGGGGAGGGGAGGGGAGGGG 20  
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 Db 3 AGGGGAGGGGAGGGGAGGGG 22  
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 RESULT 4  
 AZ462959/c  
 LOCUS  
 DEFINITION 1M0271G04R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0271G04 R, genomic survey sequence.  
 ACCESSION AZ462959

**VERSION**  
**KEYWORDS**  
**SOURCE**  
**ORGANISM**  
**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**  
**COMMENT**  
**FEATURES**  
**source**  
**ORIGIN**  
**RESULT 5**  
**LOCUS**  
**DEFINITION**

A2462959.1 GI:10621084  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 26)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Stokes, R., Tingle, A., von  
 Niederhausern, A. and Wright, D. Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0271 row: G column: 04  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 26.  
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 /mol\_type="genomic DNA"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, P-"  
 /clone\_lib="Mouse 10kb plasmid UUGCim library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 87.0%; Score 17.4; DB 9; Length 26;  
 Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGAGGGGAGGGGAGGG 20  
 Db 25 GCGGAGGGGAGGGGAGGG 7

CL661180  
 LOCUS  
 DEFINITION

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0244 row: G column: 20  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 32.  
 Location/Qualifiers

## FEATURES

source

1..32  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0244G20"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 32;  
 Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
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 Db 7 GGGGAGGGGAGGGAGGGG 25

RESULT 7  
 AZ802326/c  
 LOCUS  
 DEFINITION 2M0061L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0061L09 F, genomic survey sequence.  
 ACCSSION AZ802326  
 VERSION GSS.  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 33)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0061 row: L column: 09  
 Seq primer: CGTTGTAATAACGACGCCAGCT  
 Class: plasmid ends  
 High quality sequence stop: 33.  
 Location/Qualifiers

## FEATURES

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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0061L09"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 33;  
 Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
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 Db 20 GGAGAGGGGAGGGAGGGG 2

RESULT 8  
 BX004665  
 LOCUS  
 DEFINITION BX004665 38 bp DNA linear GSS 01-APR-2004 Arabidopsis thaliana T-DNA flanking sequence GK-400A12-017894, genomic survey sequence.  
 ACCSSION BX004665  
 VERSION GSS.  
 KEYWORDS  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1  
 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weissshaar, B.  
 GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 Bioinformatics 19 (11), 1441-1442 (2003)  
 12874060  
 2  
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissshaar, B.  
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 JOURNAL  
 PUBMED  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 PUBMED  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL



PUBMED 14756321  
 REFERENCE 3  
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehovep, P., Dekker, K.A. and Weishaar, B.  
 TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)  
 PUBMED 14682050  
 REFERENCE 4  
 AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 COMMENT This sequence has been recovered from the left border of the T-DNA. Details on the protocols used for generation of the sequence are described in References 1-3. Re-examination of the source from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

#### FEATURES

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 Location/Qualifiers

1..38  
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 /db\_xref="taxon:3702"  
 /clone="CGK-400A12-017894"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

#### ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 38;  
 Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GGGGAGGGGAGGGAGGGG 20  
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 Db 1 GGGGAGGGGAGGGAGGGG 19

RESULT 9  
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 LOCUS A2820833 43 bp DNA linear GSS 20-FEB-2001  
 DEFINITION clone UUGC2M00931b6 F, genomic survey sequence.  
 ACCESSION A2820833  
 VERSION A2820833.1 GI:12990741  
 GSS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 43)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0093 row: L column: 16  
 Seq primer: CGTTGTAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 43.

#### FEATURES

source  
 Location/Qualifiers

1..43  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
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 /clone="UUGC2M0093L16"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnates/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 43;  
 Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GGGGAGGGGAGGGAGGGG 20  
 |||||  
 Db 38 GGGGAGGGGAGGGAGGGG 20

RESULT 10  
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 LOCUS A2375586 45 bp DNA linear GSS 02-OCT-2000  
 DEFINITION 1M0129G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0129G03 F, genomic survey sequence.  
 ACCESSION A2375586  
 VERSION A2375586.1 GI:10489286  
 GSS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 45)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0129 row: G column: 03  
Seq primer: CGTGTAAACGAGCGGCAGT  
Class: plasmid ends  
High quality sequence stop: 45.  
Location/Qualifiers

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 45;  
Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
|||||  
Db 39 GGGGAGGGGAGGGAGGGG 21

RESULT 11  
AJ793526/c

LOCUS  
DEFINITION  
AJ793526 Antirrhinum majus whole plant Antirrhinum majus cDNA clone  
018.3.02.k18, mRNA sequence.  
AJ793526  
AJ793526.1 GI:51108854

KEYWORDS  
SOURCE

ORGANISM  
Antirrhinum majus (snapdragon)  
Antirrhinum majus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Lamiales; Plantaginaceae; Antirrhineae;  
Antirrhinum.  
1 (bases 1 to 47)  
Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H.,  
Siedler, H., and Zachgo, S.  
Characterization of Antirrhinum Petal Development and  
Identification of Target Genes of the Class B MADS Box Gene  
DEFICIENS  
Plant Cell 16 (12), 3197-3215 (2004)  
15539471

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED

COMMENT

Contact: Schwarz-Sommer Z  
Molekulare Pflanzen-genetik  
MPI fuer Zuechtungsforschung  
Carl-von-Linne Weg 10, D-50829, Germany.

FEATURES  
source

1. .47  
Location/Qualifiers  
/organism="Antirrhinum majus"  
/mol\_type="mRNA"  
/db\_xref="taxon:4151"  
/clone="018.3.02.k18"  
/tissue\_type="whole plant"  
/clone\_lib="Antirrhinum majus whole plant"

ORIGIN

Query Match 87.0%; Score 17.4; DB 1; Length 47;  
Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
|||||  
Db 29 GGGGAGGGGAGGGAGGGG 11

RESULT 12  
AZ800436

LOCUS  
DEFINITION  
AZ800436 Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0058L20 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 50)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0058 row: L column: 20  
Seq primer: CGTGTAAACGAGCGGCAGT  
Class: plasmid ends  
High quality sequence stop: 50.  
Location/Qualifiers

FEATURES  
source

1. .50  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC2M0058L20"  
/sex="Male"  
/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 50;  
 Best Local Similarity 94.7%; Pred. No. 4.2e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGG 19  
 |||||  
 Db 32 AGAGGAGGGGAGGGAGGG 50

RESULT 13  
 AZ780325/c  
 LOCUS  
 DEFINITION 25 bp DNA linear GSS 16-FEB-2001  
 clone UUGC2M0017N06 R, genomic survey sequence.

ACCESSION AZ780325  
 VERSION AZ780325.1 GI:12911872  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 25)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)

CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0017 row: N column: 06

Seq primer: CACACAGGAAACAGCTATGACC  
 Class: Plasmid ends

High quality sequence stop: 25.  
 Location/Qualifiers

## FEATURES

1..25  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0017N06"  
 /sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 25;  
 Best Local Similarity 90.0%; Pred. No. 6.8e+04;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGGG 20  
 |||||  
 Db 23 AGGGGAGGGGAGGGAGGGG 4

RESULT 14  
 AL935924/c  
 LOCUS  
 DEFINITION 30 bp DNA linear GSS 31-MAR-2004  
 Arabidopsis thaliana T-DNA flanking sequence GK-009H02-016930, genomic survey sequence.

ACCESSION AL935924  
 VERSION AL935924.1 GI:24367549  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1  
 Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.  
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 Bioinformatics 19 (11), 1441-1442 (2003)

2  
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 14756321

3  
 Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weisshaar, B.

High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 BioTechniques 35 (6), 1164-1168 (2003)

4 (bases 1 to 30)  
 Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.

Direct Submission  
 Submitted (31-MAR-2004) Weisshaar, B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA. Details on the protocols used for generation of the sequence are described in References 1-3. Re-examination of the source from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

```

http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
  source
    Location/Qualifiers
      1..30
        /organism="Arabidopsis thaliana"
        /mol_type="genomic DNA"
        /db_xref="taxon:3702"
        /clone="GK-009H02-016930"
        /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
        /ecotype="Col-0"
        /note="PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector pAC106 (GenBank accession number: AJ537513). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."
ORIGIN
  Query Match      84.0%; Score 16.8; DB 10; Length 30;
  Best Local Similarity 90.0%; Pred. No. 6.8e+04;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 23 AGGGGGGGGGGGGGGGGG 4

RESULT 15
AZ652279/c
LOCUS
DEFINITION
  1M0525K06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0525K06 R, genomic survey sequence.
ACCESSION
  AZ652279
VERSION
  AZ652279.1 GI:11788802
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 33)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0525 row: K column: 06
  Seq primer: CACACGAGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 33.
  Location/Qualifiers
    1..33
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0525K06"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

FEATURES
  source
    Location/Qualifiers
      1..38
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0203B05"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pW42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
  Query Match      84.0%; Score 16.8; DB 9; Length 33;
  Best Local Similarity 90.0%; Pred. No. 6.7e+04;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 31 AGGGAGAGGAGGGAGGGAG 12

RESULT 16
AZ424085/c
LOCUS
DEFINITION
  1M0203B05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0203B05 R, genomic survey sequence.
ACCESSION
  AZ424085
VERSION
  AZ424085.1 GI:10548098
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 38)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0203 row: B column: 05
  Seq primer: CACACGAGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 38.
  Location/Qualifiers
    1..38
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0203B05"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.

```



/clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 43;  
 Best Local Similarity 90.0%; Pred. No. 6.7e+04;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20

Db 41 AGGGAGGGGAGAGGAGG 22

## RESULT 19

AI800153

LOCUS

DEFINITION

tr23a06.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2219122 3', similar to SW:PRPB\_HUMAN P02814 PROLINE-RICH PEPTIDE P-B.; contains element MSR1 repetitive element ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 37)

NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..37

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2219122"

/tissue\_type="tumor, 5 pooled (see description)"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Ov23"

## FEATURES

source

Query Match 82.0%; Score 16.4; DB 1; Length 46;  
 Best Local Similarity 94.4%; Pred. No. 9e+04;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGAGGGGAGGGAGGGG 20

Db 16 GGGAGGGGAGGGAGGGG 33

/note="Organ: ovary; Vector: pcwv-sport6; Site.1: SalI;  
 Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.35 kb. tumor types include: mixed  
 Mullerian tumor, papillary serous, clear cell, spindle  
 cell. All are primary tumors, metastasis positive. Life  
 Technologies catalog #: 11534-013"

## ORIGIN

Query Match 82.0%; Score 16.4; DB 1; Length 37;  
 Best Local Similarity 94.4%; Pred. No. 9e+04;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGAGGGGAGGGAGGGG 20

Db 17 GGGAGGGGAGGGAGGGG 34

## RESULT 20

AI597960

LOCUS

DEFINITION

t804f05.x1 NCI\_CGAP\_Pan1 Homo sapiens cDNA clone IMAGE:2227617 3', similar to SW:PRPB\_HUMAN P02814 PROLINE-RICH PEPTIDE P-B.; contains TARI.t2 MSR1 repetitive element ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 46)

NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 3675 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

FEATURES

source

1..46

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2227617"

/tissue\_type="adenocarcinoma"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Pan1"

/note="Organ: pancreas; Vector: pcwv-sport6; Site.1: SalI;  
 Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.72 kb. Life Technologies catalog #:  
 11548-013"



```
Db
19 GGGAGGGGGGGGGGGGGG

RESULT 23
AZ645269/c
LOCUS
DEFINITION
  1M0510B10R Mouse 10kb plasmid UGCLM library Mus musculus genomic
  clone UGCLM0510B10 R, genomic survey sequence.
ACCESSION
AZ645269
VERSION
AZ645269.1 GI:11774602
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0510B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0510B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 79.0%; Score 15.8; DB 9; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GGGAGGGGGGGGGGGGGG

Db
19 GGGAGGGGGGGGGGGGGG

RESULT 24
AZ772707/c
LOCUS
DEFINITION
  1M0583L18R Mouse 10kb plasmid UGCLM library Mus musculus genomic
  clone UGCLM0583L18 R, genomic survey sequence.
ACCESSION
AZ772707
VERSION
AZ772707.1 GI:12896303
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0583 row: L column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0583L18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 79.0%; Score 15.8; DB 9; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GGGAGGGGGGGGGGGGGG
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Db      20 GGGGGGGGGAGGGGGGGG 2
||||| ||||| ||||| ||||| |||||
RESULT 25
AZ583408      21 bp      DNA      linear      GSS 13-DEC-2000
LOCUS      1M0378N23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0378N23 F, genomic survey sequence.
ACCESSION      AZ583408
VERSION      AZ583408.1 GI:11703261
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: N column: 23
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0378N23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES      source
1..21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0378N23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
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(http://www.jax.org/resources/documents/dnares/). The DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      79.0%; Score 15.8; DB 9; Length 21;
Best Local Similarity      89.5%; Pred. No. 1.4e+05;
Matches      17; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Db      20 GGGGGGGGGAGGGGGGGG 2
||||| ||||| ||||| ||||| |||||
RESULT 26
AZ653464      21 bp      DNA      linear      GSS 14-DEC-2000
LOCUS      1M0527G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0527G11 F, genomic survey sequence.
ACCESSION      AZ653464
VERSION      AZ653464.1 GI:11790610
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0527 row: G column: 11
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0527G11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      79.0%; Score 15.8; DB 9; Length 21;
Best Local Similarity      89.5%; Pred. No. 1.4e+05;
Matches      17; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

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Best Local Similarity 89.5%; Pred. No. 1.4e+05;          0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2; Indels 0;

QY 2 GGGGAGGGGAGGGAGGGG 20
    |||||
DB 1 GGGGGGGGGAGGGGGGGG 19

RESULT 29
AZ447246/c
LOCUS AZ447246
DEFINITION 22 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0244E23 F, genomic survey sequence.
ACCESSION AZ447246
VERSION AZ447246.1 GI:10599040
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: E column: 23
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244E23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0429D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
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inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

```

```

Query Match 79.0%; Score 15.8; DB 9; Length 22;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20
    |||||
DB 21 GGGGGGGGGGGAGGGGGG 3

RESULT 30
AZ607348/c
LOCUS AZ607348
DEFINITION 22 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0429D18 R, genomic survey sequence.
ACCESSION AZ607348
VERSION AZ607348.1 GI:11729538
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: D column: 18
Seq primer: CACACAGGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0429D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0429D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

```

```

Query Match      79.0%; Score 15.8; DB 9; Length 22;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGAGGGG 20
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Db  22 GGGGGGGGGAGGGGGGGG 4

RESULT 31
AZ645874/c      22 bp      DNA      linear      GSS 14-DEC-2000
LOCUS
DEFINITION      IM0511C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0511C07 R, genomic survey sequence.
ACCESSION      AZ645874
VERSION        AZ645874.1 GI:11775791
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarctontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511C07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
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electrophoresis. Vector DNA was prepared from a derivative
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purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

## ORIGIN

```

Query Match      79.0%; Score 15.8; DB 9; Length 22;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGAGGGG 20
    |||||
Db  19 GGGGAGGGGGGGGGGGGG 1

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## RESULT 32

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AZ488138/c      23 bp      DNA      linear      GSS 05-OCT-2000
LOCUS
DEFINITION      IM0318E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0318E13 F, genomic survey sequence.
ACCESSION      AZ488138
VERSION        AZ488138.1 GI:10656541
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarctontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0318 row: E column: 13
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0318E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

```

## FEATURES source

and selected for ampicillin resistance."

# ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 23;  
 Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
 |||||  
 Db 22 GGGGGGGGAGGGGGGGG 4

# RESULT 33

AZ581259/c  
 LOCUS  
 DEFINITION 1M0369N11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0369N11 R, genomic survey sequence.

AZ581259

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.

# REFERENCE

AUTHORS  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

# TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

# JOURNAL

COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0369 row: N column: 11

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

# FEATURES

source

1. .23  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0369N11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into

# ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 23;  
 Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
 |||||  
 Db 23 GGGGGGGGAGGGGGGGG 5

# RESULT 34

AZ800632/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0058 row: E column: 17

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0058E17"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into

adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 23;  
 Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 GGGAGGGGAGGGAGGGG 20  
 |||||  
 Db 19 GGGAGGGGAGGGAGGGG 1

## RESULT 35

AZ404465

LOCUS

DEFINITION AZ404465 24 bp DNA linear GSS 03-OCT-2000  
 clone UUGC1M0172P09 R, genomic survey sequence.

ACCESSION

AZ404465

VERSION

AZ404465.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0172 row: P column: 09

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0172P09"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [g14732114[gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 24;  
 Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 GGGAGGGGAGGGAGGGG 20  
 |||||  
 Db 4 GGGGGGGGAGGAGAGGGG 22

## RESULT 36

AZ640795/c

LOCUS

DEFINITION AZ640795 24 bp DNA linear GSS 14-DEC-2000  
 clone UUGC1M0503D04 F, genomic survey sequence.

ACCESSION

AZ640795

VERSION

AZ640795.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0503 row: D column: 04

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0503D04"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [g14732114[gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

```

Query Match      79.0%; Score 15.8; DB 9; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 GGGGAGGGAGGGAGGGGG 20
    ||||| ||||| ||||| |||||
DB   23 GGGGGGGGGAGGGGGGGG 5

```

```

RESULT 37
AZ789161/c
LOCUS      24 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION clone UUGC2M0036A15 R, genomic survey sequence.
ACCESSION  AZ789161
VERSION     AZ789161.1  GI:12929693
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

```

REFERENCE
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts

```

```

JOURNAL
COMMENT    Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0036 row: A column: 15
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 24.

```

## FEATURES

```

Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0036A15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

```

Query Match      79.0%; Score 15.8; DB 9; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 GGGGAGGGAGGGAGGGGG 20
    ||||| ||||| ||||| |||||
DB   20 GGGGAGGGGGGGGGGGGG 2

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```

RESULT 38
AZ823931
LOCUS      24 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION clone UUGC2M0098F17 F, genomic survey sequence.
ACCESSION  AZ823931
VERSION     AZ823931.1  GI:12993839
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

```

REFERENCE
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts

```

```

JOURNAL
COMMENT    Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0098 row: F column: 17
          Seq primer: CGTTGTAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 24.

```

## FEATURES

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Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0098F17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
```

of pMDA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 24;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 5 GGGGAGGGGAGGGGAGGGG 23

RESULT 19

AZ468549/c  
LOCUS  
DEFINITION  
IM0281D10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0281D10 R, genomic survey sequence.

ACCESSION  
AZ468549  
VERSION  
AZ468549.1 GI:10626674

KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0281 row: D column: 10

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 25.

FEATURES

source

1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0281D10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 23 GGGGAGGGGAGGGGAGGGG 5

RESULT 40

AZ602480/c

LOCUS

DEFINITION

IM0421F16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0421F16 F, genomic survey sequence.

ACCESSION  
AZ602480

VERSION  
AZ602480.1 GI:11724670

KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 25)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0421 row: F column: 16

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 25.

FEATURES

source

1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0421F16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."



10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* Xl10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
|||||

Db 25 GGGGGGGGAGGGGAGGGG 7  
|||||

RESULT 41  
TA33E11P/c

LOCUS TA33E11P 25 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 33e11, forward sequence,  
genomic survey sequence.

ACCESSION AL453376  
VERSION AL453376.1 GI:11854702

KEYWORDS GSS.

## SOURCE

ORGANISM Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

1 (bases 1 to 25)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).

Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source

1..25  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="33e11"

## ORIGIN

Query Match 79.0%; Score 15.8; DB 11; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
|||||

Db 20 GGGGGGGGAGGGGAGGGG 2  
|||||

RESULT 42  
BX626114

LOCUS BX626114 26 bp mRNA linear EST 08-AUG-2003  
DEFINITION NAP1 Anopheles gambiae cDNA clone ANGNP1181G08T7, mRNA  
sequence.

ACCESSION BX626114

VERSION BX626114.1 GI:33552251

KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 26)

AUTHORS Lobo, N.L., Gardner, M., Romans, P. and Collins, P.H.

TITLE Anopheles gambiae EST, Center for Tropical Disease Research and  
Training

JOURNAL Unpublished (2003)

COMMENT Contact: Frank H. Collins

Center for Tropical Disease Research and Training

University of Notre Dame

Notre Dame, IN 46556, USA

Tel: 574-631-9245

Fax: 574-631-3996

Email: frank.h.collins.75@nd.edu.

Location/Qualifiers

1..26

/organism="Anopheles gambiae"

/mol\_type="mRNA"

/db\_xref="taxon:7165"

/clone="ANGNP1181G08T7"

/lab\_host="E. coli DH10B"

/clone\_lib="NAP1"

/note="Vector: pT7T3D-Pac (Pharmacia); Site.1: NotI;

Site 2: EcoRI; ESTs sequenced from the T7 priming site

that reads from the 5' end of cDNA. The NAP1 is a

directionally cloned and normalized, oligo-T primed cDNA

library constructed from a mixture of Anopheles gambiae

developmental stages according to: Bonaldo, Lennon &

Soares (1996): Normalization and Subtraction: Two

Approaches To Facilitate Gene Discovery, Genome Research

6, 791-806."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 5; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
|||||

Db 1 GGGGAGGGGAGGGGAGGGG 19  
|||||

RESULT 43  
AZ307654/c

LOCUS AZ307654 26 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0009F22R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0009F22 R, genomic survey sequence.

ACCESSION AZ307654

VERSION AZ307654.1 GI:10346867

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Mus.

1 (bases 1 to 26)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0009 row: F column: 22  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers

## FEATURES

source

1..26  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0009F22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20

||||| ||||| ||||| |||||

Db 22 GGGGGGGGGAGGGGGGGG 4

## RESULT 44

AZ447254/c

LOCUS

DEFINITION 1M0244020F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0244020 F, genomic survey sequence.

ACCESSION AZ447254

VERSION AZ447254.1 GI:10599055

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 26)

## REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0244 row: O column: 20  
Seq primer: CGTTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers

## FEATURES

source

1..26  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0244020"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20

||||| ||||| ||||| |||||

Db 24 GGGGGGGGGAGGGGGGGG 6

## RESULT 45

AZ810458/c

LOCUS

DEFINITION 2M0076C02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0076C02 F, genomic survey sequence.

ACCESSION AZ810458

VERSION AZ810458.1 GI:12977740

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 26)

## REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0076 row: C column: 02  
Seq primer: CTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.

## FEATURES

source

1. 26  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0076C02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20

|||||

Db 26 GGGGAGGGGAGGGAGGGG 8

## RESULT 46

AZ861534/c

LOCUS

DEFINITION 2M0168K19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0168K19 F, genomic survey sequence.

ACCESSION AZ861534

VERSION AZ861534.1 GI:13057950

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

COMMENT

plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0168 row: K column: 19  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.

## FEATURES

source

1. 26  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0168K19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20

|||||

Db 23 GGGGAGGGGAGGGAGGGG 5

## RESULT 47

AZ604434/c

LOCUS

DEFINITION 1M0425I19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0425I18 F, genomic survey sequence.

ACCESSION AZ604434

VERSION AZ604434.1 GI:11726624

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 27)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0425 row: I column: 18  
Seq primer: CGTTGTAACACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 27.

FEATURES source

1. .27  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0425118"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 27;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 GGGGAGGGAGGGAGGGG 20  
||| ||||| ||||| |||||  
Db 24 GGGGGGGGGAGGGGGGGG 6

RESULT 48  
AZ649949/C  
LOCUS AZ649949 27 bp DNA linear GSS 14-DEC-2000  
DEFINITION IM0519P18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0519P18 R, genomic survey sequence.  
ACCESSION AZ649949  
VERSION AZ649949.1 GI:11783942  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von

TITLE Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0519 row: P column: 18  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.

FEATURES source

1. .27  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0519P18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 27;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 GGGGAGGGAGGGAGGGG 20  
||| ||||| ||||| |||||  
Db 25 GGGGGGGGGAGGGGGGGG 7

RESULT 49  
AZ327022  
LOCUS AZ327022 28 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0050I112F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0050I12 F, genomic survey sequence.  
ACCESSION AZ327022  
VERSION AZ327022.1 GI:10385356  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 28)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhauser,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0050 row: 1 column: 12  
Seq primer: CGTTGTAACACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 28.  
Location/Qualifiers

# FEATURES

source

1..28  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0050112"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

# ORIGIN

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGGAGGGGAGGGAGGG 19  
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DB 9 AGGGAAGTGGAGGGAGGG 27

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LOCUS  
DEFINITION  
AZ486749 28 bp DNA linear GSS 05-OCT-2000  
1M0315G02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
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ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 28)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhauser,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Class: plasmid ends  
High quality sequence stop: 28.  
Location/Qualifiers

# FEATURES

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

# ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 28;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GGGGAGGGGAGGGAGGGG 20  
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DB 26 GGGGAGGGGAGGGAGGGG 8

Search completed: February 15, 2006, 21:10:50  
Job time : 1343.25 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:56:18 ; Search time 44.9587 Seconds  
(without alignments)  
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Perfect score: 20  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| c 143 | 13.2 | 66.0 | 18 | 6 | PCT-US96-11786-43  | Sequence 43, Appl  | c 216 | 13.2 | 66.0 | 31 | 3 | US-09-896-650C-6  | Sequence 6, Appli |
| c 144 | 13.2 | 66.0 | 19 | 3 | US-09-109-663-31   | Sequence 31, Appl  | c 217 | 13.2 | 66.0 | 31 | 3 | US-09-896-650C-7  | Sequence 7, Appli |
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256 13.2 66.0 38 6 PCT-US96-11786-2  
257 13.2 66.0 39 3 US-09-052-995-7  
258 13.2 66.0 40 2 US-08-199-507B-48  
259 13.2 66.0 40 2 US-08-441-828-48  
260 13.2 66.0 44 2 US-07-931-473B-44  
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262 13.2 66.0 44 2 US-08-412-110-44  
263 13.2 66.0 44 2 US-08-409-442A-44  
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265 13.2 66.0 44 3 US-09-143-190-44  
266 13.2 66.0 44 3 US-09-502-344-44  
267 13.2 66.0 44 3 US-10-037-986-44  
268 13.2 66.0 47 2 US-08-171-389-59  
269 13.2 66.0 47 2 US-08-123-936-59  
270 13.2 66.0 47 2 US-08-475-228A-59  
271 13.2 66.0 47 3 US-08-482-080A-59  
272 13.2 66.0 47 3 US-09-354-947-59  
273 13.2 66.0 47 3 US-09-422-978-2397  
274 13.2 66.0 47 6 PCT-US93-346-59  
275 13.2 66.0 48 3 US-09-993-12388-59  
276 13.2 66.0 48 3 US-09-896-650C-32  
277 13.2 66.0 50 3 US-10-131-827-5223  
278 13.2 66.0 50 3 US-10-131-827-5224  
279 13.2 66.0 50 3 US-10-131-827-7271  
280 12.8 64.0 17 2 US-08-173-489C-95  
281 12.8 64.0 17 2 US-08-173-489C-96  
282 12.8 64.0 17 3 US-09-495-140-26  
283 12.8 64.0 17 3 US-10-059-877-26  
284 12.8 64.0 18 2 US-08-758-306-1351  
285 12.8 64.0 20 3 US-09-400-046-10  
286 12.8 64.0 20 3 US-09-509-595B-25  
287 12.8 64.0 21 2 US-08-424-663-8  
288 12.8 64.0 21 2 US-09-109-663-22  
289 12.8 64.0 21 3 US-09-280-270A-8  
290 12.8 64.0 21 3 US-09-425-804-27  
291 12.8 64.0 22 3 US-09-400-046-9  
292 12.8 64.0 23 3 US-09-400-046-8  
293 12.8 64.0 28 3 US-09-400-046-3  
294 12.8 64.0 29 3 US-09-400-046-4  
295 12.8 64.0 29 3 US-09-400-046-5  
296 12.8 64.0 29 3 US-09-342-681C-41  
297 12.8 64.0 30 3 US-09-400-046-1  
298 12.8 64.0 30 3 US-09-400-046-2  
299 12.8 64.0 30 3 US-09-400-046-7  
300 12.8 64.0 30 3 US-09-400-046-7

## ALIGNMENTS

RESULT 1  
US-08-460-890A-14/C  
; Sequence 14, Application US/08460890A  
; Patent No. 5994109  
; GENERAL INFORMATION:  
; APPLICANT: Woo, Savio L.C.  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Cristiano, Richard J.  
; APPLICANT: Gottchalk, Stephen  
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
; METHODS OF USE

; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FASTSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,890A  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167,641  
; FILING DATE: December 14, 1993  
; APPLICATION NUMBER: 07/855,389  
; FILING DATE: March 20, 1992  
; APPLICATION NUMBER: PCT/US93/02725  
; FILING DATE: March 19, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 212/066  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
; FEATURE: "C" stands for 5-methylcytosine  
; OTHER INFORMATION: "C" stands for 5-methylcytosine  
US-08-460-890A-14  
Query Match 87.0%; Score 17.4; DB 2; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.3e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 AGGGGAGGGGAGGGAGGG 19  
Db 24 AAGGGAGGGGAGGGAGGG 6  
RESULT 2  
US-08-460-890A-15  
; Sequence 15, Application US/08460890A  
; Patent No. 5994109  
; GENERAL INFORMATION:  
; APPLICANT: Woo, Savio L.C.  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Cristiano, Richard J.  
; APPLICANT: Gottchalk, Stephen  
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
; METHODS OF USE  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.

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;
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,890A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,641
; FILING DATE: December 14, 1993
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-460-890A-15

Query Match 87.0%; Score 17.4; DB 2; Length 27;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AGGGAGGGAGGGAGGG 19
Db 4 AAGGGAGGGAGGGAGGG 22

RESULT 3
US-08-167-641C-14/c
; Sequence 14, Application US/08167641C
; Patent No. 6033884
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,641C
; FILING DATE: December 14, 1993
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992/02725
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; FEATURE:
; OTHER INFORMATION: "C" stands for 5-methylcytosine
; US-08-167-641C-14

Query Match 87.0%; Score 17.4; DB 3; Length 27;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AGGGAGGGAGGGAGGG 19
Db 24 AAGGGAGGGAGGGAGGG 6

RESULT 4
US-08-167-641C-15
; Sequence 15, Application US/08167641C
; Patent No. 6033884
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,641C
; FILING DATE: December 14, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/012
```

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-167-641C-15

Query Match 87.0%; Score 17.4; DB 3; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGGAGGG 19  
DB 4 AAGGGAGGGGAGGGGAGGG 22

## RESULT 5

US-08-460-971A-14/c  
; Sequence 14, Application US/08460971A  
; Patent No. 6150168

; GENERAL INFORMATION:  
; APPLICANT: Woo, Savio L.C.  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Cristiano, Richard J.  
; APPLICANT: Gottchalk, Stephen  
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
; TITLE OF INVENTION: METHODS OF USE  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,971A  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167,641  
; FILING DATE: December 14, 1993  
; APPLICATION NUMBER: 07/855,389  
; FILING DATE: March 20, 1992  
; APPLICATION NUMBER: PCT/US93/02725  
; FILING DATE: March 19, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 212/063  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: Other nucleic acid  
; FEATURE:  
; OTHER INFORMATION: "C" stands for 5-methylcytosine  
US-08-460-971A-14

Query Match 87.0%; Score 17.4; DB 3; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGGAGGG 19  
DB 24 AAGGGAGGGGAGGGGAGGG 6

## RESULT 6

US-08-460-971A-15  
; Sequence 15, Application US/08460971A  
; Patent No. 6150168

; GENERAL INFORMATION:  
; APPLICANT: Woo, Savio L.C.  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Cristiano, Richard J.  
; APPLICANT: Gottchalk, Stephen  
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
; TITLE OF INVENTION: METHODS OF USE  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,971A  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167,641  
; FILING DATE: December 14, 1993  
; APPLICATION NUMBER: 07/855,389  
; FILING DATE: March 20, 1992  
; APPLICATION NUMBER: PCT/US93/02725  
; FILING DATE: March 19, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 212/063  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-460-971A-15

Query Match 87.0%; Score 17.4; DB 3; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGGAGGG 19

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Db      4 AAGGAGGGAGGGAGGG 22
|||||
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
FEATURE:
OTHER INFORMATION: "C" stands for 5-methylcytosine
US-08-462-040-14
Query Match      87.0%; Score 17.4; DB 3; Length 27;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 AGGGAGGGAGGGAGGG 19
|||||
Db      24 AAGGAGGGAGGGAGGG 6
|||||
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-462-040-15
Query Match      87.0%; Score 17.4; DB 3; Length 27;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 AGGGAGGGAGGGAGGG 19
|||||
Db      4 AAGGAGGGAGGGAGGG 22
|||||
RESULT 9
US-08-460-890A-13
; Sequence 13, Application US/08460890A
; Patent No. 5994109
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; RESULT 8
US-08-462-040-15
; Sequence 15, Application US/08462040
; Patent No. 6177554
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; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,641C
; FILING DATE: December 14, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-167-641C-13

Query Match      87.0%; Score 17.4; DB 3; Length 39;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels

QY      1 AGGGGAGGGGAGGGAGGG 19
Db      10 AAGGGAGGGGAGGGAGGG 28
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          |||||

RESULT 11
US-08-460-971A-13
; Sequence 13, Application US/08460971A
; Patent No. 6150168
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; METHOD OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,971A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,641
; FILING DATE: December 14, 1993
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725

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; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-460-971A-13
;
; Query Match 87.0%; Score 17.4; DB 3; Length 39;
; Best Local Similarity 94.7%; Pred. No. 4.3e+02;
; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
Qy 1 AGGGAGGGAGGGAGGG 19
| | | | | | | | | | | | | | | | | | | | |
Db 10 AAGGGAGGGAGGGAGGG 28
| | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-08-462-040-13
; Sequence 13, Application US/08462040
; Patent No. 6177554
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.040
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,641
; FILING DATE: December 14, 1993
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 13:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-462-040-13
;
; Query Match 87.0%; Score 17.4; DB 3; Length 39;
; Best Local Similarity 94.7%; Pred. No. 4.3e+02;
; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
Qy 1 AGGGAGGGAGGGAGGG 19
| | | | | | | | | | | | | | | | | | | | |
Db 10 AAGGGAGGGAGGGAGGG 28
| | | | | | | | | | | | | | | | | | | | |

RESULT 13
PCT-US93-02352-2
; Sequence 2, Application PC/TUS9302352
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology,
; APPLICANT: Pasadena, California 91125, U.S.A.
; TITLE OF INVENTION: Triple helix recognition of DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02352
; FILING DATE: 19930311
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/850,503
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: FP-56557/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 5..43
; OTHER INFORMATION: /note= "Sticky single-stranded end
; OTHER INFORMATION: from base 1 to 4. Double stranded from base 5 to
; OTHER INFORMATION: 43 to complementary strand, SEQ ID NO:3."
; PCT-US93-02352-2
;
; Query Match 82.0%; Score 16.4; DB 6; Length 43;
; Best Local Similarity 89.5%; Pred. No. 9.8e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
Qy 1 AGGGAGGGAGGGAGGG 19
| | | | | | | | | | | | | | | | | | | | |
Db 14 AAGGNGGGAGGGAGGG 32
| | | | | | | | | | | | | | | | | | | | |
```

RESULT 14  
PCT-US93-02352-3/c  
; Sequence 3, Application PC/TUS9302352  
; GENERAL INFORMATION:  
; APPLICANT: California Institute of Technology,  
; APPLICANT: Pasadena, California 91125, U.S.A.  
; TITLE OF INVENTION: Triple helix recognition of DNA  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Richard F. Trecartin  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/02352  
; FILING DATE: 19930311  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER: 07/850,503  
; FILING DATE: 13-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: FP-56557/RFT  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: misc binding  
; LOCATION: 5..43  
; OTHER INFORMATION: /note= "sticky single-stranded end  
; OTHER INFORMATION: from base 1 to 4. Double-stranded from base 5 to  
; OTHER INFORMATION: 37 to complementary strand, SEQ ID NO:2."  
PCT-US93-02352-3

Query Match 82.0%; Score 16.4; DB 6; Length 43;  
Best Local Similarity 89.5%; Pred. No. 9.8e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 34 AAGGGGAGGGGAGGGAGGG 16

RESULT 15  
US-08-956-171E-2153/c  
; Sequence 2153, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; Gil H. Choi  
; Patrick S. Dillon  
; Craig A. Rosen  
; Steven C. Barash  
; Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,171E  
; FILING DATE: 20-Oct-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB248P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 2153:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2153:  
US-08-956-171E-2153

Query Match 82.0%; Score 16.4; DB 3; Length 50;  
Best Local Similarity 89.5%; Pred. No. 9.8e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 28 GGGGGGGGGGGAGGGGG 10

RESULT 16  
US-08-781-986A-2153/c  
; Sequence 2153, Application US/08781986A  
; Patent No. 6737248  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,986A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-2153

Query Match      82.0%; Score 16.4; DB 3; Length 50;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  28 GGGGGGGGGGGGGGGGG 10

RESULT 17
US-09-622-745B-20/c
; Sequence 20, Application US/09622745B
; Patent No. 6933124
; GENERAL INFORMATION:
; APPLICANT: Astrazeneca AB
; APPLICANT: Edlund, Anders
; APPLICANT: Ekstrand, Jonas
; APPLICANT: Johansson, Thore
; APPLICANT: Leonardsson, Goran
; TITLE OF INVENTION: HUMAN GABA B RECEPTOR 1 PROMOTERS
; FILE REFERENCE: 1103326-0633
; CURRENT APPLICATION NUMBER: US/09/622,745B
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/SE00/00878
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: P R 1b GCVI Fwd
US-09-622-745B-20

Query Match      79.0%; Score 15.8; DB 3; Length 27;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 AGGGAGGGGAGGGAGGGG 19
    ||| ||||| ||||| |||||
Db  19 AGGTTAGGGAGGGAGGGG 1

RESULT 18
US-09-622-745B-21
; Sequence 21, Application US/09622745B
; Patent No. 6933124
; GENERAL INFORMATION:
; APPLICANT: Astrazeneca AB
; APPLICANT: Edlund, Anders
; APPLICANT: Ekstrand, Jonas
; APPLICANT: Johansson, Thore
; APPLICANT: Leonardsson, Goran
; TITLE OF INVENTION: HUMAN GABA B RECEPTOR 1 PROMOTERS
; FILE REFERENCE: 1103326-0633
; CURRENT APPLICATION NUMBER: US/09/622,745B
; CURRENT FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: PCT/SE00/00878
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: P R 1b GCVI Rev
US-09-622-745B-21

Query Match      79.0%; Score 15.8; DB 3; Length 27;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 AGGGAGGGGAGGGAGGGG 19
    ||| ||||| ||||| |||||
Db  9 AGGTTAGGGAGGGAGGGG 27

RESULT 19
5182196-21
; Patent No. 5182196
; APPLICANT: ALLET, BERNARD; KAWASHIMA, ERIC H.
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR OVERPRODUCTION OF
; DESIRED PROTEINS
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,281
; FILING DATE: 27-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 53,398
; FILING DATE: 18-MAY-1987
; APPLICATION NUMBER: 785,847
; FILING DATE: 09-OCT-1985
; SEQ ID NO:21
; LENGTH: 42
5182196-21

Query Match      79.0%; Score 15.8; DB 9; Length 42;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  17 GGGGGGGGGGGGGGGGG 35

RESULT 20
US-09-118-752-2
; Sequence 2, Application US/09118752
; Patent No. 6114154
; GENERAL INFORMATION:
; APPLICANT: Li, Huiwu
; TITLE OF INVENTION: Direct Construction and Isolation Full Length Target
; FILE REFERENCE: 12660-0100
; CURRENT APPLICATION NUMBER: US/09/118,752
; CURRENT FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 37
; TYPE: DNA
; ORGANISM: murine
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: primer_bind
; LOCATION: (1)..(22)
US-09-118-752-2
```



Query Match 76.0%; Score 15.2; DB 3; Length 37;  
Best Local Similarity 85.0%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20  
Db 16 AGGGAAGGGGGGGGGGGG 35

RESULT 21  
US-08-324-001-2/c  
; Sequence 2, Application US/08324001  
; Patent No. 5624803  
; GENERAL INFORMATION:  
; APPLICANT: NOONBERG, SARAH B.  
; APPLICANT: HUNT, C. ANTHONY  
; TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND  
; TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING  
; TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/324,001  
; FILING DATE: 13-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MONROY, GLADYS H.  
; REGISTRATION NUMBER: 32,430  
; REFERENCE/DOCKET NUMBER: 22000-20544.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-324-001-2

Query Match 76.0%; Score 15.2; DB 2; Length 38;  
Best Local Similarity 85.0%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20  
Db 27 AGGGAGGGAGGGAAGGG 8

RESULT 22  
US-09-230-222-18/c  
; Sequence 18, Application US/09230222A  
; Patent No. 6159720  
; GENERAL INFORMATION:  
; APPLICANT: MURASHIMA, KOUICHIROU  
; APPLICANT: MORIYA, TATSUKI  
; APPLICANT: HAMAYA, TORU  
; APPLICANT: KOGA, JINICHIRO  
; APPLICANT: SUMIDA, NAOMI  
; APPLICANT: AOYAGI, KAORU  
; APPLICANT: MURAKAMI, TAKESHI

Query Match 74.0%; Score 14.8; DB 3; Length 30;  
Best Local Similarity 88.9%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGG 18  
Db 25 AGCGGAGGAGGAGGGAGG 8

RESULT 23  
US-09-230-225B-25/c  
; Sequence 25, Application US/09230225B  
; Patent No. 6403362  
; GENERAL INFORMATION:  
; APPLICANT: Meiji Seika Kaisha, Ltd.  
; APPLICANT: Moriya, Tatsuki  
; TITLE OF INVENTION: Systems for the Mass Production of Proteins or Peptides by Micro  
; TITLE OF INVENTION: of the Genus Humicola  
; FILE REFERENCE: VX990054  
; CURRENT APPLICATION NUMBER: US/09/230,225B  
; CURRENT FILING DATE: 1999-03-03  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 25  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Humicola insolens  
US-09-230-225B-25

Query Match 74.0%; Score 14.8; DB 3; Length 30;  
Best Local Similarity 88.9%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGG 18  
Db 25 AGCGGAGGAGGAGGGAGG 8

RESULT 24  
US-09-254-352B-31  
; Sequence 31, Application US/09254352B  
; Patent No. 6365350  
; GENERAL INFORMATION:  
; APPLICANT: HAYASHIZAKI, Yoshihide  
; TITLE OF INVENTION: METHOD OF DNA SEQUENCING  
; FILE REFERENCE: 024705-080  
; CURRENT APPLICATION NUMBER: US/09/254,352B  
; CURRENT FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/JP98/03039  
; PRIOR FILING DATE: 1998-07-06  
; PRIOR APPLICATION NUMBER: JP 10-155847  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: JP 9-196478  
; PRIOR FILING DATE: 1997-07-07  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 31

```
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T7 RNA polymerase (WT)
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: Nucleotide 25 is n wherein n = any nucleotide.
US-09-254-352B-31

Query Match          74.0%; Score 14.8; DB 3; Length 31;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  3 GGGAGGGGAGGGGAGGGG 20
    ||||| ||||| |||||
Db  1 GGGAGGGGAGGGGAGGGG 18

RESULT 25
US-09-254-344-17
; Sequence 17, Application US/09254344
; Patent No. 6867027
; GENERAL INFORMATION:
; APPLICANT: HAYASHIZAKI, Yoshihide
; APPLICANT: WATAHIKI, Masanori
; TITLE OF INVENTION: RNA Polymerase
; FILE REFERENCE: 024705-077
; CURRENT APPLICATION NUMBER: US/09/254,344
; CURRENT FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/JP98/03037
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: JP 9/180883
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: JP 10/155759
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Bacteriophage T7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(31)
; OTHER INFORMATION: Mutant T7 RNA polymerase wild type.
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: Nucleotide 25 is "n" wherein "n" = any nucleotide.
US-09-254-344-17

Query Match          74.0%; Score 14.8; DB 3; Length 31;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  3 GGGAGGGGAGGGGAGGGG 20
    ||||| ||||| |||||
Db  1 GGGAGGGGAGGGGAGGGG 18

RESULT 26
US-08-777-708C-16/c
; Sequence 16, Application US/08777708C
; Patent No. 6159334
; GENERAL INFORMATION:
; APPLICANT: Pescovitz, Ora H.
; TITLE OF INVENTION: USE OF GHRH-RP TO STIMULATE STEM CELL FACTOR PRODUCTION
; FILE REFERENCE: 7037-175/1U-62
; CURRENT APPLICATION NUMBER: US/08/777,708C
; CURRENT FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: US 60/008,933
; PRIOR FILING DATE: 1995-12-20
; NUMBER OF SEQ ID NOS: 23
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-08-777-708C-16

Query Match          72.0%; Score 14.4; DB 3; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5 GAGGGAGGGGAGGGG 20
    ||||| ||||| |||||
Db  20 GAGGGAGGGTGAAGGG 5

RESULT 27
US-09-875-453B-66
; Sequence 66, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453B-66

Query Match          72.0%; Score 14.4; DB 3; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2 GGGAGGGGAGGGGAG 17
    ||||| ||||| |||||
Db  1 GGTGAGGGGAGGGGAG 16

RESULT 28
US-09-197-951-2/c
; Sequence 2, Application US/09197951
; Patent No. 6197554
; GENERAL INFORMATION:
; APPLICANT: LIN, SHI-LUNG
; APPLICANT: CHUNG, CHENG-MING
; APPLICANT: YING, SHAO-YAO
; TITLE OF INVENTION: Method for Generating Full-Length cDNA
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David & Raymond Patent Firm
; STREET: 108 N. Ynez Ave., Suite 128
; CITY: Monterey Park
; STATE: CA
; COUNTRY: USA
```

ZIP: 91754  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/197,951  
FILING DATE: 20-NO. 6197554-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chan, Raymond Y.C.  
REGISTRATION NUMBER: 37,484  
REFERENCE/DOCKET NUMBER: USP8462A-SL(3)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 571-9812  
TELEFAX: (626) 571-9813  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic"  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-197-951-2

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 20 GGGGGGGGGGGGGGGGGG 20

## RESULT 29

US-09-082-649B-55/c  
Sequence 55, Application US/09082649B  
Patent No. 6339068  
GENERAL INFORMATION:  
APPLICANT: Davis, Heather L.  
APPLICANT: Krieg, Arthur M.  
APPLICANT: Schorr, Joachim  
APPLICANT: Wu, Tong  
TITLE OF INVENTION: Vectors and Methods for Immunization or  
FILE REFERENCE: C1039/7009  
CURRENT APPLICATION NUMBER: US/09/082,649B  
CURRENT FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: US 60/047,233  
PRIOR FILING DATE: 1997-05-20  
PRIOR APPLICATION NUMBER: US 60/047,209  
PRIOR FILING DATE: 1997-05-20  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 55  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic oligonucleotide  
US-09-082-649B-55

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||

Db 20 GGGGGGGGGGGGGGGGGG 20

## RESULT 30

US-09-965-101-55/c  
Sequence 55, Application US/09965101  
Patent No. 6821957  
GENERAL INFORMATION:  
APPLICANT: Davis, Heather L.  
APPLICANT: Krieg, Arthur M.  
APPLICANT: Schorr, Joachim  
APPLICANT: Wu, Tong  
TITLE OF INVENTION: Vectors and Methods for Immunization or  
FILE REFERENCE: C1039/7057 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/09/965,101  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 09/082,649  
PRIOR FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: US 60/047,233  
PRIOR FILING DATE: 1997-05-20  
PRIOR APPLICATION NUMBER: US 60/047,209  
PRIOR FILING DATE: 1997-05-20  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 55  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic oligonucleotide  
US-09-965-101-55

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 20 GGGGGGGGGGGGGGGGGG 20

## RESULT 31

US-09-672-126B-134  
Sequence 134, Application US/09672126B  
Patent No. 6949520  
GENERAL INFORMATION:  
APPLICANT: Hartmann, Gunther L.  
APPLICANT: Bratzler, Robert L.  
APPLICANT: Krieg, Arthur  
TITLE OF INVENTION: Methods Related to Immunostimulatory  
FILE REFERENCE: C1039/7044  
CURRENT APPLICATION NUMBER: US/09/672,126B  
CURRENT FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/156,147  
PRIOR FILING DATE: 1999-09-29  
NUMBER OF SEQ ID NOS: 169  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 134  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-672-126B-134

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||



REFERENCE/DOCKET NUMBER: ISIS-1229  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-403-888A-42

Query Match 71.0%; Score 14.2; DB 2; Length 21;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
Db 1 GGGGCGGGCGGGCGGGG 19

## RESULT 35

US-08-863-639A-11/C  
Sequence 11, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel WordPerfect 8 version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph E. Mueth  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-11

Query Match 71.0%; Score 14.2; DB 2; Length 21;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
Db 21 GGGGCGGGCGGGCGGGG 3

## RESULT 36

US-08-863-639A-12  
Sequence 12, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel WordPerfect 8 version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph E. Mueth  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-12

Query Match 71.0%; Score 14.2; DB 2; Length 21;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
Db 1 GGGGCGGGCGGGCGGGG 19

## RESULT 37

US-09-696-791-4484/C  
Sequence 4484, Application US/09696791  
Patent No. 6770633  
GENERAL INFORMATION:  
APPLICANT: Robbins, Joan M.  
APPLICANT: Tritz, Richard  
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
DISEASES  
FILE REFERENCE: 480124.407  
CURRENT APPLICATION NUMBER: US/09/696,791  
CURRENT FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 4523  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4484  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
OTHER INFORMATION: PDGF A ribozyme recognition site  
US-09-696-791-4484

Query Match 71.0%; Score 14.2; DB 2; Length 21;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
Db 21 GGGGCGGGCGGGCGGGG 3

Query Match 71.0%; Score 14.2; DB 3; Length 21;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
||||| ||||| |||||  
Db 19 GGGGTGGGACGGAAGGGG 1

RESULT 38  
PCT-US92-10770-15  
Sequence 15, Application US/07808452  
Patent No. 6063612  
GENERAL INFORMATION:  
APPLICANT: Jayasena, Suredha D.  
APPLICANT: Johnston, Brian H.  
TITLE OF INVENTION: Antiviral Reagents Based on  
RNA-Binding Proteins  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/808,452  
FILING DATE: 19911213  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 8255-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: SINGLE STRAND OLIGONUCLEOTIDE,  
INDIVIDUAL ISOLATE: 12/C-1

Query Match 71.0%; Score 14.2; DB 3; Length 23;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
||||| ||||| |||||  
Db 5 GGAGAGGGGAGAGGGGGG 23

RESULT 39  
PCT-US92-10770-15  
Sequence 15, Application PC/TUS9210770  
GENERAL INFORMATION:  
APPLICANT: Jayasena, Suredha D.  
APPLICANT: Johnston, Brian H.  
TITLE OF INVENTION: Antiviral Reagents Based on  
RNA-Binding Proteins

NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SRI International  
STREET: 333 Ravenswood Avenue  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10770  
FILING DATE: 19921211  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,452  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: P-2962  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 859-4550  
TELEFAX: (415) 859-3880  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: SINGLE STRAND OLIGONUCLEOTIDE,  
INDIVIDUAL ISOLATE: 12/C-1  
PCT-US92-10770-15

Query Match 71.0%; Score 14.2; DB 6; Length 23;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
||||| ||||| |||||  
Db 5 GGAGAGGGGAGAGGGGGG 23

RESULT 40  
PCT-US92-10792-13  
Sequence 13, Application PC/TUS9210792  
GENERAL INFORMATION:  
APPLICANT: Jayasena, Suredha D.  
APPLICANT: Johnston, Brian H.  
TITLE OF INVENTION: Triple Helix Formation at  
PunPyN - (PunPyN) - (PunPyN) Tracts  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SRI International  
STREET: 333 Ravenswood Avenue  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10792  
FILING DATE: 19921211

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,934
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,452
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: P-3141
; TELEPHONE: (415) 859-4550
; TELEFAX: (415) 859-3880
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: FIGURE 10, C-1
; PCT-US92-10792-13

Query Match 71.0%; Score 14.2; DB 6; Length 23;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGAGGGGGAGGGGGGGG 20
DB 5 GGAGAGGGGAGAGGGGGG 23

RESULT 41
US-08-014-943A-7
; Sequence 7, Application US/08014943A
; Patent No. 5545551
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: Cloning And Expression Of Pur Protein
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,943A
; FILING DATE: 02-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-014-943A-7

Query Match 71.0%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGAGGGGGAGGGGGGGG 20
DB 1 GGGGGGGGGGGGGGGGGG 19

RESULT 42
US-08-486-421-49
; Sequence 49, Application US/08486421
; Patent No. 5672479
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,421
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-486-421-49

Query Match 71.0%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGAGGGGGAGGGGGGGG 20
DB 1 GGGGGGGGGGGGGGGGGG 19

RESULT 43
US-08-470-911-49
; Sequence 49, Application US/08470911
; Patent No. 5756684
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.

```

```

; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,911
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-470-911-49

Query Match 71.0%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGAGGGAGGGGG 20
   ||||| ||||| ||||| |||||
Db 1 GGGGGGGGGGGGGGGGGG 19

RESULT 44
US-08-486-809-49
; Sequence 49, Application US/08486809
; Patent No. 5869622
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,809
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-486-809-49

Query Match 71.0%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGAGGGAGGGGG 20
   ||||| ||||| ||||| |||||
Db 1 GGGGGGGGGGGGGGGGGG 19

RESULT 45
US-08-960-190A-31
; Sequence 31, Application US/08960190A
; Patent No. 6232445
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Acevedo, Jorge
; APPLICANT: Burkhardt, Martin
; APPLICANT: Jiao, Jin-an
; APPLICANT: Wong, Hing C.
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: usa
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,190A
; FILING DATE: 29-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 48002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-960-190A-31

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Query Match 71.0%; Score 14.2; DB 3; Length 24;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGGAGGGAGGGAGGGG 20  
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DB 3 GGGGAGGGAGGGAGGGG 21

RESULT 46  
US-08-976-427-26/c  
; Sequence 26, Application US/08976427A  
; Patent No. 6322968  
; GENERAL INFORMATION:  
; APPLICANT: Head, Steven R.  
; APPLICANT: Golet, Philip  
; APPLICANT: Karn, Jonathan  
; APPLICANT: Boyce-Jacino, Michael  
; TITLE OF INVENTION: De No. 6322968 or "Universal" Sequencing Array  
; FILE REFERENCE: 04990.0049  
; CURRENT APPLICATION NUMBER: US/08/976,427A  
; CURRENT FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic primer  
US-08-976-427-26

Query Match 71.0%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGGAGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
DB 25 GGGGAGGGAGGGAGGGG 7

RESULT 47  
US-09-648-312-26/c  
; Sequence 26, Application US/09648312  
; Patent No. 6337188  
; GENERAL INFORMATION:  
; APPLICANT: Head, Steven R.  
; APPLICANT: Golet, Philip  
; APPLICANT: Karn, Jonathan  
; APPLICANT: Boyce-Jacino, Michael  
; TITLE OF INVENTION: De No. 6337188 or "Universal" Sequencing Array  
; FILE REFERENCE: 04990.0049  
; CURRENT APPLICATION NUMBER: US/09/648,312  
; CURRENT FILING DATE: 2000-08-25  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic primer  
US-09-648-312-26

Query Match 71.0%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGGAGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
DB 25 GGGGAGGGAGGGAGGGG 7

RESULT 48  
US-09-896-650C-26/c  
; Sequence 26, Application US/09896650C  
; Patent No. 6946249  
; GENERAL INFORMATION:  
; APPLICANT: Head, Steven R.  
; APPLICANT: Golet, Philip  
; APPLICANT: Karn, Jonathan  
; APPLICANT: Boyce-Jacino, Michael  
; TITLE OF INVENTION: De No. 6946249 or Universal Sequencing Array  
; FILE REFERENCE: 13019-2  
; CURRENT APPLICATION NUMBER: US/09/896,650C  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 08/976,427  
; PRIOR FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Primer  
US-09-896-650C-26

Query Match 71.0%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGGAGGGAGGGAGGGG 20  
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DB 25 GGGGAGGGAGGGAGGGG 7

RESULT 49  
US-08-208-486-80/c  
; Sequence 80, Application US/08208486  
; Patent No. 5389531  
; GENERAL INFORMATION:  
; APPLICANT: Ito, Junetsu  
; APPLICANT: Yoo, Seung-Ku  
; TITLE OF INVENTION: METHODS TO REPLICATE DNA IN VITRO USING  
; PRD1-CATALYZED DNA REPLICATION SYSTEMS  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cahill, Sutton & Thomas  
; STREET: 155 Park One, 2141 E. Highland Ave.  
; CITY: Phoenix  
; STATE: Arizona  
; COUNTRY: U.S.A.  
; ZIP: 85016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb  
; COMPUTER: Packard Bell (IBM PC/AT compatible)  
; OPERATING SYSTEM: MS-Dos, Version 5.0  
; SOFTWARE: WordPerfect Version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208,486  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/869,916  
; FILING DATE: April 14, 1992  
; APPLICATION NUMBER: Japan 240525/91  
; FILING DATE: August 26, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janelle Faunce Raupp  
; REGISTRATION NUMBER: 30,485  
; REFERENCE/DOCKET NUMBER: #3954-A-7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (602) 956-7000  
; TELEFAX: (602) 495-9475

;  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)  
US-08-208-486-80

Query Match 71.0%; Score 14.2; DB 2; Length 27;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGGGGGGGGG 20  
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Db 27 GGGGGGGGGGGGGGGG 9

RESULT 50  
US-08-208-486-81  
; Sequence 81, Application US/08208486  
; Patent No. 5389531  
; GENERAL INFORMATION:  
; APPLICANT: Ito, Junetsu  
; APPLICANT: Yoo, Seung-Ku  
; TITLE OF INVENTION: METHODS TO REPLICATE DNA IN VITRO USING  
; TITLE OF INVENTION: PRD1-CATALYZED DNA REPLICATION SYSTEMS  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cahill, Sutton & Thomas  
; STREET: 155 Park One, 2141 E. Highland Ave.  
; CITY: Phoenix  
; STATE: Arizona  
; COUNTRY: U.S.A.  
; ZIP: 85016

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb  
; COMPUTER: Packard Bell (IBM PC/AT compatible)  
; OPERATING SYSTEM: MS-Dos, Version 5.0  
; SOFTWARE: WordPerfect Version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208,486  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/869,916  
; FILING DATE: April 14, 1992  
; APPLICATION NUMBER: Japan 240525/91  
; FILING DATE: August 26, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janelle Faunce Raupp  
; REGISTRATION NUMBER: 30,485  
; REFERENCE/DOCKET NUMBER: #3954-A-7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (602) 956-7000  
; TELEFAX: (602) 495-9475  
; INFORMATION FOR SEQ ID NO: 81:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)  
US-08-208-486-81

Query Match 71.0%; Score 14.2; DB 2; Length 27;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGGGGGGGGG 20  
||||| ||||| ||||| ||||| |||||  
Db 1 GGGGGGGGGGGGGGGG 19

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OM nucleic - nucleic search, using sw model

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569.815 Million cell updates/sec

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Perfect score: 20  
Sequence: 1 agggaggaggaggaggagg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
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| 1          | 20    | 100.0       | 20     | 3  | US-09-776-479-906    |
| 2          | 20    | 100.0       | 20     | 3  | US-09-776-479-906    |
| 3          | 20    | 100.0       | 20     | 5  | US-10-112-653-875    |
| 4          | 20    | 100.0       | 20     | 5  | US-10-017-995-906    |
| 5          | 20    | 100.0       | 20     | 6  | US-10-314-578-906    |
| 6          | 20    | 100.0       | 20     | 8  | US-10-831-778-906    |
| 7          | 17.4  | 87.0        | 30     | 5  | US-10-010-920-43     |
| 8          | 17.4  | 87.0        | 30     | 5  | US-10-008-721-43     |
| 9          | 17.4  | 87.0        | 33     | 9  | US-10-971-736-159    |
| 10         | 16.8  | 84.0        | 23     | 3  | US-09-263-959-699    |
| 11         | 16.4  | 82.0        | 25     | 10 | US-11-060-756-220152 |
| 12         | 16.4  | 82.0        | 50     | 7  | US-08-781-986A-2153  |
| 13         | 16.4  | 82.0        | 50     | 7  | US-10-329-624-2153   |
| 14         | 15.8  | 79.0        | 19     | 3  | US-09-263-959-923    |
| 15         | 15.8  | 79.0        | 26     | 5  | US-10-010-476-38     |
| 16         | 15.2  | 76.0        | 22     | 6  | US-10-407-449-41     |
| 17         | 15.2  | 76.0        | 22     | 6  | US-10-407-449-44     |
| 18         | 15.2  | 76.0        | 22     | 8  | US-10-820-487-5      |
| 19         | 15.2  | 76.0        | 22     | 6  | US-10-903-975-5      |
| 20         | 15.2  | 76.0        | 24     | 6  | US-10-407-449-43     |
| 21         | 15.2  | 76.0        | 27     | 9  | US-10-931-077-28     |
| 22         | 15.2  | 76.0        | 35     | 7  | US-10-239-176-13     |
| 23         | 15.2  | 76.0        | 39     | 7  | US-10-239-176-3      |

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|-------------------|------|------|----|----|---------------------|-------------------|
| Sequence 4, Appli | 76.0 | 15.2 | 24 | 7  | US-10-239-176-4     | Sequence 443, App |
| Sequence 1181, Ap | 75.0 | 15   | 25 | 15 | US-09-263-959-443   | Sequence 55, Appl |
| Sequence 5376, Ap | 75.0 | 15   | 26 | 41 | US-10-035-833A-1181 | Sequence 107, App |
| Sequence 55, Appl | 74.0 | 14.8 | 27 | 26 | US-10-010-476-55    | Sequence 93, Appl |
| Sequence 13, Appl | 74.0 | 14.8 | 28 | 26 | US-10-010-476-107   | Sequence 6318, Ap |
| Sequence 9, Appli | 74.0 | 14.8 | 29 | 40 | US-10-224-683-93    | Sequence 100, App |
| Sequence 133, App | 74.0 | 14.8 | 30 | 40 | US-10-942-561A-93   | Sequence 66, Appl |
| Sequence 431, App | 74.0 | 14.8 | 31 | 40 | US-10-035-833A-6318 | Sequence 432, App |
| Sequence 432, App | 74.0 | 14.8 | 32 | 41 | US-10-397-943-9     | Sequence 432, App |
| Sequence 2, Appli | 72.0 | 14.4 | 33 | 18 | US-09-943-944E-100  | Sequence 133, App |
| Sequence 133, App | 72.0 | 14.4 | 34 | 3  | US-09-875-453-66    | Sequence 133, App |
| Sequence 431, App | 72.0 | 14.4 | 35 | 3  | US-10-617-070-431   | Sequence 431, App |
| Sequence 432, App | 72.0 | 14.4 | 36 | 39 | US-10-617-070-432   | Sequence 432, App |
| Sequence 431, App | 72.0 | 14.4 | 37 | 39 | US-10-956-507-431   | Sequence 432, App |
| Sequence 432, App | 72.0 | 14.4 | 38 | 39 | US-10-956-507-432   | Sequence 2, Appli |
| Sequence 2, Appli | 71.0 | 14.2 | 39 | 3  | US-09-916-369A-2    | Sequence 133, App |
| Sequence 133, App | 71.0 | 14.2 | 40 | 20 | US-09-800-266A-133  | Sequence 133, App |
| Sequence 133, App | 71.0 | 14.2 | 41 | 20 | US-09-895-007A-133  | Sequence 168, App |
| Sequence 168, App | 71.0 | 14.2 | 42 | 20 | US-09-920-313-133   | Sequence 169, App |
| Sequence 429, App | 71.0 | 14.2 | 43 | 20 | US-09-888-326-168   | Sequence 429, App |
| Sequence 430, App | 71.0 | 14.2 | 44 | 20 | US-09-888-326-169   | Sequence 429, App |
| Sequence 429, App | 71.0 | 14.2 | 45 | 20 | US-09-888-326-429   | Sequence 257, App |
| Sequence 257, App | 71.0 | 14.2 | 46 | 20 | US-09-888-326-430   | Sequence 530, App |
| Sequence 530, App | 71.0 | 14.2 | 47 | 20 | US-09-776-479-257   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 48 | 20 | US-09-776-479-530   | Sequence 811, App |
| Sequence 811, App | 71.0 | 14.2 | 49 | 20 | US-09-776-479-531   | Sequence 811, App |
| Sequence 811, App | 71.0 | 14.2 | 50 | 20 | US-09-776-479-811   | Sequence 257, App |
| Sequence 257, App | 71.0 | 14.2 | 51 | 20 | US-09-776-479-811   | Sequence 530, App |
| Sequence 530, App | 71.0 | 14.2 | 52 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 53 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 54 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 55 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 56 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 57 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 58 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 59 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 60 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 61 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 62 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 63 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 64 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 65 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 66 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 67 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 68 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 69 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 70 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 71 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 72 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 73 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 74 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 75 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 76 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 77 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 78 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 79 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 80 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 81 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 82 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 83 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 84 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 85 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 86 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 87 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 88 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 89 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 90 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 91 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 92 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 93 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 94 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 95 | 20 | US-09-776-479-811   | Sequence 531, App |
| Sequence 531, App | 71.0 | 14.2 | 96 | 20 | US-09-776-479-811   | Sequence 531, App |

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|-------|------|------|----|----|----------------------|----------------------|-------|------|------|----|----|----------------------|----------------------|
| c 97  | 14.2 | 71.0 | 20 | 8  | US-10-831-778-531    | Sequence 531, App    | c 170 | 14.2 | 71.0 | 40 | 7  | US-10-661-355-22     | Sequence 22, Appl    |
| c 98  | 14.2 | 71.0 | 20 | 8  | US-10-831-778-811    | Sequence 811, App    | c 171 | 14.2 | 71.0 | 40 | 7  | US-10-661-099-21     | Sequence 21, Appl    |
| c 99  | 14.2 | 71.0 | 20 | 8  | US-10-831-778-987    | Sequence 987, App    | c 172 | 14.2 | 71.0 | 40 | 7  | US-10-661-099-22     | Sequence 22, Appl    |
| c 100 | 14.2 | 71.0 | 20 | 8  | US-10-838-659-55     | Sequence 55, Appl    | c 173 | 14.2 | 71.0 | 40 | 8  | US-10-661-415-21     | Sequence 21, Appl    |
| c 101 | 14.2 | 71.0 | 20 | 9  | US-10-661-402-13     | Sequence 13, Appl    | c 174 | 14.2 | 71.0 | 40 | 8  | US-10-661-415-22     | Sequence 22, Appl    |
| c 102 | 14.2 | 71.0 | 20 | 9  | US-10-661-402-14     | Sequence 14, Appl    | c 175 | 14.2 | 71.0 | 40 | 9  | US-10-661-402-21     | Sequence 21, Appl    |
| c 103 | 14.2 | 71.0 | 20 | 9  | US-10-661-403-13     | Sequence 13, Appl    | c 176 | 14.2 | 71.0 | 40 | 9  | US-10-661-402-22     | Sequence 22, Appl    |
| c 104 | 14.2 | 71.0 | 20 | 9  | US-10-661-403-14     | Sequence 14, Appl    | c 177 | 14.2 | 71.0 | 40 | 9  | US-10-661-403-21     | Sequence 21, Appl    |
| c 105 | 14.2 | 71.0 | 20 | 9  | US-10-969-812A-12    | Sequence 12, Appl    | c 178 | 14.2 | 71.0 | 40 | 9  | US-10-661-403-22     | Sequence 22, Appl    |
| c 106 | 14.2 | 71.0 | 20 | 9  | US-10-969-812A-13    | Sequence 13, Appl    | c 179 | 14.2 | 71.0 | 40 | 9  | US-10-969-812A-20    | Sequence 20, Appl    |
| c 107 | 14.2 | 71.0 | 20 | 9  | US-10-969-812A-21    | Sequence 21, Appl    | c 180 | 14.2 | 71.0 | 40 | 9  | US-10-969-812A-21    | Sequence 21, Appl    |
| c 108 | 14.2 | 71.0 | 20 | 10 | US-11-056-463-134    | Sequence 134, App    | c 181 | 14.2 | 71.0 | 40 | 9  | US-09-896-650A-1     | Sequence 1, Appl     |
| c 109 | 14.2 | 71.0 | 22 | 9  | US-10-487-869-12     | Sequence 12, Appl    | c 182 | 14.2 | 71.0 | 50 | 3  | US-09-896-650A-29    | Sequence 29, Appl    |
| c 110 | 14.2 | 71.0 | 24 | 3  | US-09-766-378A-31    | Sequence 31, Appl    | c 183 | 14.2 | 71.0 | 50 | 3  | US-09-993-346-522    | Sequence 522, App    |
| c 111 | 14.2 | 71.0 | 24 | 3  | US-09-888-326-170    | Sequence 170, Appl   | c 184 | 14.2 | 71.0 | 50 | 6  | US-10-131-827-2115   | Sequence 2115, App   |
| c 112 | 14.2 | 71.0 | 24 | 3  | US-09-776-479-428    | Sequence 428, App    | c 185 | 14.2 | 71.0 | 50 | 6  | US-10-131-827-4165   | Sequence 4165, App   |
| c 113 | 14.2 | 71.0 | 24 | 3  | US-09-776-479-963    | Sequence 963, App    | c 186 | 14   | 70.0 | 14 | 3  | US-08-263-359-632    | Sequence 632, App    |
| c 114 | 14.2 | 71.0 | 24 | 3  | US-09-776-479-963    | Sequence 428, App    | c 187 | 14   | 70.0 | 14 | 3  | US-10-131-827-4819   | Sequence 4819, App   |
| c 115 | 14.2 | 71.0 | 24 | 3  | US-09-776-479-963    | Sequence 963, App    | c 188 | 14   | 70.0 | 50 | 6  | US-10-131-827-4820   | Sequence 4820, App   |
| c 116 | 14.2 | 71.0 | 24 | 5  | US-10-112-653-410    | Sequence 410, App    | c 189 | 13.8 | 69.0 | 19 | 9  | US-10-923-115-73     | Sequence 73, Appl    |
| c 117 | 14.2 | 71.0 | 24 | 5  | US-10-112-653-921    | Sequence 921, App    | c 190 | 13.8 | 69.0 | 19 | 9  | US-10-923-115-189    | Sequence 189, App    |
| c 118 | 14.2 | 71.0 | 24 | 5  | US-10-017-995-428    | Sequence 428, App    | c 191 | 13.8 | 69.0 | 25 | 8  | US-10-719-900-630483 | Sequence 630483, App |
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| c 120 | 14.2 | 71.0 | 24 | 6  | US-10-314-578-428    | Sequence 428, App    | c 193 | 13.8 | 69.0 | 25 | 10 | US-11-060-756-254379 | Sequence 254379, App |
| c 121 | 14.2 | 71.0 | 24 | 6  | US-10-314-578-963    | Sequence 963, App    | c 194 | 13.8 | 69.0 | 29 | 3  | US-09-847-232-13     | Sequence 13, Appl    |
| c 122 | 14.2 | 71.0 | 24 | 7  | US-10-374-307-14     | Sequence 14, Appl    | c 195 | 13.8 | 69.0 | 29 | 3  | US-10-623-810A-69    | Sequence 69, Appl    |
| c 123 | 14.2 | 71.0 | 24 | 7  | US-10-374-307-15     | Sequence 15, Appl    | c 196 | 13.8 | 69.0 | 29 | 10 | US-11-083-617-13     | Sequence 13, Appl    |
| c 124 | 14.2 | 71.0 | 24 | 8  | US-10-831-778-428    | Sequence 428, App    | c 197 | 13.8 | 69.0 | 30 | 7  | US-10-676-248B-204   | Sequence 204, App    |
| c 125 | 14.2 | 71.0 | 24 | 8  | US-10-831-778-963    | Sequence 963, App    | c 198 | 13.8 | 69.0 | 36 | 8  | US-10-466-894-1864   | Sequence 1864, App   |
| c 126 | 14.2 | 71.0 | 25 | 3  | US-09-828-034-13     | Sequence 13, Appl    | c 199 | 13.8 | 69.0 | 36 | 8  | US-10-035-833A-6319  | Sequence 6319, App   |
| c 127 | 14.2 | 71.0 | 25 | 3  | US-09-896-650A-26    | Sequence 26, Appl    | c 200 | 13.8 | 69.0 | 41 | 7  | US-10-035-833A-145   | Sequence 145, App    |
| c 128 | 14.2 | 71.0 | 25 | 8  | US-10-719-900-145261 | Sequence 145261, App | c 201 | 13.8 | 69.0 | 41 | 7  | US-10-035-833A-658   | Sequence 658, App    |
| c 129 | 14.2 | 71.0 | 25 | 9  | US-10-956-157-133269 | Sequence 133269, App | c 202 | 13.8 | 69.0 | 41 | 7  | US-10-035-833A-1954  | Sequence 1954, App   |
| c 130 | 14.2 | 71.0 | 25 | 9  | US-10-956-157-261874 | Sequence 261874, App | c 203 | 13.8 | 69.0 | 41 | 7  | US-10-035-833A-4549  | Sequence 4549, App   |
| c 131 | 14.2 | 71.0 | 25 | 10 | US-11-060-756-168206 | Sequence 168206, App | c 204 | 13.8 | 69.0 | 41 | 7  | US-10-035-833A-5484  | Sequence 5484, App   |
| c 132 | 14.2 | 71.0 | 25 | 10 | US-11-060-756-168207 | Sequence 168207, App | c 205 | 13.8 | 69.0 | 47 | 6  | US-10-170-097-679    | Sequence 679, App    |
| c 133 | 14.2 | 71.0 | 25 | 10 | US-11-060-756-249632 | Sequence 249632, App | c 206 | 13.8 | 69.0 | 47 | 6  | US-10-349-143-285    | Sequence 285, App    |
| c 134 | 14.2 | 71.0 | 25 | 10 | US-11-060-756-279354 | Sequence 279354, App | c 207 | 13.8 | 69.0 | 47 | 6  | US-10-349-143-3218   | Sequence 3218, App   |
| c 135 | 14.2 | 71.0 | 26 | 5  | US-10-117-108A-11    | Sequence 11, Appl    | c 208 | 13.8 | 69.0 | 47 | 6  | US-10-926-684-679    | Sequence 679, App    |
| c 136 | 14.2 | 71.0 | 26 | 5  | US-10-010-476-40     | Sequence 40, Appl    | c 209 | 13.8 | 69.0 | 50 | 6  | US-10-131-827-5327   | Sequence 5327, App   |
| c 137 | 14.2 | 71.0 | 27 | 9  | US-10-931-077-27     | Sequence 27, Appl    | c 210 | 13.6 | 68.0 | 21 | 9  | US-10-708-204-3690   | Sequence 3690, App   |
| c 138 | 14.2 | 71.0 | 28 | 3  | US-09-888-326-171    | Sequence 171, App    | c 211 | 13.6 | 68.0 | 24 | 3  | US-08-894-799-21     | Sequence 21, Appl    |
| c 139 | 14.2 | 71.0 | 28 | 3  | US-09-776-479-770    | Sequence 770, App    | c 212 | 13.6 | 68.0 | 24 | 7  | US-10-648-984-21     | Sequence 21, Appl    |
| c 140 | 14.2 | 71.0 | 28 | 3  | US-09-776-479-770    | Sequence 770, App    | c 213 | 13.6 | 68.0 | 25 | 3  | US-09-863-049A-67    | Sequence 67, Appl    |
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| c 144 | 14.2 | 71.0 | 28 | 6  | US-10-314-578-770    | Sequence 770, App    | c 217 | 13.6 | 68.0 | 25 | 10 | US-11-060-756-217870 | Sequence 217870, App |
| c 145 | 14.2 | 71.0 | 29 | 5  | US-10-831-778-770    | Sequence 770, App    | c 218 | 13.6 | 68.0 | 25 | 10 | US-11-060-756-217871 | Sequence 217871, App |
| c 146 | 14.2 | 71.0 | 30 | 6  | US-10-314-578-1096   | Sequence 1096, App   | c 219 | 13.6 | 68.0 | 26 | 5  | US-10-010-476-84     | Sequence 84, Appl    |
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| c 148 | 14.2 | 71.0 | 32 | 9  | US-10-688-745-55     | Sequence 55, Appl    | c 221 | 13.6 | 68.0 | 28 | 7  | US-10-660-897-4      | Sequence 4, Appl     |
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| c 150 | 14.2 | 71.0 | 32 | 9  | US-10-849-431-5      | Sequence 5, Appl     | c 223 | 13.6 | 68.0 | 28 | 9  | US-10-903-975-4      | Sequence 4, Appl     |
| c 151 | 14.2 | 71.0 | 35 | 3  | US-09-888-326-172    | Sequence 172, App    | c 224 | 13.6 | 68.0 | 30 | 3  | US-09-978-333B-7     | Sequence 7, Appl     |
| c 152 | 14.2 | 71.0 | 35 | 3  | US-09-776-479-771    | Sequence 771, App    | c 225 | 13.6 | 68.0 | 32 | 9  | US-10-495-629A-5     | Sequence 5, Appl     |
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| c 154 | 14.2 | 71.0 | 35 | 5  | US-10-027-632-53376  | Sequence 53376, A    | c 227 | 13.6 | 68.0 | 47 | 7  | US-10-035-833A-2350  | Sequence 2350, App   |
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| c 156 | 14.2 | 71.0 | 35 | 5  | US-10-017-995-771    | Sequence 771, App    | c 229 | 13.6 | 68.0 | 50 | 6  | US-10-131-827-3003   | Sequence 3003, App   |
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| c 166 | 14.2 | 71.0 | 40 | 7  | US-10-661-088-22     | Sequence 22, Appl    | c 239 | 13.4 | 67.0 | 41 | 7  | US-10-035-833A-2047  | Sequence 2047, App   |
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| c 168 | 14.2 | 71.0 | 40 | 7  | US-10-661-088-22     | Sequence 22, Appl    | c 241 | 13.4 | 67.0 | 41 | 7  | US-10-035-833A-5344  | Sequence 5344, App   |
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## ALIGNMENTS

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; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; Treatment of Asthma and Allergy
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; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
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; PRIOR FILING DATE: 2000-02-03
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; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
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; OTHER INFORMATION: Synthetic Sequence
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; Publication No. US20030050268A1
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; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060 (AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
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; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
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; PRIOR FILING DATE: 2000-12-14
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; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
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; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fournon, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
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US-10-831-778-906

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; CURRENT APPLICATION NUMBER: US/10/010,920
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer ON-TATaDel
US-10-010-920-43

Query Match      87.0%; Score 17.4; DB 5; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



```
US-08-781-986A-2153/c
; Sequence 2153, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781.986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: P8248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-2153
Query Match 82.0%; Score 16.4; DB 2; Length 50;
Best Local Similarity 89.5%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
| | | | | | | | | |
Db 28 GGGGGGGGGGGAGGGG 10

RESULT 13
US-10-329-624-2153/c
; Sequence 2153, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
```

```
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329.624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956.171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: P8248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2153:
US-10-329-624-2153
Query Match 82.0%; Score 16.4; DB 7; Length 50;
Best Local Similarity 89.5%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
| | | | | | | | | |
Db 28 GGGGGGGGGGGAGGGG 10

RESULT 14
US-09-263-959-923
; Sequence 923, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 923:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
```



```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-923

Query Match      79.0%; Score 15.8; DB 3; Length 19;
Best Local Similarity 89.5%; Pred. No. 9.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  1 GGGGCGGGAGGGCGGGG 19

RESULT 15
US-10-010-476-38
; Sequence 38, Application US/10010476
; Publication No. US20030114402A1
; GENERAL INFORMATION:
; APPLICANT: Reich, No. US20030114402Albert O.
; APPLICANT: Flynn, James
; TITLE OF INVENTION: MODULATORS OF DNA CYTOSINE-5
; METHYLTRANSFERASE AND METHODS FOR USE THEREOF
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,476
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/485,071
; FILING DATE: 12-Jun-1998
; APPLICATION NUMBER: 60/057,411
; FILING DATE: 29-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Canady, Karen S
; REGISTRATION NUMBER: 39,927
; REFERENCE/DOCKET NUMBER: 30794.30W001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-010-476-38

Query Match      79.0%; Score 15.8; DB 5; Length 26;
Best Local Similarity 89.5%; Pred. No. 8.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  2 GGGGTGGGAGCGGAGGGG 20

RESULT 16
US-10-407-449-41

; Sequence 41, Application US/10407449
; Publication No. US20040005601A1
; GENERAL INFORMATION:
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Hurley, Laurence
; APPLICANT: Farrell, Thomas
; APPLICANT: Grand, Cory
; APPLICANT: Bears, David
; TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLIX DNA
; FILE REFERENCE: 53223-20004.00
; CURRENT APPLICATION NUMBER: US/10/407,449
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/404,966
; PRIOR FILING DATE: 2002-08-04
; PRIOR APPLICATION NUMBER: US 60/370,358
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: Unknown
; PRIOR FILING DATE: 2003-03-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Generalized quadruplex structure for RET
US-10-407-449-41

Query Match      76.0%; Score 15.2; DB 6; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1 AGGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  1 AGGGCGGGCGGGCGGGG 20

RESULT 17
US-10-407-449-44
; Sequence 44, Application US/10407449
; Publication No. US20040005601A1
; GENERAL INFORMATION:
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Hurley, Laurence
; APPLICANT: Farrell, Thomas
; APPLICANT: Grand, Cory
; APPLICANT: Bears, David
; TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLIX DNA
; FILE REFERENCE: 53223-20004.00
; CURRENT APPLICATION NUMBER: US/10/407,449
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/404,966
; PRIOR FILING DATE: 2002-08-04
; PRIOR APPLICATION NUMBER: US 60/370,358
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: Unknown
; PRIOR FILING DATE: 2003-03-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the TMPyP4-induced photocleavage site
US-10-407-449-44

Query Match      76.0%; Score 15.2; DB 6; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1 AGGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
```

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Db 1 AGGGCGGGCGGGCGGGG 20
||||| |||| |||| |||| ||||
RESULT 18
US-10-820-487-5
; Sequence 5, Application US/10820487
; Publication No. US20050004160A1
; GENERAL INFORMATION:
; APPLICANT: WHITTEN, Jeffrey P.
; APPLICANT: SCHWABE, Michael
; APPLICANT: MORAN, Terrance
; TITLE OF INVENTION: HETEROCYCLIC SUBSTITUTED
; TITLE OF INVENTION: 1,4-DIHYDRO-4-OXO-1,8-NAPHTHYRIDINE ANALOGS
; FILE REFERENCE: 532232001200
; CURRENT APPLICATION NUMBER: US/10/820,487
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/461,205
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/519,569
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-820-487-5
Query Match 76.0%; Score 15.2; DB 8; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20
||||| |||| |||| |||| ||||
Db 1 AGGGCGGGCGGGCGGGG 20
||||| |||| |||| |||| ||||
RESULT 19
US-10-903-975-5
; Sequence 5, Application US/10903975
; Publication No. US20050085468A1
; GENERAL INFORMATION:
; APPLICANT: WHITTEN, Jeffrey P.
; APPLICANT: SCHWABE, Michael
; APPLICANT: SIDDIQUI-JAIN, Adam
; APPLICANT: MORAN, Terrance
; TITLE OF INVENTION: SUBSTITUTED QUINOBENZOXAZINE ANALOGS
; FILE REFERENCE: 532232001120
; CURRENT APPLICATION NUMBER: US/10/903,975
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 10/821,243
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/461,271
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 60/463,171
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/519,535
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US 60/532,727
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-903-975-5
Query Match 76.0%; Score 15.2; DB 9; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20
||||| |||| |||| |||| ||||
Db 1 AGGGCGGGCGGGCGGGG 20
||||| |||| |||| |||| ||||
RESULT 20
US-10-407-449-43
; Sequence 43, Application US/10407449
; Publication No. US20040005601A1
; GENERAL INFORMATION:
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Hurley, Laurence
; APPLICANT: Farrell, Thomas
; APPLICANT: Grand, Cory
; APPLICANT: Bearss, David
; TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
; FILE REFERENCE: 53223-20004.00
; CURRENT APPLICATION NUMBER: US/10/407,449
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/404,966
; PRIOR FILING DATE: 2002-08-04
; PRIOR APPLICATION NUMBER: US 60/370,358
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: Unknown
; PRIOR FILING DATE: 2003-03-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RET quadruplex-forming nucleotide sequence
US-10-407-449-43
Query Match 76.0%; Score 15.2; DB 6; Length 24;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20
||||| |||| |||| |||| ||||
Db 1 AGGGCGGGCGGGCGGGG 20
||||| |||| |||| |||| ||||
RESULT 21
US-10-931-077-28/c
; Sequence 28, Application US/10931077
; Publication No. US20050204432A1
; GENERAL INFORMATION:
; APPLICANT: Pioneer Hi-Bred International, Inc.
; APPLICANT: Multani, Dilbag
; APPLICANT: Niu, Xiaomu
; APPLICANT: Tones, Dwight T
; APPLICANT: Wang, Haiyin
; APPLICANT: Xu, Deping
; TITLE OF INVENTION: BR2 AND DW3 PROMOTERS AND METHODS OF USE
; FILE REFERENCE: 035718/281933
; CURRENT APPLICATION NUMBER: US/10/931,077
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: 60/499,580
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Zea mays
US-10-931-077-28
Query Match 76.0%; Score 15.2; DB 9; Length 27;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20
||||| |||| |||| |||| ||||
```

Db 26 AGGGAGGAGGAGGGAGGGG 7  
||||| ||||| ||||| |||||

RESULT 22  
US-10-239-176-13/c  
; Sequence 13, Application US/10239176  
; Publication No. US20040086856A1  
; GENERAL INFORMATION:  
; APPLICANT: TAKAHASHI, MASAYOSHI  
; APPLICANT: OKADA, JUN  
; APPLICANT: HASHIMOTO, KOJI  
; TITLE OF INVENTION: NUCLEIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF  
; TITLE OF INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME  
; FILE REFERENCE: 228763US0SRDPT  
; CURRENT APPLICATION NUMBER: US/10/239,176  
; CURRENT FILING DATE: 2003-03-19  
; PRIOR APPLICATION NUMBER: PCT/JPO2/08670  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: JP 2002-218644  
; PRIOR FILING DATE: 2002-07-26  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic DNA  
US-10-239-176-13

Query Match 76.0%; Score 15.2; DB 7; Length 35;  
Best Local Similarity 85.0%; Pred. No. 1.2e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGAGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 22 AGGGAGGAGGAGGGAGGGG 3

RESULT 23  
US-10-239-176-3/c  
; Sequence 3, Application US/10239176  
; Publication No. US20040086856A1  
; GENERAL INFORMATION:  
; APPLICANT: TAKAHASHI, MASAYOSHI  
; APPLICANT: OKADA, JUN  
; APPLICANT: HASHIMOTO, KOJI  
; TITLE OF INVENTION: NUCLEIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF  
; TITLE OF INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME  
; FILE REFERENCE: 228763US0SRDPT  
; CURRENT APPLICATION NUMBER: US/10/239,176  
; CURRENT FILING DATE: 2003-03-19  
; PRIOR APPLICATION NUMBER: PCT/JPO2/08670  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: JP 2002-218644  
; PRIOR FILING DATE: 2002-07-26  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic DNA  
US-10-239-176-3

Query Match 76.0%; Score 15.2; DB 7; Length 39;  
Best Local Similarity 85.0%; Pred. No. 1.2e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGAGGAGGGAGGGG 20  
||||| ||||| ||||| |||||

Db 21 AGGGAGGAGGAGGGAGGGG 2

RESULT 24  
US-10-239-176-4/c  
; Sequence 4, Application US/10239176  
; Publication No. US20040086856A1  
; GENERAL INFORMATION:  
; APPLICANT: TAKAHASHI, MASAYOSHI  
; APPLICANT: OKADA, JUN  
; APPLICANT: HASHIMOTO, KOJI  
; TITLE OF INVENTION: NUCLEIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF  
; TITLE OF INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME  
; FILE REFERENCE: 228763US0SRDPT  
; CURRENT APPLICATION NUMBER: US/10/239,176  
; CURRENT FILING DATE: 2003-03-19  
; PRIOR APPLICATION NUMBER: PCT/JPO2/08670  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: JP 2002-218644  
; PRIOR FILING DATE: 2002-07-26  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic DNA  
US-10-239-176-4

Query Match 76.0%; Score 15.2; DB 7; Length 48;  
Best Local Similarity 85.0%; Pred. No. 1.1e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGAGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 30 AGGGAGGAGGAGGGAGGGG 11

RESULT 25  
US-09-263-959-443/c  
; Sequence 443, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 443:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-263-959-443

Query Match 75.0%; Score 15; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0;

Qy 5 GAGGGGAGGGGAGGG 19  
 Db 15 GAGGGGAGGGGAGGG 1

RESULT 26

US-10-035-833A-1181  
 ; Sequence 1181, Application US/10035833A  
 ; Publication No. US20040072156A1  
 ; GENERAL INFORMATION:

APPLICANT: Nakamura, Yuho  
 APPLICANT: Sekine, Akihiro  
 APPLICANT: Iida, Aritoshi  
 APPLICANT: Saito, Osamu  
 TITLE OF INVENTION: Detection of Genetic Polymorphisms  
 FILE REFERENCE: FORS-06904  
 CURRENT APPLICATION NUMBER: US/10/035,833A  
 CURRENT FILING DATE: 2001-12-27  
 NUMBER OF SEQ ID NOS: 7669  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 1181  
 LENGTH: 41  
 TYPE: DNA  
 ORGANISM: Homo sapiens

US-10-035-833A-1181

Query Match 75.0%; Score 15; DB 7; Length 41;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0;

Qy 4 GGAGGGAGGGAGGGG 20  
 Db 10 GGAAGGAGGGAGGGG 26

RESULT 27

US-10-035-833A-5376  
 ; Sequence 5376, Application US/10035833A  
 ; Publication No. US20040072156A1  
 ; GENERAL INFORMATION:

APPLICANT: Nakamura, Yuho  
 APPLICANT: Sekine, Akihiro  
 APPLICANT: Iida, Aritoshi  
 APPLICANT: Saito, Osamu  
 TITLE OF INVENTION: Detection of Genetic Polymorphisms  
 FILE REFERENCE: FORS-06904  
 CURRENT APPLICATION NUMBER: US/10/035,833A  
 CURRENT FILING DATE: 2001-12-27  
 NUMBER OF SEQ ID NOS: 7669  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 5376  
 LENGTH: 41  
 TYPE: DNA  
 ORGANISM: Homo sapiens

US-10-035-833A-5376

Query Match 75.0%; Score 15; DB 7; Length 41;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0;

Qy 4 GGAGGGAGGGAGGGG 20  
 Db 10 GGAAGGAGGGAGGGG 26

Db 10 GGAAGGAGGGAGGGG 26

RESULT 28

US-10-010-476-55  
 ; Sequence 55, Application US/10010476  
 ; Publication No. US20030114402A1  
 ; GENERAL INFORMATION:

APPLICANT: Reich, No. US20030114402Albert O.  
 APPLICANT: Flynn, James  
 TITLE OF INVENTION: MODULATORS OF DNA CYTOSINE-5  
 METHYLTRANSFERASE AND METHODS FOR USE THEREOF  
 NUMBER OF SEQUENCES: 110  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
 STREET: 11150 Santa Monica Boulevard, Suite 400  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 90025

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/010,476  
 FILING DATE: 07-Dec-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/485,071  
 FILING DATE: 12-Jun-1998  
 APPLICATION NUMBER: 60/057,411  
 FILING DATE: 29-AUG-1997

ATTORNEY/AGENT INFORMATION:  
 NAME: Canady, Karen S  
 REGISTRATION NUMBER: 39,927  
 REFERENCE/DOCKET NUMBER: 30794.30WO01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 310 445-1140  
 TELEFAX: 310 445-9031

INFORMATION FOR SEQ ID NO: 55:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 26 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear

US-10-010-476-55

Query Match 74.0%; Score 14.8; DB 5; Length 26;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+04;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGGGGAGGGAGGGG 20  
 Db 3 GGGGGGGAGGGAGGGG 20

RESULT 29

US-10-010-476-107  
 ; Sequence 107, Application US/10010476  
 ; Publication No. US20030114402A1  
 ; GENERAL INFORMATION:

APPLICANT: Reich, No. US20030114402Albert O.  
 APPLICANT: Flynn, James  
 TITLE OF INVENTION: MODULATORS OF DNA CYTOSINE-5  
 METHYLTRANSFERASE AND METHODS FOR USE THEREOF  
 NUMBER OF SEQUENCES: 110  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
 STREET: 11150 Santa Monica Boulevard, Suite 400

```

, CITY: Los Angeles
, STATE: CA
, COUNTRY: USA
, ZIP: 90025
, COMPUTER READABLE FORM:
, MEDIUM TYPE: diskette
, COMPUTER: IBM Compatible
, OPERATING SYSTEM: DOS
, SOFTWARE: FastSEQ for Windows Version 2.0
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/10/010,476
, FILING DATE: 07-Dec-2001
, CLASSIFICATION: <unknown>
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US/09/485,071
, FILING DATE: 12-Jun-1998
, APPLICATION NUMBER: 60/057,411
, FILING DATE: 29-AUG-1997
, ATTORNEY/AGENT INFORMATION:
, NAME: Canady, Karen S
, REGISTRATION NUMBER: 39,927
, REFERENCE/DOCKET NUMBER: 30794.30W001
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 310 445-1140
, TELEFAX: 310 445-9031
, TELEX: <unknown>
, INFORMATION FOR SEQ ID NO: 107:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 26 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: double
, TOPOLOGY: linear
, SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-10-010-476-107

```

|                       |              |                    |               |            |
|-----------------------|--------------|--------------------|---------------|------------|
| Query Match           | 74.0%;       | Score 14.8;        | DB 5;         | Length 26; |
| Best Local Similarity | 88.9%;       | Pred. No. 1.9e+04; |               |            |
| Matches 16;           | Conservative | 0;                 | Mismatches 2; | Indels 0;  |
| Gaps                  | 0;           |                    |               |            |

```

RESULT 30
US-10-224-683-93
; Sequence 93, Application US/10224683
; Publication No. US20030162192A1
; GENERAL INFORMATION:
; APPLICANT: Sotos, John
; APPLICANT: Rienhoff, Jr., Hugh
; APPLICANT: Guida, Marco
; APPLICANT: Curtan, Mark
; TITLE OF INVENTION: Polymorphisms Associated with Ion-Channel Disease
; FILE REFERENCE: 4389-33
; CURRENT APPLICATION NUMBER: US/10/224,683
; CURRENT FILING DATE: 2002-01-06
; PRIOR APPLICATION NUMBER: 60/314,331
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/378,521
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-224-683-93

```

```

Qy      2  GCGGAGGGGAGGGGAGGG 19
      | | | | | | | | | |
Db      3  GAGGAGGGGAGGGGAGGG 20

RESULT 31
US-10-942-561A-93
; Sequence 93. Application US/10942561A
; Publication No. US20050089905A1
; GENERAL INFORMATION:
; APPLICANT: Sotos, John
; APPLICANT: Rienhoff, Jr., Hugh
; APPLICANT: Guida, Marco
; APPLICANT: Curran, Mark
; TITLE OF INVENTION: Polymorphisms AS
; FILE REFERENCE: DNA-33US2
; CURRENT APPLICATION NUMBER: US/10/94
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 10/224,683
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/314,331
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/378,521
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-942-561A-93

```

```

RESULT 32
US-10-035-833A-6318/c
; Sequence 6318, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7689
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6318
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: c is present or absent.
US-10-035-833A-6318

```

|    | Query Match           | 74.0%             | Score 14.8;        | DB 7;         | Length 41; |
|----|-----------------------|-------------------|--------------------|---------------|------------|
|    | Best Local Similarity | 88.9%;            | Pred. No. 1.6e+04; |               |            |
|    | Matches 16;           | Conservative      | 0;                 | Mismatches 2; | Indels 0;  |
|    | Gaps                  | 0;                |                    |               |            |
| Qy | 2                     | GGGGAGGGGAGGGAGGG | 19                 |               |            |
| Dh | 31                    | GGGGCGGGGAGGGGGGG | 14                 |               |            |



Best Local Similarity 93.8%; Pred. No. 2.3e+04; Mismatches 0; Gaps 0; Indels 1;

Qy 5 GAGGGGAGGGGAGGGG 20  
Db 23 GTGGGGAGGGGAGGGG 38

## RESULT 37

US-10-617-070-432  
; Sequence 432, Application US/10617070  
; Publication No. US20040096874A1  
; GENERAL INFORMATION:  
; APPLICANT: Neville, Matt  
; APPLICANT: de Arruda Indig, Monika  
; APPLICANT: Cao, Feng  
; APPLICANT: Oldenburg, Mary C.  
; APPLICANT: Koelbl, Jim C.  
; APPLICANT: Aizenstein, Brian D.  
; APPLICANT: Davey, Keith  
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes  
; FILE REFERENCE: FORS-08195  
; CURRENT APPLICATION NUMBER: US/10/617,070  
; CURRENT FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: 10/411,954  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/371,819  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 529  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 432  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-10-617-070-432

Query Match 72.0%; Score 14.4; DB 7; Length 39;  
Best Local Similarity 93.8%; Pred. No. 2.3e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GAGGGGAGGGGAGGGG 20  
Db 23 GTGGGGAGGGGAGGGG 38

## RESULT 38

US-10-956-507-431  
; Sequence 431, Application US/10956507  
; Publication No. US20050196771A1  
; GENERAL INFORMATION:  
; APPLICANT: Neville, Matt  
; APPLICANT: de Arruda Indig, Monika  
; APPLICANT: Cao, Feng  
; APPLICANT: Oldenburg, Mary C.  
; APPLICANT: Koelbl, Jim C.  
; APPLICANT: Aizenstein, Brian D.  
; APPLICANT: Davey, Keith  
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes  
; FILE REFERENCE: FORS-08195  
; CURRENT APPLICATION NUMBER: US/10/956,507  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: US/10/617,070  
; PRIOR FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: 10/411,954  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/371,819  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 529  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 431  
; LENGTH: 39

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-10-956-507-431

Query Match 72.0%; Score 14.4; DB 9; Length 39;  
Best Local Similarity 93.8%; Pred. No. 2.3e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GAGGGGAGGGGAGGGG 20  
Db 23 GTGGGGAGGGGAGGGG 38

## RESULT 39

US-10-956-507-432  
; Sequence 432, Application US/10956507  
; Publication No. US20050196771A1  
; GENERAL INFORMATION:  
; APPLICANT: Neville, Matt  
; APPLICANT: de Arruda Indig, Monika  
; APPLICANT: Cao, Feng  
; APPLICANT: Oldenburg, Mary C.  
; APPLICANT: Koelbl, Jim C.  
; APPLICANT: Aizenstein, Brian D.  
; APPLICANT: Davey, Keith  
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes  
; FILE REFERENCE: FORS-08195  
; CURRENT APPLICATION NUMBER: US/10/956,507  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: US/10/617,070  
; PRIOR FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: 10/411,954  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/371,819  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 529  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 432  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-10-956-507-432

Query Match 72.0%; Score 14.4; DB 9; Length 39;  
Best Local Similarity 93.8%; Pred. No. 2.3e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GAGGGGAGGGGAGGGG 20  
Db 23 GTGGGGAGGGGAGGGG 38

## RESULT 40

US-09-916-369A-2/c  
; Sequence 2, Application US/09916369A  
; Publication No. US20020058802A1  
; GENERAL INFORMATION:  
; APPLICANT: Dellinger, Douglas J  
; APPLICANT: Perboost, Michael GM  
; APPLICANT: Caruthers, Marvin H  
; APPLICANT: Betley, Jason R  
; TITLE OF INVENTION: Synthesis of Polynucleotides Using Combined Oxidation/Deprotection  
; FILE REFERENCE: 10003869-1  
; CURRENT APPLICATION NUMBER: US/09/916,369A  
; CURRENT FILING DATE: 2001-07-21  
; PRIOR APPLICATION NUMBER: US 09/627,249  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 9

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-09-916-369A-2

Query Match          71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  20 GGGGGGGGGGGGGGGGGG 20

RESULT 41
US-09-800-266A-133
; Sequence 133, Application US/09800266A
; Patent No. US20020156033A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
; TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
; FILE REFERENCE: C1037/7017 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/800,266A
; PRIOR FILING DATE: 2001-03-05
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-800-266A-133

Query Match          71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  1 GGGGGGGGGGGGGGGGGG 19

RESULT 42
US-09-895-007A-133
; Sequence 133, Application US/09895007A
; Patent No. US20020165178A1
; GENERAL INFORMATION:
; APPLICANT: Schetter, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; FILE REFERENCE: C1041/7014 (AWS)
; CURRENT APPLICATION NUMBER: US/09/895,007A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/214,369
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-895-007A-133

Query Match          71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  1 GGGGGGGGGGGGGGGGGG 19

RESULT 43
US-09-920-313-133
; Sequence 133, Application US/09920313
; Publication No. US20020198165A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; TITLE OF INVENTION: Treatment of Gastric Ulcers
; FILE REFERENCE: C1037/7019 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/920,313
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/222,248
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-920-313-133

Query Match          71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  1 GGGGGGGGGGGGGGGGGG 19

RESULT 44
US-09-888-326-168/c
; Sequence 168, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 168
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-168

```



Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy**

2 GGGAGCGGACGGCAGCGG 20

|||||

**Db**

20 GGGGGGGGGGGGGGGGGGG 2

## RESULT 45

```

US-09-888-326-169/C
; Sequence 169, Application US/09888326
; Publication NO. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 169
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-169

```

|                       |              |                    |              |            |
|-----------------------|--------------|--------------------|--------------|------------|
| Query Match           | 71.0%;       | Score 14.2;        | DB 3;        | Length 20; |
| Best Local Similarity | 84.2%;       | Pred. NO. 3.4e+04; |              |            |
| Matches 16:           | Conservative | 0;                 | Mismatches 3 | Indels     |

Qy 2 GGGAGCGGAGCGGAGGG 20  
|||||  
Dp 20 GGGGGGGGGGGGGGGGG 2

RESULT 46

```

US-09-888-326-429
; Sequence 429, Application US/09888326
; Publication NO. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 429
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-429

```

|                          |        |                    |        |            |
|--------------------------|--------|--------------------|--------|------------|
| Query Match              | 71.0%; | Score 14.2;        | DB 3;  | Length 20; |
| Best Local Similarity    | 84.2%; | Pred. No. 3.4e+04; |        |            |
| Matches 16: Conservative | 0;     | Mismatches 3       | Indels |            |

Qy 2 GGGAGGGAGGGAGGG 20  
pb 1 GGGGGGGGGGGGGGGG 19

RESULT 47

```

US-09-888-326-430
; Sequence 430, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 430
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-430

```

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels

Qy 2 GGGAGGGAGGGAGGG 20  
||| ||| ||| ||| |||  
pb 1 GGGGGGGGGGGGGGGG 19

RESULT 48

```

US-09-776-479-257/C
; Sequence 257, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 257
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-09-776-479-257

Query Match 71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%;
Pred. No. 3.4e+04;

```

|                       |        |                    |       |            |
|-----------------------|--------|--------------------|-------|------------|
| Query Match           | 71.0%; | Score 14.2;        | DB 3; | Length 20; |
| Best Local Similarity | 84.2%; | Pred. No. 3.4e+04; |       |            |

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20  
|||||  
Db 20 GGGGGGGGGGGGGGGG 2

RESULT 49  
US-09-776-479-530/c  
; Sequence 530, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 530  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-530

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20  
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Db 20 GGGGGGGGGGGGGGGG 2

RESULT 50  
US-09-776-479-531  
; Sequence 531, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 531  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-531

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20  
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Db 1 GGGGGGGGGGGGGGGG 19

Search completed: February 16, 2006, 02:34:15  
Job time : 293.248 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 02:03:53 ; Search time 186.446 Seconds  
(without alignments)  
98.157 Million cell updates/sec

Title: US-09-669-187A-906

Perfect score: 20

Sequence: 1 aggggagggaggaggagg 20

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 11812030

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA-New:\*

1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

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8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*

9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*

10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2          | 20    | 100.0       | 26     | 7  | US-10-310-914A-1295111 |
| 3          | 19    | 95.0        | 19     | 7  | US-10-310-914A-7761511 |
| 4          | 19    | 95.0        | 19     | 7  | US-10-310-914A-776152  |
| 5          | 19    | 95.0        | 20     | 7  | US-10-310-914A-739686  |
| 6          | 19    | 95.0        | 20     | 7  | US-10-310-914A-162719  |
| 7          | 19    | 95.0        | 21     | 7  | US-10-310-914A-1162726 |
| 8          | 19    | 95.0        | 21     | 7  | US-10-310-914A-1295143 |
| 9          | 19    | 95.0        | 21     | 7  | US-10-310-914A-1295144 |
| 10         | 19    | 95.0        | 23     | 7  | US-10-310-914A-1295148 |
| 11         | 19    | 95.0        | 23     | 7  | US-10-310-914A-1295149 |
| 12         | 19    | 95.0        | 26     | 7  | US-10-310-914A-739676  |
| 13         | 19    | 95.0        | 27     | 7  | US-10-310-914A-1162727 |
| 14         | 19    | 95.0        | 28     | 7  | US-10-310-914A-1162700 |
| 15         | 18.4  | 92.0        | 20     | 7  | US-10-310-914A-1155402 |
| 16         | 18.4  | 92.0        | 24     | 7  | US-10-310-914A-162906  |
| 17         | 18.4  | 92.0        | 24     | 7  | US-10-310-914A-162961  |
| 18         | 18.4  | 92.0        | 24     | 7  | US-10-310-914A-162974  |
| 19         | 18.4  | 92.0        | 28     | 7  | US-10-310-914A-282266  |
| 20         | 18    | 90.0        | 19     | 7  | US-10-310-914A-906589  |
| 21         | 18    | 90.0        | 22     | 7  | US-10-310-914A-1295146 |

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| c 95  | 16.4 | 82.0 | 19 | 7 | US-10-310-914A-1162720 | Sequence 1162720,  | 168   | 15.8 | 79.0 | 21 | 7  | US-10-310-914A-678373  | Sequence 678373,  |
| c 96  | 16.4 | 82.0 | 19 | 7 | US-10-310-914A-1162721 | Sequence 1162721,  | 169   | 15.8 | 79.0 | 21 | 7  | US-10-310-914A-845519  | Sequence 845519,  |
| c 97  | 16.4 | 82.0 | 20 | 7 | US-10-310-914A-172750  | Sequence 172750,   | 170   | 15.8 | 79.0 | 21 | 7  | US-10-310-914A-127157  | Sequence 127157,  |
| c 98  | 16.4 | 82.0 | 20 | 7 | US-10-310-914A-271793  | Sequence 271793,   | c 171 | 15.8 | 79.0 | 21 | 7  | US-10-310-914A-130734  | Sequence 130734,  |
| c 99  | 16.4 | 82.0 | 20 | 7 | US-10-310-914A-282308  | Sequence 282308,   | 172   | 15.8 | 79.0 | 22 | 7  | US-10-310-914A-130734  | Sequence 130734,  |
| c 100 | 16.4 | 82.0 | 20 | 7 | US-10-310-914A-628863  | Sequence 628863,   | 173   | 15.8 | 79.0 | 22 | 7  | US-10-310-914A-130795  | Sequence 130795,  |
| c 101 | 16.4 | 82.0 | 20 | 7 | US-10-310-914A-628863  | Sequence 628863,   | 174   | 15.8 | 79.0 | 22 | 7  | US-10-310-914A-369359  | Sequence 369359,  |
| c 102 | 16.4 | 82.0 | 20 | 7 | US-10-310-914A-1240445 | Sequence 1240445,  | 175   | 15.8 | 79.0 | 22 | 7  | US-10-310-914A-369359  | Sequence 369359,  |
| c 103 | 16.4 | 82.0 | 21 | 7 | US-10-310-914A-100306  | Sequence 100306,   | 176   | 15.8 | 79.0 | 22 | 7  | US-10-310-914A-390269  | Sequence 390269,  |
| c 104 | 16.4 | 82.0 | 21 | 7 | US-10-310-914A-496762  | Sequence 496762,   | 177   | 15.8 | 79.0 | 22 | 7  | US-10-310-914A-391201  | Sequence 391201,  |
| c 105 | 16.4 | 82.0 | 21 | 7 | US-10-310-914A-560700  | Sequence 560700,   | 178   | 15.8 | 79.0 | 22 | 7  | US-10-310-914A-955344  | Sequence 955344,  |
| c 106 | 16.4 | 82.0 | 21 | 7 | US-10-310-914A-732268  | Sequence 732268,   | c 177 | 15.8 | 79.0 | 22 | 7  | US-10-310-914A-1185318 | Sequence 1185318, |
| c 107 | 16.4 | 82.0 | 21 | 7 | US-10-310-914A-758538  | Sequence 758538,   | 179   | 15.8 | 79.0 | 23 | 7  | US-10-310-914A-130713  | Sequence 130713,  |
| c 108 | 16.4 | 82.0 | 21 | 7 | US-10-310-914A-1240416 | Sequence 1240416,  | 180   | 15.8 | 79.0 | 23 | 7  | US-10-310-914A-327849  | Sequence 327849,  |
| c 109 | 16.4 | 82.0 | 21 | 7 | US-10-310-914A-1283269 | Sequence 1283269,  | 181   | 15.8 | 79.0 | 23 | 7  | US-10-310-914A-390256  | Sequence 390256,  |
| c 110 | 16.4 | 82.0 | 21 | 7 | US-10-310-914A-1302766 | Sequence 1302766,  | 182   | 15.8 | 79.0 | 23 | 7  | US-10-310-914A-391202  | Sequence 391202,  |
| c 111 | 16.4 | 82.0 | 22 | 7 | US-10-310-914A-810508  | Sequence 810508,   | c 183 | 15.8 | 79.0 | 23 | 7  | US-10-310-914A-424313  | Sequence 424313,  |
| c 112 | 16.4 | 82.0 | 22 | 7 | US-10-310-914A-898815  | Sequence 898815,   | 184   | 15.8 | 79.0 | 23 | 7  | US-10-310-914A-659288  | Sequence 659288,  |
| c 113 | 16.4 | 82.0 | 22 | 7 | US-10-310-914A-988521  | Sequence 988521,   | 185   | 15.8 | 79.0 | 23 | 7  | US-10-310-914A-702282  | Sequence 702282,  |
| c 114 | 16.4 | 82.0 | 22 | 7 | US-10-310-914A-1240527 | Sequence 1240527,  | 186   | 15.8 | 79.0 | 23 | 7  | US-10-310-914A-728892  | Sequence 728892,  |
| c 115 | 16.4 | 82.0 | 23 | 7 | US-10-310-914A-59881   | Sequence 59881, A  | c 187 | 15.8 | 79.0 | 23 | 7  | US-10-310-914A-1066133 | Sequence 1066133, |
| c 116 | 16.4 | 82.0 | 23 | 7 | US-10-310-914A-433723  | Sequence 433723,   | 188   | 15.8 | 79.0 | 24 | 7  | US-10-310-914A-271796  | Sequence 271796,  |
| c 117 | 16.4 | 82.0 | 24 | 7 | US-10-310-914A-595326  | Sequence 595326,   | 189   | 15.8 | 79.0 | 24 | 7  | US-10-310-914A-281031  | Sequence 281031,  |
| c 118 | 16.4 | 82.0 | 24 | 7 | US-10-310-914A-598776  | Sequence 598776, A | 190   | 15.8 | 79.0 | 24 | 7  | US-10-310-914A-281091  | Sequence 281091,  |
| c 119 | 16.4 | 82.0 | 24 | 7 | US-10-310-914A-590304  | Sequence 590304,   | c 191 | 15.8 | 79.0 | 24 | 7  | US-10-310-914A-879624  | Sequence 879624,  |
| c 120 | 16.4 | 82.0 | 24 | 7 | US-10-310-914A-689570  | Sequence 689570,   | 192   | 15.8 | 79.0 | 25 | 7  | US-10-310-914A-121551  | Sequence 121551,  |
| c 121 | 16.4 | 82.0 | 25 | 7 | US-10-310-914A-732087  | Sequence 732087,   | 193   | 15.8 | 79.0 | 25 | 7  | US-10-310-914A-298907  | Sequence 298907,  |
| c 122 | 16.4 | 82.0 | 25 | 7 | US-10-310-914A-659207  | Sequence 659207,   | 194   | 15.8 | 79.0 | 25 | 11 | US-10-310-914A-298907  | Sequence 298907,  |
| c 123 | 16.4 | 82.0 | 25 | 7 | US-10-310-914A-826277  | Sequence 826277,   | 195   | 15.8 | 79.0 | 25 | 11 | US-11-121-849-23512    | Sequence 23512, A |
| c 124 | 16.4 | 82.0 | 25 | 7 | US-10-310-914A-912851  | Sequence 912851,   | 196   | 15.8 | 79.0 | 26 | 7  | US-10-310-914A-38847   | Sequence 38847, A |
| c 125 | 16.4 | 82.0 | 25 | 7 | US-10-310-914A-271802  | Sequence 271802,   | 197   | 15.8 | 79.0 | 26 | 7  | US-10-310-914A-137621  | Sequence 137621,  |
| c 126 | 16.4 | 82.0 | 26 | 7 | US-10-310-914A-433727  | Sequence 433727,   | c 198 | 15.8 | 79.0 | 26 | 7  | US-10-310-914A-137639  | Sequence 137639,  |
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| c 128 | 16.4 | 82.0 | 27 | 7 | US-10-310-914A-612117  | Sequence 612117,   | c 200 | 15.8 | 79.0 | 27 | 7  | US-10-310-914A-678220  | Sequence 678220,  |
| c 129 | 16.4 | 82.0 | 18 | 7 | US-10-310-914A-612117  | Sequence 612117,   | c 201 | 15.8 | 79.0 | 27 | 11 | US-10-310-914A-840062  | Sequence 840062,  |
| c 130 | 16.4 | 82.0 | 19 | 7 | US-10-310-914A-1047392 | Sequence 1047392,  | c 202 | 15.8 | 79.0 | 27 | 11 | US-11-177-000-20       | Sequence 20, Appl |
| c 131 | 16.4 | 82.0 | 19 | 7 | US-10-310-914A-271757  | Sequence 271757,   | c 203 | 15.8 | 79.0 | 27 | 11 | US-11-177-000-21       | Sequence 21, Appl |
| c 132 | 16.4 | 82.0 | 19 | 7 | US-10-310-914A-1047384 | Sequence 1047384,  | c 204 | 15.4 | 77.0 | 18 | 7  | US-10-310-914A-282309  | Sequence 282309,  |
| c 133 | 16.4 | 82.0 | 19 | 7 | US-10-310-914A-1047387 | Sequence 1047387,  | c 205 | 15.4 | 77.0 | 18 | 7  | US-10-310-914A-496354  | Sequence 496354,  |
| c 134 | 16.4 | 82.0 | 20 | 7 | US-10-310-914A-612127  | Sequence 612127,   | c 206 | 15.4 | 77.0 | 18 | 7  | US-10-310-914A-496354  | Sequence 496354,  |
| c 135 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-612134  | Sequence 612134,   | c 207 | 15.4 | 77.0 | 18 | 7  | US-10-310-914A-551203  | Sequence 551203,  |
| c 136 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-162959  | Sequence 162959,   | c 208 | 15.4 | 77.0 | 18 | 7  | US-10-310-914A-758543  | Sequence 758543,  |
| c 137 | 15.8 | 79.0 | 19 | 7 | US-10-310-914A-325657  | Sequence 325657,   | c 209 | 15.4 | 77.0 | 19 | 7  | US-10-310-914A-959337  | Sequence 959337,  |
| c 138 | 15.8 | 79.0 | 19 | 7 | US-10-310-914A-673482  | Sequence 673482,   | c 210 | 15.4 | 77.0 | 19 | 7  | US-10-310-914A-227821  | Sequence 227821,  |
| c 139 | 15.8 | 79.0 | 19 | 7 | US-10-310-914A-689749  | Sequence 689749,   | c 211 | 15.4 | 77.0 | 19 | 7  | US-10-310-914A-229386  | Sequence 229386,  |
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| c 142 | 15.8 | 79.0 | 19 | 7 | US-10-310-914A-1302929 | Sequence 1302929,  | c 214 | 15.4 | 77.0 | 19 | 7  | US-10-310-914A-278047  | Sequence 278047,  |
| c 143 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-90712   | Sequence 90712, A  | c 215 | 15.4 | 77.0 | 19 | 7  | US-10-310-914A-298911  | Sequence 298911,  |
| c 144 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-130775  | Sequence 130775,   | c 216 | 15.4 | 77.0 | 19 | 7  | US-10-310-914A-443852  | Sequence 443852,  |
| c 145 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-137638  | Sequence 137638,   | c 217 | 15.4 | 77.0 | 19 | 7  | US-10-310-914A-490785  | Sequence 490785,  |
| c 146 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-148912  | Sequence 148912,   | c 218 | 15.4 | 77.0 | 19 | 7  | US-10-310-914A-732307  | Sequence 732307,  |
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| c 148 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-168717  | Sequence 168717,   | c 220 | 15.4 | 77.0 | 19 | 7  | US-10-310-914A-1289847 | Sequence 1289847, |
| c 149 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-287572  | Sequence 287572,   | c 221 | 15.4 | 77.0 | 19 | 7  | US-10-310-914A-1305555 | Sequence 1305555, |
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| c 151 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-761167  | Sequence 761167,   | c 223 | 15.4 | 77.0 | 20 | 7  | US-10-310-914A-391173  | Sequence 391173,  |
| c 152 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-774755  | Sequence 774755,   | c 224 | 15.4 | 77.0 | 20 | 7  | US-10-310-914A-500346  | Sequence 500346,  |
| c 153 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-845518  | Sequence 845518,   | c 225 | 15.4 | 77.0 | 20 | 7  | US-10-310-914A-560704  | Sequence 560704,  |
| c 154 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-879479  | Sequence 879479,   | c 226 | 15.4 | 77.0 | 20 | 7  | US-10-310-914A-758567  | Sequence 758567,  |
| c 155 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-939253  | Sequence 939253,   | c 227 | 15.4 | 77.0 | 20 | 7  | US-10-310-914A-1289907 | Sequence 1289907, |
| c 156 | 15.8 | 79.0 | 20 | 7 | US-10-310-914A-1037971 | Sequence 1037971,  | c 228 | 15.4 | 77.0 | 21 | 7  | US-10-310-914A-257955  | Sequence 257955,  |
| c 157 | 15.8 | 79.0 | 21 | 7 | US-10-310-914A-65142   | Sequence 65142, A  | c 229 | 15.4 | 77.0 | 21 | 7  | US-10-310-914A-282326  | Sequence 282326,  |
| c 158 | 15.8 | 79.0 | 21 | 7 | US-10-310-914A-121502  | Sequence 121502,   | c 230 | 15.4 | 77.0 | 21 | 7  | US-10-310-914A-351069  | Sequence 351069,  |
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| c 164 | 15.8 | 79.0 | 21 | 7 | US-10-310-914A-386842  | Sequence 386842,   | c 236 | 15.4 | 77.0 | 22 | 7  | US-10-310-914A-172788  | Sequence 172788,  |
| c 165 | 15.8 | 79.0 | 21 | 7 | US-10-310-914A-390315  | Sequence 390315,   | c 237 | 15.4 | 77.0 | 22 | 7  | US-10-310-914A-455481  | Sequence 455481,  |
| c 166 | 15.8 | 79.0 | 21 | 7 | US-10-310-914A-390316  | Sequence 390316,   | c 238 | 15.4 | 77.0 | 22 | 7  | US-10-310-914A-1065863 | Sequence 1065863, |
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c 255 15.4 77.0 29 7 US-10-310-914A-490746  
c 256 15.2 76.0 20 7 US-10-310-914A-253916  
c 257 15.2 76.0 20 7 US-10-310-914A-362674  
c 258 15.2 76.0 20 7 US-10-310-914A-1072829  
c 259 15.2 76.0 21 7 US-10-310-914A-121454  
c 260 15.2 76.0 21 7 US-10-310-914A-138032  
261 15.2 76.0 21 7 US-10-310-914A-220594  
262 15.2 76.0 21 7 US-10-310-914A-253917  
263 15.2 76.0 21 7 US-10-310-914A-313487  
264 15.2 76.0 21 7 US-10-310-914A-939225  
c 265 15.2 76.0 21 7 US-10-310-914A-995316  
c 266 15.2 76.0 21 7 US-10-310-914A-1185247  
c 267 15.2 76.0 21 7 US-10-310-914A-1194774  
268 15.2 76.0 22 7 US-10-310-914A-131311  
269 15.2 76.0 22 7 US-10-310-914A-348780  
270 15.2 76.0 22 7 US-10-310-914A-391284  
271 15.2 76.0 22 8 US-11-106-909-5  
272 15.2 76.0 23 7 US-10-310-914A-288141  
c 273 15.2 76.0 23 7 US-10-310-914A-367876  
c 274 15.2 76.0 23 7 US-10-310-914A-497156  
275 15.2 76.0 23 7 US-10-310-914A-678353  
276 15.2 76.0 23 7 US-10-310-914A-718705  
277 15.2 76.0 23 7 US-10-310-914A-767802  
278 15.2 76.0 23 7 US-10-310-914A-840057  
279 15.2 76.0 23 7 US-10-310-914A-993088  
280 15.2 76.0 24 7 US-10-310-914A-63005  
281 15.2 76.0 24 7 US-10-310-914A-80883  
c 282 15.2 76.0 24 7 US-10-310-914A-172569  
283 15.2 76.0 24 7 US-10-310-914A-203029  
c 284 15.2 76.0 24 7 US-10-310-914A-239883  
285 15.2 76.0 24 7 US-10-310-914A-253942  
286 15.2 76.0 24 7 US-10-310-914A-285672  
c 287 15.2 76.0 24 7 US-10-310-914A-443940  
c 288 15.2 76.0 24 7 US-10-310-914A-571568  
c 289 15.2 76.0 24 7 US-10-310-914A-710243  
290 15.2 76.0 24 7 US-10-310-914A-969660  
291 15.2 76.0 24 7 US-10-310-914A-993073  
c 292 15.2 76.0 25 7 US-10-310-914A-367906  
c 293 15.2 76.0 25 7 US-10-310-914A-367909  
294 15.2 76.0 25 7 US-10-310-914A-682082  
c 295 15.2 76.0 25 7 US-10-310-914A-840058  
c 296 15.2 76.0 25 7 US-10-310-914A-845336  
297 15.2 76.0 25 11 US-11-121-849-23511  
298 15.2 76.0 26 7 US-10-310-914A-76617  
299 15.2 76.0 26 7 US-10-310-914A-348779  
c 300 15.2 76.0 26 7 US-10-310-914A-444004

ALIGNMENTS

RESULT 1  
US-11-127-654-875  
; Sequence 875, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

; TITLE OF INVENTION: INFLAMMATORY DISEASES  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 875  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-875  
  
Query Match 100.0%; Score 20; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 AGGGAGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGGGAGGGAGGGAGGGG 20  
  
RESULT 2  
US-10-310-914A-1295111  
; Sequence 1295111, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1295111  
; LENGTH: 26  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1295111  
  
Query Match 100.0%; Score 20; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 AGGGAGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGGGAGGGAGGGAGGGG 20  
  
RESULT 3  
US-10-310-914A-776151/c  
; Sequence 776151, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 776151  
; LENGTH: 19  
; TYPE: RNA

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; ORGANISM: Human
US-10-310-914A-776151

Query Match          95.0%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGAGGGGAGGGAGGGG 20
    |||||
Db   19 GGGAGGGGAGGGAGGGG 1

RESULT 4
US-10-310-914A-776152/c
; Sequence 776152, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 776152
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-776152

Query Match          95.0%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGAGGGGAGGGAGGGG 20
    |||||
Db   19 GGGAGGGGAGGGAGGGG 1

RESULT 5
US-10-310-914A-739686
; Sequence 739686, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 739686
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-739686

Query Match          95.0%; Score 19; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGAGGGGAGGGAGGGG 20
    |||||
Db   1 GGGAGGGGAGGGAGGGG 19

RESULT 6
US-10-310-914A-1162719/c
; Sequence 1162719, Application US/10310914A
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1162719
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1162719

Query Match          95.0%; Score 19; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGAGGGGAGGGAGGGG 20
    |||||
Db   19 GGGAGGGGAGGGAGGGG 1

RESULT 7
US-10-310-914A-1162726/c
; Sequence 1162726, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1162726
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1162726

Query Match          95.0%; Score 19; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGAGGGGAGGGAGGGG 20
    |||||
Db   21 GGGAGGGGAGGGAGGGG 3

RESULT 8
US-10-310-914A-1295143
; Sequence 1295143, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1295143
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
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## US-10-310-914A-1295143

Query Match 95.0%; Score 19; DB 7; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 3 AGGGAGGGAGGGAGGG 21

## RESULT 9

US-10-310-914A-1295144  
; Sequence 1295144, Application US/10310914A  
; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1295144  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human

## US-10-310-914A-1295144

Query Match 95.0%; Score 19; DB 7; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 3 AGGGAGGGAGGGAGGG 21

## RESULT 10

US-10-310-914A-1295148  
; Sequence 1295148, Application US/10310914A  
; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1295148  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human

## US-10-310-914A-1295148

Query Match 95.0%; Score 19; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 5 AGGGAGGGAGGGAGGG 23

## RESULT 11

US-10-310-914A-1295149  
; Sequence 1295149, Application US/10310914A  
; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1295149  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human

## US-10-310-914A-1295149

Query Match 95.0%; Score 19; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 5 AGGGAGGGAGGGAGGG 23

## RESULT 12

US-10-310-914A-739676  
; Sequence 739676, Application US/10310914A  
; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 739676  
; LENGTH: 26  
; TYPE: RNA  
; ORGANISM: Human

## US-10-310-914A-739676

Query Match 95.0%; Score 19; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | | | | |  
Db 6 GGGGAGGGAGGGAGGGG 24

## RESULT 13

US-10-310-914A-1162727/c  
; Sequence 1162727, Application US/10310914A  
; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1162727  
; LENGTH: 27  
; TYPE: RNA  
; ORGANISM: Human

## US-10-310-914A-1162727

Query Match 95.0%; Score 19; DB 7; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 20  
|||||  
Db 21 GGGGAGGGAGGGAGGGG 3  
|||||

RESULT 14  
US-10-310-914A-1162700/c  
; Sequence 1162700, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1162700  
; LENGTH: 28  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1162700

Query Match 95.0%; Score 19; DB 7; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 20  
|||||  
Db 25 GGGGAGGGAGGGAGGGG 7  
|||||

RESULT 15  
US-10-310-914A-1155402  
; Sequence 1155402, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1155402  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1155402

Query Match 92.0%; Score 18.4; DB 7; Length 20;  
Best Local Similarity 95.0%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20  
|||||  
Db 1 AGGGAGGGAGGGAGGGG 20  
|||||

RESULT 16  
US-10-310-914A-162906  
; Sequence 162906, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 162906  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-162906

Query Match 92.0%; Score 18.4; DB 7; Length 24;  
Best Local Similarity 95.0%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20  
|||||  
Db 3 AGGGAGGGAGGGAGGGG 22  
|||||

RESULT 17  
US-10-310-914A-162961  
; Sequence 162961, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 162961  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-162961

Query Match 92.0%; Score 18.4; DB 7; Length 24;  
Best Local Similarity 95.0%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20  
|||||  
Db 5 AGGGAGGGAGGGAGGGG 24  
|||||

RESULT 18  
US-10-310-914A-162974  
; Sequence 162974, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 162974  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-162974



```
Query Match          92.0%; Score 18.4; DB 7; Length 24;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 5 AGGGAGGGAGGGAGGGG 24
    ||||| ||||| ||||| |||||

RESULT 19
US-10-310-914A-282266
; Sequence 282266, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 282266
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-282266

Query Match          92.0%; Score 18.4; DB 7; Length 28;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 7 AGGGAGGGAGGGAGGGG 26
    ||||| ||||| ||||| |||||

RESULT 20
US-10-310-914A-906589
; Sequence 906589, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 906589
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-906589

Query Match          90.0%; Score 18; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 19
    ||||| ||||| ||||| |||||
Db 2 GGGGAGGGAGGGAGGGG 19
    ||||| ||||| ||||| |||||

RESULT 21
US-10-310-914A-1295146
; Sequence 1295146, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
```

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; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1295146
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1295146

Query Match          90.0%; Score 18; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 19
    ||||| ||||| ||||| |||||
Db 5 GGGGAGGGAGGGAGGGG 22
    ||||| ||||| ||||| |||||

RESULT 22
US-10-310-914A-739675
; Sequence 739675, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 739675
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-739675

Query Match          90.0%; Score 18; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 19
    ||||| ||||| ||||| |||||
Db 6 GGGGAGGGAGGGAGGGG 23
    ||||| ||||| ||||| |||||

RESULT 23
US-10-310-914A-1047386
; Sequence 1047386, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1047386
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1047386

Query Match          90.0%; Score 18; DB 7; Length 23;
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; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162912
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-162912

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGAGGGAGGGAGGGG 20
    |||||
Db 2 GGGAGGGAGGGAGGGG 19

RESULT 24
US-10-310-914A-100302/c
; Sequence 100302, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 100302
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-100302

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGAGGGAGGGAGGGG 20
    |||||
Db 19 GGGGTGGGAGGGAGGGG 1

RESULT 25
US-10-310-914A-148888
; Sequence 148888, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148888
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148888

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGAGGGAGGGAGGGG 20
    |||||
Db 1 GGGGUGGGAGGGAGGGG 19

RESULT 26
US-10-310-914A-162912
; Sequence 162912, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
```

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; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162912
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-162912

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGAGGGAGGGAGGG 19
    |||||
Db 1 AGGGAGGGAGGGAGGG 19

RESULT 27
US-10-310-914A-386824
; Sequence 386824, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386824
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386824

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGAGGGAGGGAGGG 19
    |||||
Db 1 AGGGAGGGAGGGAGGG 19

RESULT 28
US-10-310-914A-386825
; Sequence 386825, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386825
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386825

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGAGGGAGGGAGGG 19
    |||||
Db 1 AGGGAGGGAGGGAGGG 19
```

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Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGG 19
|||||
Db 1 AGGGAGGGGAGGGAGGG 19

RESULT 29
US-10-310-914A-386850
; Sequence 386850, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386850
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386850

Query Match 87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGAGGGGAGGGAGGGG 20
|||||
Db 1 GGGAGGGGAGGGAGGGG 19

RESULT 30
US-10-310-914A-288225
; Sequence 288225, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 288225
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-288225

Query Match 87.0%; Score 17.4; DB 7; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGAGGGGAGGGAGGGG 20
|||||
Db 1 GGGAGGGGAGGGAGGGG 19

RESULT 31
US-10-310-914A-588532
; Sequence 588532, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
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; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 588532
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-588532

Query Match 87.0%; Score 17.4; DB 7; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGAGGGGAGGGAGGGG 20
|||||
Db 1 GGGAGGGGAGGGAGGGG 19

RESULT 32
US-10-310-914A-628864
; Sequence 628864, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 628864
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-628864

Query Match 87.0%; Score 17.4; DB 7; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGG 19
|||||
Db 2 AGGGAGGGGAGGGAGGG 20

RESULT 33
US-10-310-914A-1155411
; Sequence 1155411, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1155411
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1155411

Query Match 87.0%; Score 17.4; DB 7; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGG 19
|||||
Db 2 AGGGAGGGGAGGGAGGG 20

RESULT 34
US-10-310-914A-1155411
; Sequence 1155411, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1155411
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1155411

Query Match 87.0%; Score 17.4; DB 7; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 GGGGAGGGGAGGGAGGGG 20  
Db 1 GGGGAGUGGAGGGAGGGG 19

RESULT 34  
US-10-310-914A-100342/c  
; Sequence 100342, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 100342  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-100342

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20  
Db 20 GGGGAGGGGAGGGGAAGGG 2

RESULT 35  
US-10-310-914A-288226  
; Sequence 288226, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 288226  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-288226

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20  
Db 1 GGGGAGGGGAGGGAGCGG 19

RESULT 36  
US-10-310-914A-288227  
; Sequence 288227, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 288227  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-288227

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20  
Db 1 GGGGAGGGGAGGGAGCGG 19

RESULT 37  
US-10-310-914A-386839  
; Sequence 386839, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386839  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386839

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGAGGGG 19  
Db 2 AAGGGAGGGGAGGGAGGGG 20

RESULT 38  
US-10-310-914A-386841  
; Sequence 386841, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386841  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386841

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGAGGGGAGGGAGGG 19  
Db 3 AAGGGAGGGAGGGAGGG 21

RESULT 39  
US-10-310-914A-386851  
; Sequence 386851, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386851  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386851

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGAGGGGAGGGAGGGG 20  
Db 1 GGGAGGGGAGGGAGGGG 19

RESULT 40  
US-10-310-914A-659280  
; Sequence 659280, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 659280  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-659280

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGAGGGGAGGGAGGG 19  
Db 3 AGGGAGGGGAGGGAGGG 21

RESULT 41  
US-10-310-914A-1345469  
; Sequence 1345469, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1345469  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1345469

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGAGGGGAGGGAGGGG 20  
Db 2 GGGAGGGGAGGGAGGGG 20

RESULT 42  
US-10-310-914A-282307  
; Sequence 282307, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 282307  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-282307

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGAGGGGAGGGAGGG 19  
Db 4 AGGGAGGGGAGGGAGGG 22

RESULT 43  
US-10-310-914A-386862  
; Sequence 386862, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386862  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386862

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGAGGGGAGGGAGGG 19

Db 4 AGGGGAGGGAGGGAGGG 22  
||||| ||||| ||||| |||||

## RESULT 44

US-10-310-914A-560684  
; Sequence 560684, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 560684  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-560684

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGAGGGAGGG 19  
||||| ||||| ||||| |||||

Db 1 AGGGGUGGGAGGGAGGG 19

## RESULT 45

US-10-310-914A-628966  
; Sequence 628966, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 628966  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-628966

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGAGGGAGGG 19  
||||| ||||| ||||| |||||

Db 4 AGGGGAGGGAGGGAGGG 22

## RESULT 46

US-10-310-914A-659284  
; Sequence 659284, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 659284  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-659284

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGAGGGAGGG 19  
||||| ||||| ||||| |||||

Db 4 AGGGGAGGGAGGGAGGG 22

## RESULT 47

US-10-310-914A-1345363/c  
; Sequence 1345363, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1345363  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1345363

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||

Db 20 GGGGAGGGAGGGAGGGG 2

## RESULT 48

US-10-310-914A-1345365/c  
; Sequence 1345365, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1345365  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1345365

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||

Db 19 GGGGAGGGGACGGGGGGGG 1

## RESULT 49

US-10-310-914A-100318/c  
; Sequence 100318, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 100318  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-100318

Query Match 87.0%; Score 17.4; DB 7; Length 23;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGGGGG 20

Db 22 GGGGAGGGGAGGGGAAGGG 4

## RESULT 50

US-10-310-914A-162972  
; Sequence 162972, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 162972  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-162972

Query Match 87.0%; Score 17.4; DB 7; Length 23;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGGAGGG 19

Db 5 AGGGGAGGGGAGGGGAGGG 23

Search completed: February 16, 2006, 02:53:09  
Job time : 189.446 secs

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